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TI - Evidence-Based Malaria Control and Elimination in the Amazon:
Input from
the International Center of Excellence in Malaria Research
Network in
Peru and Brazil.
PG - 160-167
LID - 10.4269/ajtmh.21-1272 [doi]
AB - Malaria remains endemic in 17 countries in the Americas, where
723,000
cases were reported in 2019. The majority (> 90%) of the
regional malaria
burden is found within the Amazon Basin, which includes nine
countries
and territories in South America. Locally generated evidence
is critical
to provide information to public health decision makers upon
which the
design of efficient and regionally directed malaria control
and
elimination programs can be built. Plasmodium vivax is the
predominant
malaria parasite in the Amazon Basin. This parasite species
appears to be
more resilient to malaria control strategies worldwide.
Asymptomatic
Plasmodium infections constitute a potentially infectious
reservoir that
is typically missed by routine microscopy-based surveillance
and often
remains untreated. The primary Amazonian malaria vector,
Nyssorhynchus
(formerly Anopheles) darlingi, has changed its behavior to
feed and rest
predominantly outdoors, reducing the efficiency of core vector
control
measures such as indoor residual spraying and distribution of
long-
lasting insecticide-treated bed nets. We review public health
implications of recent field-based research carried out by the
Amazonia
International Center of Excellence in Malaria Research in Peru
and
Brazil. We discuss the relative role of traditional and novel
tools and

strategies for better malaria control and elimination across the Amazon, including improved diagnostic methods, new anti-relapse medicines, and biological larvicides, and emphasize the need to integrate research and public health policymaking.

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TI - Malaria Resilience in South America: Epidemiology, Vector
Biology, and
Immunology Insights from the Amazonian International Center of
Excellence
in Malaria Research Network in Peru and Brazil.
PG - 168-181
LID - 10.4269/ajtmh.22-0127 [doi]
AB - The 1990s saw the rapid reemergence of malaria in Amazonia,
where it
remains an important public health priority in South America.
The
Amazonian International Center of Excellence in Malaria
Research (ICEMR)
was designed to take a multidisciplinary approach toward
identifying
novel malaria control and elimination strategies. Based on
geographically
and epidemiologically distinct sites in the Northeastern
Peruvian and
Western Brazilian Amazon regions, synergistic projects
integrate malaria
epidemiology, vector biology, and immunology. The Amazonian
ICEMR's
overarching goal is to understand how human behavior and other
sociodemographic features of human reservoirs of transmission-
predominantly asymptotically parasitemic people-interact
with the major
Amazonian malaria vector, *Nyssorhynchus* (formerly *Anopheles*)

darlingi,
and with human immune responses to maintain malaria resilience
and
continued endemicity in a hypoendemic setting. Here, we will
review
Amazonian ICEMR's achievements on the synergies among malaria
epidemiology, Plasmodium-vector interactions, and immune
response, and
how those provide a roadmap for further research, and, most
importantly,
point toward how to achieve malaria control and elimination in
the
Americas.

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TI - Drug resistance and population structure of Plasmodium
falciparum and

Plasmodium vivax in the Peruvian Amazon.

PG - 16474

LID - 10.1038/s41598-022-21028-3 [doi]

AB - Malaria is a major health problem in Peru despite substantial
progress

achieved by the ongoing malaria elimination program. This
study explored
the population genetics of 63 Plasmodium falciparum and 170 P.
vivax

cases collected in the Peruvian Amazon Basin between 2015 and
2019.

Microscopy and PCR were used for malaria detection and
positive samples

were genotyped at neutral and drug resistance-associated
regions. The P.

falciparum population exhibited a low nucleotide diversity (π
= 0.02)

whereas the P. vivax population presented a higher genetic
diversity (π

= 0.34). All P. falciparum samples (n = 63) carried
chloroquine (CQ)

resistant mutations on Pfcrt. Most P. falciparum samples (53
out of 54)

carried sulfadoxine (SD) resistant mutations on Pfdhfr and
Pfdhps. No

evidence was found of artemisinin resistance mutations on
kelch13.

Population structure showed that a single cluster accounted
for 93.4% of

the P. falciparum samples whereas three clusters were found
for P. vivax.

Our study shows a low genetic diversity for both species with significant differences in genetic sub-structuring. The high prevalence of CQ-resistance mutations could be a result of indirect selection pressures driven by the *P. vivax* treatment scheme. These results could be useful for public health authorities to safeguard the progress that Peru has achieved towards malaria elimination.

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JID - 101563288
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TI - Epidemiological characteristics of *P. vivax* asymptomatic
infections in
the Peruvian Amazon.
PG - 901423
LID - 10.3389/fcimb.2022.901423 [doi]
AB - Introduction: Herein, we tested the hypothesis that
Asymptomatic *P. vivax*
(Pv) infected individuals (Asym) feature different
epidemiological,
clinical and biochemical characteristics, as well as
hematological
parameters, potentially predictive of clinical immunity in
comparison to
symptomatic Pv infected individuals (Sym). Methodology:
Between 2018 -
2021, we conducted 11 population screenings (PS, Day 0 (D0))
in 13
different riverine communities around Iquitos city, in the
Peruvian
Amazon, to identify Pv Sym and Asym individuals. A group of
these
individuals agreed to participate in a nested case - control
study to
evaluate biochemical and hematological parameters. Pv Asym

individuals did not present common malaria symptoms (fever, headache, and chills), had a positive/negative microscopy result, a positive qPCR result, reported no history of antimalarial treatment during the last month, and were followed-up weekly until Day 21 (D21). Control individuals, had a negative malaria microscopy and qPCR result, no history of antimalarial treatment or malaria infections during the last three years, and no history of comorbidities or chronic infections. Results: From the 2159 individuals screened during PS, data revealed a low but heterogeneous Pv prevalence across the communities (11.4%), where most infections were Asym (66.7%) and submicroscopic (82.9%). A total of 29 Asym, 49 Sym, and 30 control individuals participated in the nested case - control study (n=78). Ten of the individuals that were initially Asym at D0, experienced malaria symptoms during follow up and therefore, were included in the Sym group. 29 individuals remained Asym throughout all follow-ups. High levels of eosinophils were found in Asym individuals in comparison to Sym and controls. Conclusion: For the first-time, key epidemiological, hematological, and biochemical features are reported from Pv Asym infections from the Peruvian Amazon. These results should be considered for the design and reshaping of malaria control measures as the country moves toward malaria elimination.

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OT - P. vivax
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OT - biochemical
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S0 - Front Cell Infect Microbiol. 2022 Aug 31;12:901423. doi:

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VI - 12

DP - 2022

TI - Assessment of IgG3 as a serological exposure marker for *Plasmodium vivax*

in areas with moderate-high malaria transmission intensity.

PG - 950909

LID - 10.3389/fcimb.2022.950909 [doi]

AB - A more sensitive surveillance tool is needed to identify *Plasmodium vivax*

infections for treatment and to accelerate malaria elimination efforts.

To address this challenge, our laboratory has developed an eight-antigen

panel that detects total IgG as serological markers of *P. vivax* exposure

within the prior 9 months. The value of these markers has been established for use in areas with low transmission. In

moderate-high

transmission areas, there is evidence that total IgG is more long-lived

than in areas with low transmission, resulting in poorer performance of

these markers in these settings. Antibodies that are shorter-lived may be

better markers of recent infection for use in moderate-high transmission

areas. Using a multiplex assay, the antibody temporal kinetics of total

IgG, IgG1, IgG3, and IgM against 29 *P. vivax* antigens were

measured over
36 weeks following asymptomatic *P. vivax* infection in Papua
New Guinean
children (n = 31), from an area with moderate-high
transmission
intensity. IgG3 declined faster to background than total IgG,
IgG1, and
IgM. Based on these kinetics, IgG3 performance was then
assessed for
classifying recent exposure in a cohort of Peruvian
individuals (n = 590;
age 3–85 years) from an area of moderate transmission
intensity. Using
antibody responses against individual antigens, the highest
performance
of IgG3 in classifying recent *P. vivax* infections in the prior
9 months
was to one of the Pv-fam-a proteins assessed (PVX_125728) (AUC
= 0.764).
Surprisingly, total IgG was overall a better marker of recent
P. vivax
infection, with the highest individual classification
performance to
RBP2b1986–2653 (PVX_094255) (AUC = 0.838). To understand the
acquisition
of IgG3 in this Peruvian cohort, relevant epidemiological
factors were
explored using a regression model. IgG3 levels were positively
associated
with increasing age, living in an area with (relatively)
higher
transmission intensity, and having three or more PCR-detected
blood-stage
P. vivax infections within the prior 13 months. Overall, we
found that
IgG3 did not have high accuracy for detecting recent exposure
to *P. vivax*
in the Peruvian cohort, with our data suggesting that this is
due to the
high levels of prior exposure required to acquire high IgG3
antibody
levels.

CI – Copyright (c) 2022 Tayipto, Rosado, Gamboa, White, Kiniboro,
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Beeson, Takashima, Tsuboi, Harbers, Robinson, Mueller and
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 LA - eng
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 TA - Front Cell Infect Microbiol
 JT - Frontiers in cellular and infection microbiology
 JID - 101585359
 RN - 0 (Antibodies, Protozoan)
 RN - 0 (Biomarkers)
 RN - 0 (Immunoglobulin G)
 RN - 0 (Immunoglobulin M)
 SB - IM
 MH - Adolescent
 MH - Adult
 MH - Aged
 MH - Aged, 80 and over
 MH - Antibodies, Protozoan
 MH - Asymptomatic Infections
 MH - Biomarkers
 MH - Child
 MH - Child, Preschool
 MH - Humans
 MH - Immunoglobulin G
 MH - Immunoglobulin M

MH - *Malaria
MH - *Malaria, Falciparum
MH - *Malaria, Vivax/diagnosis
MH - Middle Aged
MH - Plasmodium falciparum
MH - Plasmodium vivax
MH - Young Adult
PMC - PMC9395743
OTO - NOTNLM
OT - IgG3
OT - Plasmodium vivax
OT - antibody
OT - malaria
OT - malaria elimination
OT - multiplex assay
OT - surveillance
COIS- RL, MW, TT, and IM are inventors on patent PCT/US17/67926 on a system,
method, apparatus, and diagnostic test for P. vivax. Author MH was
employed by CellFree Sciences Co., Ltd., Yokohama, Japan. The remaining
authors declare that the research was conducted in the absence of any
commercial or financial relationships that could be construed as a
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VI - 107
IP - 1
DP - 2022 Jul 13
TI - Insights into Plasmodium vivax Asymptomatic Malaria Infections and Direct
Skin-Feeding Assays to Assess Onward Malaria Transmission in the Amazon.

PG - 154-161

LID - 10.4269/ajtmh.21-1217 [doi]

AB - Understanding the reservoir and infectivity of Plasmodium gametocytes to

vector mosquitoes is crucial to align strategies aimed at malaria

transmission elimination. Yet, experimental information is scarce

regarding the infectivity of Plasmodium vivax for mosquitoes in diverse

epidemiological settings where the proportion of asymptotically

infected individuals varies at a microgeographic scale. We measured the

transmissibility of clinical and subclinical P. vivax malaria parasite

carriers to the major mosquito vector in the Amazon Basin, Nyssorhynchus

darlingi (formerly Anopheles). A total of 105 participants with natural

P. vivax malaria infection were recruited from a cohort study in Loreto

Department, Peruvian Amazon. Four of 18 asymptomatic individuals with P.

vivax positivity by blood smear infected colony-grown Ny. darlingi (22%),

with 2.6% (19 of 728) mosquitoes infected. In contrast, 77% (44/57) of

symptomatic participants were infectious to mosquitoes with 51% (890 of

1,753) mosquitoes infected. Infection intensity was greater in symptomatic infections (mean, 17.8 oocysts/mosquito) compared

with

asymptomatic infections (mean, 0.28 oocysts/mosquito), attributed to

parasitemia/gametocytemia level. Paired experiments (N = 27) using direct

skin-feeding assays and direct membrane mosquito-feeding assays showed

that infectivity to mosquitoes was similar for both methods. Longitudinal

studies with longer follow-up of symptomatic and asymptomatic parasite

infections are needed to determine the natural variations of disease

transmissibility.

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PT - Journal Article
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DEP - 20220613
PL - United States
TA - Am J Trop Med Hyg
JT - The American journal of tropical medicine and hygiene
JID - 0370507
SB - IM
MH - Animals
MH - *Anopheles/parasitology
MH - Asymptomatic Infections/epidemiology
MH - Cohort Studies
MH - Humans
MH - *Malaria
MH - *Malaria, Vivax/parasitology
MH - Mosquito Vectors/parasitology
MH - Plasmodium vivax
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S0 - Am J Trop Med Hyg. 2022 Jun 13;107(1):154-161. doi:
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IS - 1935-2735 (Electronic)
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VI - 16
IP - 5
DP - 2022 May
TI - Malaria transmission structure in the Peruvian Amazon through
antibody
signatures to Plasmodium vivax.
PG - e0010415
LID - 10.1371/journal.pntd.0010415 [doi]
AB - BACKGROUND: The landscape of malaria transmission in the
Peruvian Amazon
is temporally and spatially heterogeneous, presenting
different micro-

geographies with particular epidemiologies. Most cases are asymptomatic and escape routine malaria surveillance based on light microscopy (LM).

Following the implementation of control programs in this region, new approaches to stratify transmission and direct efforts at an individual and community level are needed. Antibody responses to serological exposure markers (SEM) to *Plasmodium vivax* have proven diagnostic performance to identify people exposed in the previous 9 months.

METHODOLOGY: We measured antibody responses against 8 SEM to identify recently exposed people and determine the transmission dynamics of *P. vivax* in peri-urban (Iquitos) and riverine (Mazan) communities of Loreto, communities that have seen significant recent reductions in malaria transmission. Socio-demographic, geo-reference, LM and qPCR diagnosis data were collected from two cross-sectional surveys. Spatial and multilevel analyses were implemented to describe the distribution of seropositive cases and the risk factors associated with exposure to *P. vivax*.

PRINCIPAL FINDINGS: Low local transmission was detected by qPCR in both Iquitos (5.3%) and Mazan (2.7%); however, seroprevalence indicated a higher level of (past) exposure to *P. vivax* in Mazan (56.5%) than Iquitos (38.2%). Age and being male were factors associated with high odds of being seropositive in both sites. Higher antibody levels were found in individuals >15 years old. The persistence of long-lived antibodies in these individuals could overestimate the detection of recent exposure.

Antibody levels in younger populations (<15 years old) could be a better indicator of recent exposure to *P. vivax*. **CONCLUSIONS:** The large number of current and past infections detected by SEMs allows for detailed local epidemiological analyses, in contrast to data from qPCR prevalence surveys which did not produce statistically significant associations.

Serological surveillance will be increasingly important in the Peruvian

Amazon as malaria transmission is reduced by continued control and

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LA - eng
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PT - Journal Article
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JT - PLoS neglected tropical diseases
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SB - IM
MH - Adolescent
MH - Cross-Sectional Studies
MH - Female
MH - Humans
MH - *Malaria
MH - *Malaria, Falciparum/epidemiology
MH - *Malaria, Vivax/epidemiology
MH - Male
MH - Peru/epidemiology
MH - Plasmodium falciparum
MH - Plasmodium vivax
MH - Prevalence
MH - Seroepidemiologic Studies
PMC - PMC9119515
COIS- I have read the journal's policy and the authors of this manuscript have the following competing interests: MTW and IM are inventors on patent PCT/US17/67926 on a system, method, apparatus and diagnostic test for Plasmodium vivax. No other authors declare a conflict of interest.

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S0 - PLoS Negl Trop Dis. 2022 May 9;16(5):e0010415. doi: 10.1371/journal.pntd.0010415. eCollection 2022 May.

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VI - 9

DP - 2022 May

TI - Relative contribution of low-density and asymptomatic infections to

Plasmodium vivax transmission in the Amazon: pooled analysis of individual participant data from population-based cross-sectional surveys.

LID - 100169 [pii]

LID - 10.1016/j.lana.2021.100169 [doi]

AB - Background: Low-density and asymptomatic Plasmodium vivax infections

remain largely undetected and untreated and may contribute significantly to malaria transmission in the Amazon. Methods: We analysed individual participant data from population-based surveys that measured P vivax

prevalence by microscopy and polymerase chain reaction (PCR) between 2002

and 2015 and modelled the relationship between parasite density and

infectiousness to vectors using membrane feeding assay data. We estimated

the proportion of sub-patent (i.e., missed by microscopy) and asymptomatic P vivax infections and examined how parasite density relates

to clinical manifestations and mosquito infection in Amazonian settings.

Findings: We pooled 24,986 observations from six sites in Brazil and

Peru. P vivax was detected in 6.8% and 2.1% of them by PCR and microscopy, respectively. 58.5% to 92.6% of P vivax infections were

asymptomatic and 61.2% to 96.3% were sub-patent across study sites. P

vivax density thresholds associated with clinical symptoms were one order

of magnitude higher in children than in adults. We estimate that sub-

patent parasite carriers are minimally infectious and contribute 12.7% to

24.9% of the community-wide P vivax transmission, while asymptomatic

carriers are the source of 28.2% to 79.2% of mosquito infections.

Interpretation: Asymptomatic P vivax carriers constitute a vast

infectious reservoir that, if targeted by malaria elimination strategies,

could substantially reduce malaria transmission in the Amazon. Infected

children may remain asymptomatic despite high parasite densities that elicit clinical manifestations in adults. Funding: US National Institutes of Health, Fundacao de Amparo a Pesquisa do Estado de Sao Paulo, and Belgium Development Cooperation.

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LA - eng
GR - U19 AI089681/AI/NIAID NIH HHS/United States
PT - Journal Article
DEP - 20220105
PL - England
TA - Lancet Reg Health Am
JT - Lancet regional health. Americas
JID - 9918232503006676
PMC - PMC9161731
MID - NIHMS1810344
OTO - NOTNLM
OT - Amazon
OT - Plasmodium vivax
OT - asymptomatic infections
OT - fever threshold
OT - malaria
OT - sub-patent infections
EDAT- 2022/06/07 06:00
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OWN - NLM

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IS - 1756-3305 (Electronic)

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VI - 15

IP - 1

DP - 2022 Mar 28

TI - Nyssorhynchus darlingi genome-wide studies related to
microgeographic
dispersion and blood-seeking behavior.

PG - 106

LID - 10.1186/s13071-022-05219-5 [doi]

AB - BACKGROUND: In Brazil, malaria is concentrated in the Amazon
Basin, where

more than 99% of the annual cases are reported. The main goal
of this

study was to investigate the population structure and genetic
association

of the biting behavior of Nyssorhynchus (also known as
Anopheles)

darlingi, the major malaria vector in the Amazon region of
Brazil, using

low-coverage genomic sequencing data. METHODS: Samples were
collected in

the municipality of Mancio Lima, Acre state, Brazil between
2016 and

2017. Different approaches using genotype imputation and no
gene

imputation for data treatment and low-coverage sequencing
genotyping were

performed. After the samples were genotyped, population
stratification

analysis was performed. RESULTS: Weak but statistically
significant

stratification signatures were identified between
subpopulations

separated by distances of approximately 2-3 km. Genome-wide
association

studies (GWAS) were performed to compare indoor/outdoor biting
behavior

and blood-seeking at dusk/dawn. A statistically significant
association

was observed between biting behavior and single nucleotide
polymorphism

(SNP) markers adjacent to the gene associated with cytochrome
P450 (CYP)

4H14, which is associated with insecticide resistance. A
statistically

significant association between blood-seeking periodicity and SNP markers adjacent to genes associated with the circadian cycle was also observed.

CONCLUSION: The data presented here suggest that low-coverage whole-genome sequencing with adequate processing is a powerful tool to genetically characterize vector populations at a microgeographic scale in malaria transmission areas, as well as for use in GWAS. Female mosquitoes entering houses to take a blood meal may be related to a specific CYP4H14 allele, and female timing of blood-seeking is related to circadian rhythm genes.

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GR - 2018/07406-6/FAPESP
GR - U19AI089681/ICEMR (NIH)
PT - Journal Article
DEP - 20220328
PL - England
TA - Parasit Vectors
JT - Parasites & vectors
JID - 101462774
SB - IM
MH - Animals
MH - *Anopheles/genetics
MH - Disease Vectors
MH - Female
MH - Genome-Wide Association Study
MH - *Malaria
MH - Mosquito Vectors/genetics
PMC - PMC8961893
EDAT- 2022/03/30 06:00
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s13071-022-05219-5.

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LR - 20220425
IS - 0971-7196 (Print)
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VI - 45
IP - 2
DP - 2021 Jun
TI - Assessment of Plasmodium antigens and CRP in dried blood spots
with
multiplex malaria array.
PG - 479-489
LID - 10.1007/s12639-020-01325-2 [doi]
AB - Dried blood spots (DBS) typically prepared on filter papers
are an ideal
sample type for malaria surveillance by offering easy and
cost-effective
methods in terms of sample collection, storage, and transport.
The
objective of this study was to evaluate the applicability of
DBS with a
commercial multiplex malaria assay, developed to concurrently

measure

Plasmodium antigens, histidine-rich protein 2 (HRP2), Plasmodium lactate dehydrogenase (pLDH), and a host inflammatory biomarker, C-reactive protein (CRP), in whole blood. The assay conditions were optimized for DBS, and thermal stability for measurement of Plasmodium antigens and CRP in dried blood were determined. Performance of the multiplex assay on matched DBS and whole blood pellet samples was also evaluated using the clinical samples. The results indicate the acceptable performance in multiplex antigen detection using DBS samples. At cutoff levels for DBS, with a diagnostic specificity with a lower 95% confidence bound > 92%, diagnostic sensitivities against polymerase chain reaction (PCR)-confirmed malaria for HRP2, Pf LDH, Pv LDH, and Pan LDH were 93.5%, 80.4%, 21.3%, and 55.6%, respectively. The half-life of pLDH was significantly less than that of HRP2 in thermal stability studies.

Results with DBS samples collected from Peru indicate that the uncontrolled storage conditions of DBS can result in inaccurate reporting for infection with *P. falciparum* parasites with hrp2/3 deletions. With careful consideration that minimizing the unfavorable DBS storage environment is essential for ensuring integrity of heat-labile Plasmodium antigens, DBS samples can be used as an alternative to liquid whole blood to detect *P. falciparum* with hrp2/3 deletions in malaria surveillance.

SUPPLEMENTARY INFORMATION: The online version of this article (10.1007/s12639-020-01325-2) contains supplementary material, which is available to authorized users.

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LA - eng
PT - Journal Article
DEP - 20210103
PL - India
TA - J Parasit Dis
JT - Journal of parasitic diseases : official organ of the Indian
Society for
Parasitology
JID - 9713059
PMC - PMC8254675
OTO - NOTNLM
OT - Dried blood spot
OT - HRP2
OT - Immunoassay
OT - LDH
OT - Malaria
OT - Multiplex
COIS- Conflict of interestAll authors declare that they have no
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VI - 20
IP - 1
DP - 2021 May 19
TI - Multicopy targets for Plasmodium vivax and Plasmodium
falciparum
detection by colorimetric LAMP.
PG - 225
LID - 10.1186/s12936-021-03753-8 [doi]
AB - BACKGROUND: Loop-mediated isothermal amplification (LAMP) for
malaria
diagnosis at the point of care (POC) depends on the detection
capacity of
synthesized nucleic acids and the specificity of the
amplification
target. To improve malaria diagnosis, new colorimetric LAMP
tests were
developed using multicopy targets for Plasmodium vivax and
Plasmodium
falciparum detection. METHODS: The cytochrome oxidase I (COX1)
mitochondrial gene and the non-coding sequence Pvr47 for P.
vivax, and
the sub-telomeric sequence of erythrocyte membrane protein 1
(EMP1) and
the non-coding sequence Pfr364 for P. falciparum were targeted
to design
new LAMP primers. The limit of detection (LOD) of each
colorimetric LAMP
was established and assessed with DNA extracted by mini spin
column kit
and the Boil & Spin method from 28 microscopy infections, 101
malaria
submicroscopic infections detected by real-time PCR only, and

183

negatives infections by both microscopy and PCR. RESULTS: The LODs for the colorimetric LAMPs were estimated between 2.4 to 3.7 parasites/microL of whole blood. For *P. vivax* detection, the colorimetric LAMP using the COX1 target showed a better performance than the Pvr47 target, whereas the Pfr364 target was the most specific for *P. falciparum* detection. All microscopic infections of *P. vivax* were detected by PvCOX1-LAMP using the mini spin column kit DNA extraction method and 81% (17/21) were detected using Boil & Spin sample preparation. Moreover, all microscopic infections of *P. falciparum* were detected by Pfr364-LAMP using both sample preparation methods. In total, PvCOX1-LAMP and Pfr364-LAMP detected 80.2% (81 samples) of the submicroscopic infections using the DNA extraction method by mini spin column kit, while 36.6% (37 samples) were detected using the Boil & Spin sample preparation method. CONCLUSION: The colorimetric LAMPs with multicopy targets using the COX1 target for *P. vivax* and the Pfr364 for *P. falciparum* have a high potential to improve POC malaria diagnosis detecting a greater number of submicroscopic Plasmodium infections.

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LA - eng
GR - 2D43TW007120-11A1/Translational Research Development for Endemic Infectious Diseases of Amazonia - FOGARTY
PT - Journal Article
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TA - Malar J
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RN - 0 (Protozoan Proteins)
RN - EC 1.9.3.1 (Electron Transport Complex IV)
RN - LAMP assay
SB - IM
MH - Colorimetry/*methods
MH - Electron Transport Complex IV/analysis
MH - Malaria, Falciparum/*diagnosis
MH - Malaria, Vivax/*diagnosis
MH - Molecular Diagnostic Techniques/*methods
MH - Nucleic Acid Amplification Techniques/*methods
MH - Plasmodium falciparum/enzymology/*isolation & purification
MH - Plasmodium vivax/enzymology/*isolation & purification
MH - Protozoan Proteins/analysis
PMC - PMC8135177
OTO - NOTNLM
OT - Colorimetric LAMP
OT - Cox1
OT - Malaria
OT - Molecular diagnosis
OT - PfEMP1
OT - Pfr364
OT - Pvr47
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s12936-021-03753-8.

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VI - 223
IP - 12 Suppl 2
DP - 2021 Apr 27
TI - Integrating Parasitological and Entomological Observations to
Understand
Malaria Transmission in Riverine Villages in the Peruvian
Amazon.
PG - S99-S110
LID - 10.1093/infdis/jiaa496 [doi]
AB - BACKGROUND: Remote rural riverine villages account for most of
the
reported malaria cases in the Peruvian Amazon. As transmission
decreases
due to intensive standard control efforts, malaria strategies
in these
villages will need to be more focused and adapted to local
epidemiology.
METHODS: By integrating parasitological, entomological, and
environmental
observations between January 2016 and June 2017, we provided
an in-depth
characterization of malaria transmission dynamics in 4
riverine villages
of the Mazan district, Loreto department. RESULTS: Despite
variation
across villages, malaria prevalence by polymerase chain
reaction in March
2016 was high (>25% in 3 villages), caused by Plasmodium vivax
mainly and
composed of mostly submicroscopic infections. Housing without
complete
walls was the main malaria risk factor, while households close
to forest
edges were more commonly identified as spatial clusters of
malaria

prevalence. Villages in the basin of the Mazan River had a higher density of adult *Anopheles darlingi* mosquitoes, and retained higher prevalence and incidence rates compared to villages in the basin of the Napo River despite test-and-treat interventions. CONCLUSIONS: High heterogeneity in malaria transmission was found across and within riverine villages, resulting from interactions between the microgeographic landscape driving diverse conditions for vector development, housing structure, and human behavior.

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LA - eng

GR - R01 AI110112/AI/NIAID NIH HHS/United States

GR - U19 AI089681/AI/NIAID NIH HHS/United States

GR - UL1 TR001863/TR/NCATS NIH HHS/United States

PT - Journal Article

PT - Research Support, N.I.H., Extramural

PT - Research Support, Non-U.S. Gov't

PL - United States

TA - J Infect Dis

JT - The Journal of infectious diseases

JID - 0413675

SB - IM

MH - Adult

MH - Animals

MH - Anopheles/*parasitology

MH - *Bites and Stings

MH - Humans

MH - Incidence
MH - Insect Vectors
MH - Malaria/epidemiology/*transmission
MH - Mosquito Control/*methods
MH - Mosquito Vectors/*parasitology
MH - Peru/epidemiology
MH - Plasmodium vivax/genetics/*isolation & purification
MH - Polymerase Chain Reaction
MH - Prevalence
PMC - PMC8079135
OTO - NOTNLM
OT - Amazon
OT - Peru
OT - entomological inoculation rate
OT - heterogeneity
OT - human biting rate
OT - incidence
OT - malaria
OT - prevalence
OT - transmission
EDAT- 2021/04/28 06:00
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PST - ppublish
S0 - J Infect Dis. 2021 Apr 27;223(12 Suppl 2):S99-S110. doi:
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OWN - NLM
STAT- MEDLINE
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IS - 1537-6613 (Electronic)
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VI - 223
IP - 8
DP - 2021 Apr 23
TI - Temporal and Microspatial Heterogeneity in Transmission
Dynamics of
Coendemic Plasmodium vivax and Plasmodium falciparum in Two
Rural Cohort
Populations in the Peruvian Amazon.
PG - 1466-1477
LID - 10.1093/infdis/jiaa526 [doi]
AB - BACKGROUND: Malaria is highly heterogeneous: its changing
malaria
microepidemiology needs to be addressed to support malaria
elimination
efforts at the regional level. METHODS: A 3-year, population-

based cohort study in 2 settings in the Peruvian Amazon (Lupuna, Cahuide) followed participants by passive and active case detection from January 2013 to December 2015. Incidence and prevalence rates were estimated using microscopy and polymerase chain reaction (PCR). RESULTS: Lupuna registered 1828 infections (1708 Plasmodium vivax, 120 Plasmodium falciparum; incidence was 80.7 infections/100 person-years (95% confidence interval [CI] , 77.1–84.5). Cahuide detected 1046 infections (1024 P vivax, 20 P falciparum, 2 mixed); incidence was 40.2 infections/100 person-years (95% CI, 37.9–42.7). Recurrent P vivax infections predominated onwards from 2013. According to PCR data, submicroscopic predominated over microscopic infections, especially in periods of low transmission. The integration of parasitological, entomological, and environmental observations evidenced an intense and seasonal transmission resilient to standard control measures in Lupuna and a persistent residual transmission after severe outbreaks were intensively handled in Cahuide. CONCLUSIONS: In 2 exemplars of complex local malaria transmission, standard control strategies failed to eliminate submicroscopic and hypnozoite reservoirs, enabling persistent transmission.

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PT - Research Support, N.I.H., Extramural
PL - United States
TA - J Infect Dis
JT - The Journal of infectious diseases
JID - 0413675
SB - IM
MH - Cohort Studies
MH - Humans
MH - *Malaria, Falciparum/epidemiology/transmission
MH - *Malaria, Vivax/epidemiology/transmission
MH - Peru/epidemiology
MH - Plasmodium falciparum
MH - Plasmodium vivax
MH - Prevalence
PMC - PMC8064053
OTO - NOTNLM
OT - Amazon
OT - Malaria
OT - Peru
OT - human biting rate
OT - transmission
EDAT- 2020/08/22 06:00
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OWN - NLM
STAT- MEDLINE
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IS - 1932-6203 (Electronic)
IS - 1932-6203 (Linking)
VI - 16
IP - 4
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TI - Ecology and larval population dynamics of the primary malaria

vector

Nyssorhynchus darlingi in a high transmission setting dominated by fish

farming in western Amazonian Brazil.

PG - e0246215

LID - 10.1371/journal.pone.0246215 [doi]

AB - Vale do Rio Juruá in western Acre, Brazil, is a persistent malaria

transmission hotspot partly due to fish farming development that was

encouraged to improve local standards of living. Fish ponds can be

productive breeding sites for Amazonian malaria vector species, including

Nyssorhynchus darlingi, which, combined with high human density and

mobility, add to the local malaria burden. This study reports entomological profile of immature and adult *Ny. darlingi* at

three sites

in Mancio Lima, Acre, during the rainy and dry season

(February to

September, 2017). From 63 fishponds, 10,859 larvae were collected,

including 5,512 first-instar Anophelinae larvae and 4,927 second, third

and fourth-instars, of which 8.5% ($n = 420$) were *Ny. darlingi*. This

This

species was most abundant in not-abandoned fishponds and in the presence

of emerging aquatic vegetation. Seasonal analysis of immatures in urban

landscapes found no significant difference in the numbers of *Ny.*

darlingi, corresponding to equivalent population density during the rainy

to dry transition period. However, in the rural landscape, significantly

higher numbers of *Ny. darlingi* larvae were collected in August (IRR =

5.80, $p = 0.037$) and September (IRR = 6.62, $p = 0.023$) (dry season),

compared to February (rainy season), suggesting important role of

fishponds for vector population maintenance during the seasonal

transition in this landscape type. Adult sampling detected mainly *Ny.*

darlingi (~93%), with similar outdoor feeding behavior, but different

abundance according to landscape profile: urban site 1 showed higher

peaks of human biting rate in May (46 bites/person/hour), than February

(4) and September (15), while rural site 3 shows similar HBR

during the same sampling period (22, 24 and 21, respectively). This study contributes to a better understanding of the larvae biology of the main malaria vector in the Vale do Rio Jurua region and, ultimately will support vector control efforts.

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GR - UL1 TR001863/TR/NCATS NIH HHS/United States
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DEP - 20210408
PL - United States
TA - PLoS One
JT - PloS one
JID - 101285081
SB - IM
MH - Animals
MH - Anopheles/*physiology
MH - *Aquaculture
MH - Brazil
MH - Larva/physiology

MH - *Malaria
MH - Mosquito Vectors/*physiology
MH - *Ponds
MH - Population Dynamics
MH - *Seasons
PMC - PMC8031405
COIS- The authors have declared that no competing interests exist.
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S0 - PLoS One. 2021 Apr 8;16(4):e0246215. doi: 10.1371/
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OWN - NLM
STAT- MEDLINE
DCOM- 20210526
LR - 20210915
IS - 1878-3511 (Electronic)
IS - 1201-9712 (Linking)
VI - 105
DP - 2021 Apr
TI - Towards one standard treatment for uncomplicated Plasmodium
falciparum
and Plasmodium vivax malaria: Perspectives from and for the
Peruvian
Amazon.
PG - 293-297
LID - S1201-9712(21)00128-4 [pii]
LID - 10.1016/j.ijid.2021.02.042 [doi]
AB - Malaria continues to wreak havoc in the Peruvian Amazon.
Lengthy research
efforts have brought important lessons on its particular
epidemiology:
the heterogeneous levels of transmission, the large reservoir
of both
asymptomatic and submicroscopic infections, the co-
transmission of
Plasmodium vivax and Plasmodium falciparum in the same areas,
and the
limitations of current diagnostics. Based on these features,
the national
elimination program could greatly benefit from simplified
standard
treatment, with the use of artemisinin-based combination

therapy and even shorter schemes of primaquine maintaining the total dosing. It is acknowledged that there is some uncertainty regarding the true prevalence of glucose-6-phosphate dehydrogenase deficiency (G6PD) and genetic polymorphisms related to cytochrome P-450 isozyme 2D6 functioning. Once we have a better understanding, tafenoquine, whether or not in combination with a rapid G6PD enzyme test, may become a future pathway to eliminate the otherwise hidden reservoir of the *P. vivax* hypnozoite through one standard Plasmodium treatment.

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LA - eng

PT - Journal Article

DEP - 20210215

PL - Canada

TA - Int J Infect Dis

JT - International journal of infectious diseases : IJID : official publication of the International Society for Infectious

Diseases

JID - 9610933

RN - 0 (Aminoquinolines)

RN - 0 (Artemisinins)

RN - 262P8GS9L9 (tafenoquine)

RN - 9RMU91N5K2 (artemisinin)

RN - MVR3634GX1 (Primaquine)

SB - IM

MH - Adult

MH - Aminoquinolines/therapeutic use

MH - Artemisinins/therapeutic use

MH - Female

MH - Humans

MH - Malaria, Falciparum/*drug therapy/epidemiology

MH - Malaria, Vivax/*drug therapy

MH - Peru/epidemiology

MH - Plasmodium falciparum/*physiology

MH - Plasmodium vivax/*physiology

MH - Prevalence

MH - Primaquine/administration & dosage/therapeutic use

MH - Reference Standards

OTO - NOTNLM

OT - Control

OT - Elimination

OT - Peru

OT - Plasmodium falciparum

OT - Plasmodium vivax

OT - Policy

OT - South America

OT - Treatment

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j.ijid.2021.02.042.
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LR - 20210920
IS - 2076-0817 (Print)
IS - 2076-0817 (Linking)
VI - 10
IP - 3
DP - 2021 Mar 2
TI - PvMSP8 as a Novel Plasmodium vivax Malaria Sero-Marker for the
Peruvian
Amazon.
LID - 282 [pii]
LID - 10.3390/pathogens10030282 [doi]
AB - The measurement of recent malaria exposure can support malaria
control
efforts. This study evaluated serological responses to an in-
house
Plasmodium vivax Merozoite Surface Protein 8 (PvMSP8)
expressed in a
Baculovirus system as sero-marker of recent exposure to P.
vivax (Pv) in
the Peruvian Amazon. In a first evaluation, IgGs against
PvMSP8 and
PvMSP10 proteins were measured by Luminex in a cohort of 422
Amazonian
individuals with known history of Pv exposure (monthly data of
infection
status by qPCR and/or microscopy over five months). Both
serological
responses were able to discriminate between exposed and non-
exposed
individuals in a good manner, with slightly higher performance
of anti-
PvMSP10 IgGs (area under the curve AUC = 0.78 [95% CI =
0.72-0.83]) than
anti-PvMSP8 IgGs (AUC = 0.72 [95% CI = 0.67-0.78]) (p = 0.01).
In a
second evaluation, the analysis by ELISA of 1251 plasma
samples,
collected during a population-based cross-sectional survey,
confirmed the
good performance of anti-PvMSP8 IgGs for discriminating
between

individuals with Pv infection at the time of survey and/or with antecedent of Pv in the past month (AUC = 0.79 [95% CI = 0.74–0.83]).

Anti-PvMSP8 IgG antibodies can be considered as a good biomarker of recent Pv exposure in low-moderate transmission settings of the Peruvian Amazon.

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GR - Contract 218-2015-FONDECYT/Fondo Nacional de Desarrollo
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GR - U19AI089681/NH/NIH HHS/United States
GR - D43TW007120/TW/FIC NIH HHS/United States
PT - Journal Article
DEP - 20210302
PL - Switzerland
TA - Pathogens
JT - Pathogens (Basel, Switzerland)
JID - 101596317
PMC - PMC7999794
OTO - NOTNLM
OT - ELISA
OT - Luminex
OT - P. vivax
OT - PvMSP8
OT - antibodies
OT - malaria
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VI - 20
IP - 1
DP - 2021 Feb 25
TI - Performance of a fully-automated system on a WHO malaria
microscopy
evaluation slide set.
PG - 110
LID - 10.1186/s12936-021-03631-3 [doi]
AB - BACKGROUND: Manual microscopy remains a widely-used tool for
malaria
diagnosis and clinical studies, but it has inconsistent
quality in the
field due to variability in training and field practices.
Automated
diagnostic systems based on machine learning hold promise to
improve
quality and reproducibility of field microscopy. The World
Health
Organization (WHO) has designed a 55-slide set (WHO 55) for
their
External Competence Assessment of Malaria Microscopists
(ECAMM)
programme, which can also serve as a valuable benchmark for
automated
systems. The performance of a fully-automated malaria
diagnostic system,
EasyScan G0, on a WHO 55 slide set was evaluated. METHODS: The
WHO 55
slide set is designed to evaluate microscopist competence in
three areas
of malaria diagnosis using Giemsa-stained blood films, focused
on crucial
field needs: malaria parasite detection, malaria parasite
species
identification (ID), and malaria parasite quantitation. The
EasyScan G0
is a fully-automated system that combines scanning of Giemsa-
stained
blood films with assessment algorithms to deliver malaria
diagnoses. This
system was tested on a WHO 55 slide set. RESULTS: The EasyScan
G0
achieved 94.3 % detection accuracy, 82.9 % species ID
accuracy, and 50 %
quantitation accuracy, corresponding to WHO microscopy
competence Levels
1, 2, and 1, respectively. This is, to our knowledge, the best
performance of a fully-automated system on a WHO 55 set.
CONCLUSIONS:
EasyScan G0's expert ratings in detection and quantitation on
the WHO 55

slide set point towards its potential value in drug efficacy use-cases,
as well as in some case management situations with less stringent species

ID needs. Improved runtime may enable use in general case management settings.

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 LA - eng
 PT - Journal Article
 DEP - 20210225
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 TA - Malar J
 JT - Malaria journal
 JID - 101139802
 SB - IM
 MH - Automation, Laboratory
 MH - Diagnostic Tests, Routine/instrumentation/*methods
 MH - Humans
 MH - Malaria/diagnosis
 MH - Malaria, Falciparum/*diagnosis
 MH - Microscopy/*instrumentation
 MH - Plasmodium/isolation & purification
 MH - Plasmodium falciparum/*isolation & purification
 MH - Reproducibility of Results
 MH - World Health Organization
 PMC - PMC7905596
 OTO - NOTNLM

OT - Automated diagnosis
OT - Machine learning
OT - Malaria
OT - Microscopy
OT - WHO
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TI - Heterogeneity in response to serological exposure markers of recent

Plasmodium vivax infections in contrasting epidemiological contexts.

PG - e0009165

LID - 10.1371/journal.pntd.0009165 [doi]

AB - BACKGROUND: Antibody responses as serological markers of Plasmodium vivax

infection have been shown to correlate with exposure, but little is known

about the other factors that affect antibody responses in naturally

infected people from endemic settings. To address this question, we

studied IgG responses to novel serological exposure markers (SEMs) of P.

vivax in three settings with different transmission intensity. METHODOLOGY: We validated a panel of 34 SEMs in a Peruvian

cohort with up

to three years' longitudinal follow-up using a multiplex platform and

compared results to data from cohorts in Thailand and Brazil. Linear

regression models were used to characterize the association

between

antibody responses and age, the number of detected blood-stage infections

during follow-up, and time since previous infection. Receiver Operating

Characteristic (ROC) analysis was used to test the performance of SEMs to

identify *P. vivax* infections in the previous 9 months.

PRINCIPAL

FINDINGS: Antibody titers were associated with age, the number of blood-

stage infections, and time since previous *P. vivax* infection in all three

study sites. The association between antibody titers and time since

previous *P. vivax* infection was stronger in the low transmission settings

of Thailand and Brazil compared to the higher transmission setting in

Peru. Of the SEMs tested, antibody responses to RBP2b had the highest

performance for classifying recent exposure in all sites, with area under

the ROC curve (AUC) = 0.83 in Thailand, AUC = 0.79 in Brazil, and AUC =

0.68 in Peru. CONCLUSIONS: In low transmission settings, *P. vivax* SEMs

can accurately identify individuals with recent blood-stage infections.

In higher transmission settings, the accuracy of this approach diminishes

substantially. We recommend using *P. vivax* SEMs in low transmission

settings pursuing malaria elimination, but they are likely to be less

effective in high transmission settings focused on malaria control.

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GR - U19 AI089681/AI/NIAID NIH HHS/United States

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TA - PLoS Negl Trop Dis

JT - PLoS neglected tropical diseases

JID - 101291488

RN - 0 (Biomarkers)

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SB - IM

MH - Antibody Formation

MH - Biomarkers/*blood

MH - Brazil/epidemiology

MH - Cohort Studies

MH - Humans

MH - Immunoglobulin G/blood

MH - Longitudinal Studies

MH - Malaria, Vivax/blood/*diagnosis/epidemiology/immunology

MH - Peru/epidemiology

MH - Plasmodium vivax

MH - Prevalence

MH - Serologic Tests/*methods/standards

MH - Thailand/epidemiology

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COIS- I have read the journal's policy and the authors of this

manuscript have
the following competing interests: RJL, MTW, Takafumi Tsuboi
and IM are
inventors on patent PCT/US17/67926 on a system, method,
apparatus and
diagnostic test for Plasmodium vivax. No other authors declare
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TI - Malaria Situation in the Peruvian Amazon during the COVID-19
Pandemic.

PG - 1773-1776

LID - 10.4269/ajtmh.20-0889 [doi]

AB - The Peruvian Ministry of Health reports a near absence of
malaria cases

in the Amazon region during the COVID-19 pandemic. However,
the rapid
increase in SARS-CoV-2 infections has overwhelmed the Peruvian
health

system, leading to national panic and closure of public
medical

facilities, casting doubt on how accurately malaria cases'
numbers

reflect reality. In the Amazon region of Loreto, where malaria
cases are

concentrated, COVID-19 has led to near-complete closure of the
primary

healthcare system, and diagnosis and treatment of acute
febrile

illnesses, including malaria, has plummeted. Here, we describe

the

potential association of COVID-19 with a markedly reduced number of

reported malaria cases due to the reduced control activities carried out

by the Peruvian Malaria Zero Program, which could lead to malaria

resurgence and an excess of morbidity and mortality.

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TA - Am J Trop Med Hyg
JT - The American journal of tropical medicine and hygiene
JID - 0370507
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MH - Betacoronavirus
MH - COVID-19
MH - Coronavirus Infections/*epidemiology
MH - Humans
MH - Malaria/*epidemiology/prevention & control
MH - Pandemics
MH - Peru/epidemiology
MH - Pneumonia, Viral/*epidemiology
MH - SARS-CoV-2
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DCOM- 20201123
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VI - 103
IP - 4
DP - 2020 Oct
TI - Diagnosis of Plasmodium vivax by Loop-Mediated Isothermal
Amplification
in Febrile Patient Samples from Loreto, Peru.
PG - 1549-1552

LID - 10.4269/ajtmh.20-0212 [doi]

AB - Plasmodium vivax is co-endemic with Plasmodium falciparum in Peru, and

optimum management requires distinguishing these two species in the blood

of patients. For the differential identification of P. vivax and other

Plasmodium spp., the Loopamp(TM) Malaria Pan Detection Kit in combination

with the Loopamp Malaria Pv Detection Kit (Eiken Chemical Co. Ltd.,

Tokyo, Japan) was used to evaluate 559 whole blood samples collected in

2017 from febrile patients with suspected malaria attending different

health facilities in the Loreto region. The Loopamp Malaria Pan Detection

Kit showed a sensitivity of 87.7% (95% CI: 83.5-91.9) and a specificity

of 94.4% (95% CI: 91.9-96.9) and good agreement with PCR (Cohen's kappa

0.8266, 95% CI: 0.7792-0.874). By comparison, the Loopamp Malaria Pv

Detection Kit showed a similar sensitivity (84.4%, 95% CI: 79.0-89.7) and

specificity (92.4%, 95% CI: 89.7-95.0) and substantial agreement with PCR

(Cohen's kappa: 0.7661, 95% CI: 0.7088-0.8234).

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LA - eng

GR - D43 TW007120/TW/FIC NIH HHS/United States

PT - Journal Article

PT - Research Support, N.I.H., Extramural

PT - Research Support, Non-U.S. Gov't

PL - United States

TA - Am J Trop Med Hyg

JT - The American journal of tropical medicine and hygiene

JID - 0370507

SB - IM

MH - Fever

MH - Humans

MH - Malaria/*diagnosis/parasitology

MH - Malaria, Vivax/*diagnosis/parasitology

MH - Nucleic Acid Amplification Techniques

MH - Peru

MH - Plasmodium/genetics/*isolation & purification

MH - Plasmodium vivax/genetics/*isolation & purification

MH - Polymerase Chain Reaction

MH - Sensitivity and Specificity

PMC - PMC7543827

EDAT- 2020/08/05 06:00

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CRDT- 2020/08/05 06:00

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PHST- 2020/08/05 06:00 [entrez]

AID - 10.4269/ajtmh.20-0212 [doi]

PST - ppublish

S0 - Am J Trop Med Hyg. 2020 Oct;103(4):1549-1552. doi: 10.4269/ajtmh.20-0212.

PMID- 33072692

OWN - NLM

STAT- MEDLINE

DCOM- 20210514

LR - 20210514

IS - 2296-2565 (Print)

IS - 2296-2565 (Linking)

VI - 8

DP - 2020

TI - Open-Source 3D Printable GPS Tracker to Characterize the Role of Human

Population Movement on Malaria Epidemiology in River Networks:

A Proof-

of-Concept Study in the Peruvian Amazon.

PG - 526468

LID - 10.3389/fpubh.2020.526468 [doi]

AB - Human movement affects malaria epidemiology at multiple geographical

levels; however, few studies measure the role of human movement in the

Amazon Region due to the challenging conditions and cost of movement

tracking technologies. We developed an open-source low-cost 3D printable

GPS-tracker and used this technology in a cohort study to characterize

the role of human population movement in malaria epidemiology in a rural

riverine village in the Peruvian Amazon. In this pilot study

of 20 participants (mean age = 40 years old), 45,980 GPS coordinates were

recorded over 1 month. Characteristic movement patterns were observed

relative to the infection status and occupation of the participants.

Applying two analytical animal movement ecology methods, utilization

distributions (UDs) and integrated step selection functions (iSSF), we

showed contrasting environmental selection and space use patterns

according to infection status. These data suggested an important role of

human movement in the epidemiology of malaria in the Peruvian Amazon due

to high connectivity between villages of the same riverine network,

suggesting limitations of current community-based control strategies. We

additionally demonstrate the utility of this low-cost technology with

movement ecology analysis to characterize human movement in resource-poor

environments.

CI - Copyright (c) 2020 Carrasco-Escobar, Fornace, Wong, Padilla-Huamantínco,

Saldana-Lopez, Castillo-Meza, Caballero-Andrade, Manrique, Ruiz-Cabrejos,

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GR - D43 TW007120/TW/FIC NIH HHS/United States
GR - U19 AI089681/AI/NIAID NIH HHS/United States
PT - Journal Article
PT - Research Support, N.I.H., Extramural
PT - Research Support, Non-U.S. Gov't
DEP - 20200924
PL - Switzerland
TA - Front Public Health
JT - Frontiers in public health
JID - 101616579
MH - Adult
MH - Animals
MH - Cohort Studies
MH - Humans
MH - *Malaria/epidemiology
MH - Peru/epidemiology
MH - Pilot Projects
MH - *Rivers
PMC - PMC7542225
OTO - NOTNLM
OT - Amazon
OT - asymptomatic malaria
OT - connectivity
OT - human movement
OT - malaria
OT - movement ecology
OT - networks
OT - open-source
EDAT- 2020/10/20 06:00
MHDA- 2020/10/20 06:01
CRDT- 2020/10/19 05:58
PHST- 2020/01/13 00:00 [received]
PHST- 2020/08/21 00:00 [accepted]
PHST- 2020/10/19 05:58 [entrez]
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AID - 10.3389/fpubh.2020.526468 [doi]
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S0 - Front Public Health. 2020 Sep 24;8:526468. doi:
10.3389/fpubh.2020.526468. eCollection 2020.

PMID- 32189616

OWN - NLM

STAT- MEDLINE

DCOM- 20200814

LR - 20210110

IS - 1476-1645 (Electronic)

IS - 0002-9637 (Linking)

VI - 102

IP - 6

DP - 2020 Jun

TI - Multiplex Human Malaria Array: Quantifying Antigens for
Malaria Rapid
Diagnostics.

PG - 1366-1369

LID - 10.4269/ajtmh.19-0763 [doi]

AB - Malaria antigen detection through rapid diagnostic tests
(RDTs) is widely

used to diagnose malaria and estimate prevalence. To support
more

sensitive next-generation RDT development and screen
asymptomatic

malaria, we developed and evaluated the Q-Plex() Human Malaria
Array

(Quansys Biosciences, Logan, UT), which quantifies the
antigens commonly

used in RDTs-Plasmodium falciparum-specific histidine-rich
protein 2

(HRP2), P. falciparum-specific lactate dehydrogenase (Pf LDH),
Plasmodium

vivax -specific LDH (Pv LDH), and Pan malaria lactate
dehydrogenase (Pan

LDH), and human C-reactive protein (CRP), a biomarker of
severity in

malaria. At threshold levels yielding 99.5% or more diagnostic
specificity, diagnostic sensitivities against polymerase chain
reaction-

confirmed malaria for HRP2, Pf LDH, Pv LDH, and Pan LDH were
92.7%,

71.5%, 46.1%, and 83.8%, respectively. P. falciparum culture
strains and

samples from Peru indicated that HRP2 and Pf LDH combined
improves

detection of P. falciparum parasites with hrp2 and hrp3
deletions. This

array can be used for antigen-based malaria screening and
detecting

hrp2/3 deletion mutants of P. falciparum.

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LA - eng
GR - U19 AI089674/AI/NIAID NIH HHS/United States
PT - Journal Article
PL - United States
TA - Am J Trop Med Hyg
JT - The American journal of tropical medicine and hygiene
JID - 0370507
RN - 0 (Antigens, Protozoan)
RN - 0 (DNA, Protozoan)
SB - IM
MH - Antigens, Protozoan/genetics
MH - DNA, Protozoan/*genetics
MH - Diagnostic Tests, Routine
MH - Humans
MH - Malaria/*diagnosis
MH - Multiplex Polymerase Chain Reaction/*methods
MH - Plasmodium/*genetics
MH - Sensitivity and Specificity
MH - Species Specificity
PMC - PMC7253106
EDAT- 2020/03/20 06:00
MHDA- 2020/08/15 06:00
CRDT- 2020/03/20 06:00
PHST- 2020/03/20 06:00 [pubmed]
PHST- 2020/08/15 06:00 [medline]
PHST- 2020/03/20 06:00 [entrez]
AID - 10.4269/ajtmh.19-0763 [doi]
PST - ppublish
S0 - Am J Trop Med Hyg. 2020 Jun;102(6):1366-1369. doi: 10.4269/ajtmh.19-0763.

PMID- 32316981
OWN - NLM
STAT- MEDLINE
DCOM- 20201208
LR - 20201214
IS - 1475-2875 (Electronic)
IS - 1475-2875 (Linking)
VI - 19
IP - 1
DP - 2020 Apr 21
TI - Economic costs analysis of uncomplicated malaria case management in the Peruvian Amazon.
PG - 161
LID - 10.1186/s12936-020-03233-5 [doi]
AB - BACKGROUND: Case management is one of the principal strategies for malaria control. This study aimed to estimate the economic costs of uncomplicated malaria case management and explore the influence of health-seeking behaviours on those costs. METHODS: A knowledge, attitudes and practices (KAP) survey was applied to 680 households of fifteen communities in Mazan-Loreto in March 2017, then a socio-economic survey was conducted in September 2017 among 161 individuals with confirmed uncomplicated malaria in the past 3 months. Total costs per episode were estimated from both provider (Ministry of Health, MoH) and patient perspectives. Direct costs were estimated using a standard costing estimation procedure, while the indirect costs considered the loss of incomes among patients, substitute labourers and companions due to illness in terms of the monthly minimum wage. Sensitivity analysis evaluated the uncertainty of the average cost per episode. RESULTS: The KAP survey showed that most individuals (79.3%) that had malaria went to a health facility for a diagnosis and treatment, 2.7% received those services from community health workers, and 8% went to a drugstore or were self-treated at home. The average total cost per episode in the Mazan district was US\$ 161. The cost from the provider's perspective was

US\$ 30.85 per episode while from the patient's perspective the estimated cost was US\$ 131 per episode. The average costs per Plasmodium falciparum episode (US\$ 180) were higher than those per Plasmodium vivax episode (US\$ 156) due to longer time lost from work by patients with P. falciparum infections (22.2 days) than by patients with P. vivax infections (17.0 days). The delayed malaria diagnosis (after 48 h of the onset of symptoms) was associated with the time lost from work due to illness (adjusted mean ratio 1.8; 95% CI 1.3, 2.6). The average cost per malaria episode was most sensitive to the uncertainty around the lost productivity cost due to malaria. CONCLUSIONS: Despite the provision of free malaria case management by MoH, there is delay in seeking care and the costs of uncomplicated malaria are mainly borne by the families.

These costs are not well perceived by the society and the substantial financial impact of the disease can be frequently undervalued in public policy planning.

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GR - 008-2014-FONDECYT/Consejo Nacional de Ciencia, Tecnologia e
Innovacion
Tecnologica
PT - Journal Article
DEP - 20200421
PL - England
TA - Malar J
JT - Malaria journal
JID - 101139802
SB - IM
MH - Adolescent
MH - Adult
MH - Aged
MH - Aged, 80 and over
MH - Case Management/*economics
MH - Child
MH - Child, Preschool
MH - Female
MH - *Health Knowledge, Attitudes, Practice
MH - Humans
MH - Infant
MH - Malaria, Falciparum/*prevention & control
MH - Malaria, Vivax/*prevention & control
MH - Male
MH - Middle Aged
MH - Peru
MH - Young Adult
PMC - PMC7175533
OTO - NOTNLM
OT - Cost
OT - Economic
OT - Health care-seeking behaviour
OT - Malaria
OT - Management
OT - Peru
EDAT- 2020/04/23 06:00

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CRDT- 2020/04/23 06:00
PHST- 2019/11/28 00:00 [received]
PHST- 2020/04/10 00:00 [accepted]
PHST- 2020/04/23 06:00 [entrez]
PHST- 2020/04/23 06:00 [pubmed]
PHST- 2020/12/15 06:00 [medline]
AID - 10.1186/s12936-020-03233-5 [doi]
AID - 10.1186/s12936-020-03233-5 [pii]
PST - epublish
S0 - Malar J. 2020 Apr 21;19(1):161. doi: 10.1186/
s12936-020-03233-5.

PMID- 32150544
OWN - NLM
STAT- MEDLINE
DCOM- 20200512
LR - 20200512
IS - 1935-2735 (Electronic)
IS - 1935-2727 (Linking)
VI - 14
IP - 3
DP - 2020 Mar
TI - Human Plasmodium vivax diversity, population structure and
evolutionary
origin.
PG - e0008072
LID - 10.1371/journal.pntd.0008072 [doi]
AB - More than 200 million malaria clinical cases are reported each
year due
to Plasmodium vivax, the most widespread Plasmodium species in
the world.
This species has been neglected and understudied for a long
time, due to
its lower mortality in comparison with Plasmodium falciparum.
A renewed
interest has emerged in the past decade with the discovery of
antimalarial drug resistance and of severe and even fatal
human cases.
Nonetheless, today there are still significant gaps in our
understanding
of the population genetics and evolutionary history of P.
vivax,
particularly because of a lack of genetic data from Africa. To
address
these gaps, we genotyped 14 microsatellite loci in 834 samples
obtained
from 28 locations in 20 countries from around the world. We
discuss the
worldwide population genetic structure and diversity and the
evolutionary
origin of P. vivax in the world and its introduction into the
Americas.
This study demonstrates the importance of conducting genome-

wide analyses

of *P. vivax* in order to unravel its complex evolutionary history.

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LA – eng
PT – Journal Article
PT – Research Support, Non-U.S. Gov't
DEP – 20200309
PL – United States
TA – PLoS Negl Trop Dis
JT – PLoS neglected tropical diseases
JID – 101291488
SB – IM
MH – *Genetic Variation
MH – *Genotype
MH – Genotyping Techniques
MH – Global Health
MH – Humans
MH – Malaria, Vivax/*parasitology
MH – Plasmodium vivax/*classification/*genetics/isolation &
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PMC – PMC7082039
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S0 - PLoS Negl Trop Dis. 2020 Mar 9;14(3):e0008072. doi:
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STAT- MEDLINE

DCOM- 20210510

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IS - 2379-3708 (Electronic)

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VI - 5

IP - 1

DP - 2020 Jan 16

TI - Anti-MSP-10 IgG indicates recent exposure to Plasmodium vivax infection

in the Peruvian Amazon.

LID - 10.1172/jci.insight.130769 [doi]

LID - 130769 [pii]

AB - BACKGROUND Serological tools for the accurate detection of recent malaria

exposure are needed to guide and monitor malaria control efforts. IgG

responses against Plasmodium vivax and P. falciparum merozoite surface

protein-10 (MSP10) were measured as a potential way to identify recent

malaria exposure in the Peruvian Amazon. METHODS A field-based study

included 470 participants in a longitudinal cohort who completed a

comprehensive evaluation: light microscopy and PCR on enrollment, at

least 1 monthly follow-up by light microscopy, a second PCR, and serum

and dried blood spots for serological analysis at the end of the follow-

up. IgG titers against novel mammalian cell-produced recombinant PvMSP10

and PfMSP10 were determined by ELISA. RESULTS During the follow-

up period, 205 participants were infected, including 171 with P. vivax, 26 with P.

falciparum, 6 with infections by both species but at different times, and

2 with mixed infections. Exposure to P. vivax was more accurately

identified when serological responses to PvMSP10 were obtained from serum

(sensitivity, 58.1%; specificity, 81.8%; AUC: 0.76) than from dried blood

spots (sensitivity, 35.2; specificity, 83.5%; AUC: 0.64) (PAUC < 0.001).

Sensitivity was highest (serum, 82.9%; dried blood spot,

45.7%) with confirmed *P. vivax* infections occurring 7–30 days before sample collection; sensitivity decreased significantly in relation to time since last documented infection. PvMSP10 serological data did not show evidence of interspecies cross-reactivity. Anti-PfMSP10 responses poorly discriminated between *P. falciparum*-exposed and nonexposed individuals (AUC = 0.59; $P > 0.05$). CONCLUSION Anti-PvMSP10 IgG indicates recent exposure to *P. vivax* at the population level in the Amazon region. Serum, not dried blood spots, should be used for such serological tests. FUNDING Cooperative agreement U19AI089681 from the United States Public Health Service, NIH/National Institute of Allergy and Infectious Diseases, as the Amazonian International Center of Excellence in Malaria Research.

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LA - eng
GR - UL1 TR001863/TR/NCATS NIH HHS/United States
GR - U19 AI089681/AI/NIAID NIH HHS/United States
PT - Journal Article
PT - Research Support, N.I.H., Extramural
DEP - 20200116
PL - United States
TA - JCI Insight
JT - JCI insight
JID - 101676073
RN - 0 (Antigens, Protozoan)
RN - 0 (Immunoglobulin G)
RN - 0 (Protozoan Proteins)
SB - IM
MH - Adolescent
MH - Adult
MH - Antigens, Protozoan/genetics/*immunology
MH - Child
MH - Child, Preschool
MH - Cohort Studies
MH - Female
MH - Humans
MH - Immunoglobulin G/*blood
MH - Malaria, Falciparum/immunology
MH - Malaria, Vivax/diagnosis/epidemiology/*immunology
MH - Male
MH - Multivariate Analysis
MH - Peru/epidemiology
MH - Plasmodium falciparum
MH - Plasmodium vivax/*immunology

MH - Protozoan Proteins/genetics/*immunology
MH - Young Adult
PMC - PMC7030819
OTO - NOTNLM
OT - Diagnostics
OT - Epidemiology
OT - Immunology
OT - Infectious disease
OT - Malaria
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S0 - JCI Insight. 2020 Jan 16;5(1). pii: 130769. doi:
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VI - 19

IP - 1

DP - 2020 Jan 9

TI - Quantification of malaria antigens PfHRP2 and pLDH by
quantitative

suspension array technology in whole blood, dried blood spot
and plasma.

PG - 12

LID - 10.1186/s12936-019-3083-5 [doi]

AB - BACKGROUND: Malaria diagnostics by rapid diagnostic test (RDT)
relies

primarily on the qualitative detection of Plasmodium
falciparum

histidine-rich protein 2 (PfHRP2) and Plasmodium spp lactate
dehydrogenase (pLDH). As novel RDTs with increased sensitivity
are being

developed and implemented as point of care diagnostics, highly
sensitive

laboratory-based assays are needed for evaluating RDT
performance. Here,

a quantitative suspension array technology (qSAT) was
developed,

validated and applied for the simultaneous detection of PfHRP2
and pLDH

in a variety of biological samples (whole blood, plasma and dried blood spots) from individuals living in different endemic countries.

RESULTS:

The qSAT was specific for the target antigens, with analytical ranges of

6.8 to 762.8 pg/ml for PfHRP2 and 78.1 to 17076.6 pg/ml for P. falciparum

LDH (Pf-LDH). The assay detected Plasmodium vivax LDH (Pv-LDH) at a lower

sensitivity than Pf-LDH (analytical range of 1093.20 to 187288.5 pg/ml).

Both PfHRP2 and pLDH levels determined using the qSAT showed to

positively correlate with parasite densities determined by quantitative

PCR (Spearman $r = 0.59$ and 0.75 , respectively) as well as microscopy

(Spearman $r = 0.40$ and 0.75 , respectively), suggesting the assay to be a

good predictor of parasite density. CONCLUSION: This immunoassay can be

used as a reference test for the detection and quantification of PfHRP2

and pLDH, and could serve for external validation of RDT performance, to

determine antigen persistence after parasite clearance, as well as a

complementary tool to assess malaria burden in endemic settings.

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LA - eng
PT - Journal Article
DEP - 20200109
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TA - Malar J
JT - Malaria journal
JID - 101139802
RN - 0 (Antigens, Protozoan)
RN - 0 (HRP-2 antigen, Plasmodium falciparum)
RN - 0 (Protozoan Proteins)
RN - 6S06U10H04 (Biotin)
RN - EC 1.1.1.27 (L-Lactate Dehydrogenase)
SB - IM
MH - Adolescent
MH - Adult
MH - Africa
MH - Animals
MH - Antigens, Protozoan/*blood
MH - Biotin
MH - Calibration
MH - Child
MH - Cross-Sectional Studies
MH - Female
MH - High-Throughput Nucleotide Sequencing/methods
MH - Humans
MH - L-Lactate Dehydrogenase/*blood
MH - Malaria, Falciparum/blood/*diagnosis
MH - Malaria, Vivax/blood/*diagnosis
MH - Mice
MH - Microspheres
MH - Parasitemia/blood/diagnosis
MH - Pregnancy
MH - Protozoan Proteins/*blood
MH - Real-Time Polymerase Chain Reaction
MH - South America
MH - Spain
MH - Young Adult
PMC - PMC6953214
OTO - NOTNLM
OT - Histidine-rich protein 2
OT - Luminex
OT - Malaria
OT - Parasite lactate dehydrogenase
OT - Quantitative suspension array technology
OT - Rapid diagnostic test

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S0 - Malar J. 2020 Jan 9;19(1):12. doi: 10.1186/s12936-019-3083-5.

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OWN - NLM
STAT- MEDLINE
DCOM- 20200128
LR - 20200128
IS - 1873-6254 (Electronic)
IS - 0001-706X (Linking)
VI - 200
DP - 2019 Dec
TI - A pilot evaluation of alternative procedures to simplify LAMP-based malaria diagnosis in field conditions.
PG - 105125
LID - S0001-706X(19)30617-5 [pii]
LID - 10.1016/j.actatropica.2019.105125 [doi]
AB - Highly-sensitive and field-friendly diagnostic tools are needed for accurate detection of low-density malaria infections. Although loop-mediated isothermal amplification (LAMP) fulfills these conditions, operational challenges are still encountered during pilot population screenings in remote settings when employing Loopamp MALARIA Pan/Pf detection kit (Eiken Chemical Co.). This study evaluates different procedures for the simplification of sample preparation and result reading steps of current LAMP protocols. The reference 'Boil & Spin' (B&S) pre-amplification procedure was compared to three alternative methods, along with a colorimetric staining protocol based on malachite green. Results suggested that the B&S supernatant transference step may be omitted without an impact on test performance, even when colorimetry was incorporated to facilitate results visualization. Procedures skipping

centrifugation and/or heat-incubation were proved to be compatible with LAMP-based malaria DNA detection, but resulted in a low-to-moderate decrease in sensitivity and ambiguous result interpretation for the most straightforward protocol. Nevertheless, all simplified LAMP methods could still reach lower limits of detection than the currently used tools for malaria mass-screening (i.e. microscopy and rapid tests), indicating that these alternative strategies may deserve further consideration. This evaluation, therefore, demonstrates the feasibility of skipping some of the main procedural bottlenecks of LAMP-malaria protocols, a much-needed achievement to make point-of-care implementation of molecular diagnostics a reality.

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LA - eng

PT - Comparative Study
PT - Journal Article
DEP - 20190805
PL - Netherlands
TA - Acta Trop
JT - Acta tropica
JID - 0370374
SB - IM
MH - Diagnostic Tests, Routine/*methods
MH - Humans
MH - Malaria/*diagnosis
MH - Mass Screening/*methods
MH - Nucleic Acid Amplification Techniques/*methods
MH - Pilot Projects
MH - Plasmodium/*isolation & purification
MH - *Point-of-Care Systems
MH - Sensitivity and Specificity
OTO - NOTNLM
OT - Loop-mediated isothermal amplification (LAMP)
OT - Malaria infection
OT - Plasmodium
OT - Point-of-care diagnosis
OT - Sample preparation
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IS - 1935-2735 (Electronic)
IS - 1935-2727 (Linking)
VI - 13
IP - 11
DP - 2019 Nov
TI - Microsatellite analysis reveals connectivity among
geographically distant
transmission zones of Plasmodium vivax in the Peruvian Amazon:
A critical
barrier to regional malaria elimination.

PG - e0007876

LID - 10.1371/journal.pntd.0007876 [doi]

AB - Despite efforts made over decades by the Peruvian government to eliminate

malaria, *Plasmodium vivax* remains a challenge for public health decision-

makers in the country. The uneven distribution of its incidence, plus its

complex pattern of dispersion, has made ineffective control measures

based on global information that lack the necessary detail to understand

transmission fully. In this sense, population genetic tools can

complement current surveillance. This study describes the genetic

diversity and population structure from September 2012 to March 2015 in

three geographically distant settlements, Cahuide (CAH), Lupuna (LUP) and

Santa Emilia (STE), located in the Peruvian Amazon. A total 777 *P. vivax*

mono-infections, out of 3264, were genotyped. Among study areas, LUP

showed 19.7% of polyclonal infections, and its genetic diversity (Hexp)

was 0.544. Temporal analysis showed a significant increment of polyclonal

infections and Hexp, and the introduction and persistence of a new

parasite population since March 2013. In STE, 40.1% of infections were

polyclonal, with Hexp = 0.596. The presence of four genetic clusters

without signals of clonal expansion and infections with lower parasite

densities compared against the other two areas were also found. At least

four parasite populations were present in CAH in 2012, where, after June

2014, malaria cases decreased from 213 to 61, concomitant with a decrease

in polyclonal infections (from 0.286 to 0.18), and expectedly variable

Hexp. Strong signals of gene flow were present in the study areas and

wide geographic distribution of highly diverse parasite populations were

found. This study suggests that movement of malaria parasites by human

reservoirs connects geographically distant malaria transmission areas in

the Peruvian Amazon. The maintenance of high levels of parasite genetic

diversity through human mobility is a critical barrier to malaria

elimination in this region.

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GR - D43 TW007120/TW/FIC NIH HHS/United States
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GR - UL1 TR001863/TR/NCATS NIH HHS/United States
PT - Journal Article
PT - Research Support, N.I.H., Extramural
DEP - 20191111
PL - United States
TA - PLoS Negl Trop Dis
JT - PLoS neglected tropical diseases
JID - 101291488
SB - IM
MH - Adolescent
MH - Adult
MH - Aged
MH - Aged, 80 and over
MH - Child
MH - Child, Preschool
MH - *Disease Transmission, Infectious
MH - Female
MH - *Genotype
MH - Genotyping Techniques
MH - Humans
MH - Incidence
MH - Infant
MH - Infant, Newborn
MH - Longitudinal Studies
MH - Malaria, Vivax/*epidemiology/*parasitology/transmission
MH - Male
MH - Microsatellite Repeats
MH - Middle Aged
MH - Molecular Epidemiology
MH - Peru/epidemiology
MH - Plasmodium vivax/*classification/*genetics/isolation & purification
MH - Young Adult
PMC - PMC6874088
COIS- The authors have declared that no competing interests exist.
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S0 - PLoS Negl Trop Dis. 2019 Nov 11;13(11):e0007876. doi: 10.1371/journal.pntd.0007876. eCollection 2019 Nov.

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IP - 1

DP - 2019 Sep 23

TI - Evaluation of Plasmodium falciparum MSP10 and its development as a

serological tool for the Peruvian Amazon region.

PG - 327

LID - 10.1186/s12936-019-2959-8 [doi]

AB - BACKGROUND: Different antigens are needed to characterize Plasmodium

falciparum infection in terms of seroreactivity and targets for invasion

inhibition, in order to guide and identify the proper use of such

proteins as tools for the development of serological markers and/or as

vaccine candidates. METHODS: IgG responses in 84 serum samples from

individuals with *P. falciparum* infection [classified as symptomatic (Sym)

or asymptomatic (Asym)], or acute *Plasmodium vivax* infection, from the

Peruvian Amazon region, were evaluated by enzyme-linked immunosorbent

assays specific for a baculovirus-produced recombinant protein *P.*

falciparum Merozoite Surface Protein 10 (rMSP10) and for non-EGF region

selected peptides of PfMSP10 selected by a bioinformatics tool (PfMSP10-1, PfMSP10-2 and PfMSP10-3). Monoclonal antibodies

against the

selected peptides were evaluated by western blotting, confocal microscopy

and inhibition invasion assays. RESULTS: Seroreactivity analysis of the

P. falciparum Sym- and Asym-infected individuals against rMSP10 showed a

higher response as compared to the individuals with *P. vivax* acute

infection. IgG responses against peptide PfMSP10-1 were weak. Interestingly high IgG response was found against peptide

PfMSP10-2 and

the combination of peptides PfMSP10-1 + PfMSP10-2. Monoclonal antibodies

were capable of detecting native PfMSP10 on purified schizonts by western blot and confocal microscopy. A low percentage of inhibition of merozoite invasion of erythrocytes in vitro was observed when the monoclonal antibodies were compared with the control antibody against AMA-1 antigen.

Further studies are needed to evaluate the role of PfMSP10 in the merozoite invasion. CONCLUSIONS: The rMSP10 and the PfMSP10-2 peptide synthesized for this study may be useful antigens for evaluation of P.

falciparum malaria exposure in Sym and Asym individuals from the Peruvian

Amazon region. Moreover, these antigens can be used for further

investigation of the role of this protein in other malaria-endemic areas.

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LA - eng

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GR - 218-2015-FONDECYT/FONDECYT / CONCYTEC

GR - U19AI089681/NHI-USA

GR - D43TW007120/TW/FIC NIH HHS/United States

PT - Journal Article

DEP - 20190923

PL - England
TA - Malar J
JT - Malaria journal
JID - 101139802
RN - 0 (Antigens, Protozoan)
RN - 0 (Protozoan Proteins)
SB - IM
MH - Antigens, Protozoan/*analysis
MH - Humans
MH - Malaria, Falciparum/*diagnosis
MH - Peru
MH - Plasmodium falciparum/*isolation & purification
MH - Population Surveillance/*methods
MH - Protozoan Proteins/*analysis
MH - Seroepidemiologic Studies
PMC - PMC6757379
OTO - NOTNLM
OT - Monoclonal antibodies
OT - Peptides
OT - PfMSP10
OT - Plasmodium falciparum
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AID - 10.1186/s12936-019-2959-8 [doi]
AID - 10.1186/s12936-019-2959-8 [pii]
PST - epublish
S0 - Malar J. 2019 Sep 23;18(1):327. doi: 10.1186/
s12936-019-2959-8.

PMID- 31511562
OWN - NLM
STAT- MEDLINE
DCOM- 20201028
LR - 20210110
IS - 2045-2322 (Electronic)
IS - 2045-2322 (Linking)
VI - 9
IP - 1
DP - 2019 Sep 11
TI - A multiplex qPCR approach for detection of pfhrp2 and pfhrp3
gene
deletions in multiple strain infections of Plasmodium
falciparum.
PG - 13107
LID - 10.1038/s41598-019-49389-2 [doi]
AB - The rapid and accurate diagnosis of Plasmodium falciparum
malaria
infection is an essential factor in malaria control.

Currently, malaria diagnosis in the field depends heavily on using rapid diagnostic tests (RDTs) many of which detect circulating parasite-derived histidine-rich protein 2 antigen (PfHRP2) in capillary blood. *P. falciparum* strains lacking PfHRP2, due to *pfhrp2* gene deletions, are an emerging threat to malaria control programs. The novel assay described here, named qHRP2/3-del, is well suited for high-throughput screening of *P. falciparum* isolates to identify these gene deletions. The qHRP2/3-del assay identified *pfhrp2* and *pfhrp3* deletion status correctly in 93.4% of samples with parasitemia levels higher than 5 parasites/microL when compared to nested PCR. The qHRP2/3-del assay can correctly identify *pfhrp2* and *pfhrp3* gene deletions in multiple strain co-infections, particularly prevalent in Sub-Saharan countries. Deployment of this qHRP2/3-del assay will provide rapid insight into the prevalence and potential spread of *P. falciparum* isolates that escape surveillance by RDTs.

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PT - Journal Article
PT - Research Support, N.I.H., Extramural
PT - Research Support, Non-U.S. Gov't
DEP - 20190911
PL - England
TA - Sci Rep
JT - Scientific reports
JID - 101563288
RN - 0 (Antigens, Protozoan)
RN - 0 (HRP-2 antigen, Plasmodium falciparum)
RN - 0 (HRP3 protein, Plasmodium falciparum)
RN - 0 (Protozoan Proteins)
SB - IM
MH - Antigens, Protozoan/*genetics/*metabolism
MH - *Gene Deletion
MH - Plasmodium falciparum/*genetics/physiology
MH - Polymerase Chain Reaction/*methods
MH - Protozoan Proteins/*genetics/*metabolism
PMC - PMC6739368
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AID - 10.1038/s41598-019-49389-2 [doi]
AID - 10.1038/s41598-019-49389-2 [pii]
PST - epublish
S0 - Sci Rep. 2019 Sep 11;9(1):13107. doi: 10.1038/
s41598-019-49389-2.

PMID- 31358033
OWN - NLM
STAT- MEDLINE
DCOM- 20191202
LR - 20200327
IS - 1756-3305 (Electronic)
IS - 1756-3305 (Linking)
VI - 12
IP - 1
DP - 2019 Jul 29
TI - Higher risk of malaria transmission outdoors than indoors by
Nyssorhynchus darlingi in riverine communities in the Peruvian
Amazon.
PG - 374
LID - 10.1186/s13071-019-3619-0 [doi]
AB - BACKGROUND: Malaria remains an important public health problem
in Peru
where incidence has been increasing since 2011. Of over 55,000
cases
reported in 2017, Plasmodium vivax was the predominant species
(76%),
with P. falciparum responsible for the remaining 24%.
Nyssorhynchus
darlingi (previously Anopheles darlingi) is the main vector in
Amazonian
Peru, where hyperendemic Plasmodium transmission pockets have
been found.
Mazan district has pronounced spatial heterogeneity of P.
vivax malaria.
However, little is known about behavior, ecology or seasonal
dynamics of
Ny. darlingi in Mazan. This study aimed to gather baseline
information
about bionomics of malaria vectors and transmission risk
factors in a
hyperendemic malaria area of Amazonian Peru. METHODS: To
assess vector
biology metrics, five surveys (two in the dry and three in the
rainy
season), including collection of sociodemographic information,
were
conducted in four communities in 2016–2017 on the Napo (Urco

Mirano, URC;
Salvador, SAL) and Mazan Rivers (Visto Bueno, VIB; Libertad, LIB). Human-biting rate (HBR), entomological inoculation rate (EIR) and human blood index (HBI) were measured to test the hypothesis of differences in entomological indices of *Ny. darlingi* between watersheds. A generalized linear mixed effect model (GLMM) was constructed to model the relationship between household risk factors and the EIR.

RESULTS:
Nyssorhynchus darlingi comprised 95% of 7117 Anophelinae collected and its abundance was significantly higher along the Mazan River. The highest EIRs (3.03–4.54) were detected in March and June in URC, LIB and VIB, and significantly more *Ny. darlingi* were infected outdoors than indoors. Multivariate analysis indicated that the EIR was >12 times higher in URC compared with SAL. The HBI ranged from 0.42–0.75; humans were the most common blood source, followed by Galliformes and cows. There were dramatic differences in peak biting time and malaria incidence with similar bednet coverage in the villages. **CONCLUSIONS:** *Nyssorhynchus darlingi* is the predominant contributor to malaria transmission in the Mazan District, Peru. Malaria risk in these villages is higher in the peridomestic area, with pronounced heterogeneities between and within villages on the Mazan and the Napo Rivers. Spatiotemporal identification and quantification of the prevailing malaria transmission would provide new evidence to orient specific control measures for vulnerable or at high risk populations.

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GR - R01 AI110112/AI/NIAID NIH HHS/United States
GR - R01AI110112/National Institute of Allergy and Infectious Diseases
GR - T32AI05532901/Biodefense and Emerging Infectious Disease Training fellowship
GR - U19 AI089681/AI/NIAID NIH HHS/United States
GR - 201460655/TDR/WHO
PT - Journal Article
DEP - 20190729
PL - England
TA - Parasit Vectors

JT - Parasites & vectors
JID - 101462774
SB - IM
MH - Adolescent
MH - Adult
MH - Animals
MH - Anopheles/*parasitology/*physiology
MH - Bites and Stings
MH - Child
MH - Child, Preschool
MH - Female
MH - *Housing
MH - Humans
MH - Incidence
MH - Malaria/epidemiology/*transmission
MH - Malaria, Falciparum/epidemiology/transmission
MH - Malaria, Vivax/epidemiology/transmission
MH - Male
MH - Mosquito Vectors/*parasitology
MH - Peru/epidemiology
MH - Risk Factors
MH - *Rivers
MH - Seasons
MH - Young Adult
PMC - PMC6664538
OTO - NOTNLM
OT - Blood meal source
OT - Entomological inoculation rate
OT - GLMM
OT - Human blood index
OT - Mazan District
OT - Nyssorhynchus darlingi
OT - Peruvian Amazon
OT - Plasmodium
EDAT- 2019/07/31 06:00
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AID - 10.1186/s13071-019-3619-0 [doi]
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PST - epublish
S0 - Parasit Vectors. 2019 Jul 29;12(1):374. doi: 10.1186/
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PMID- 31221984
OWN - NLM
STAT- MEDLINE
DCOM- 20201027
LR - 20220302
IS - 2045-2322 (Electronic)

IS - 2045-2322 (Linking)

VI - 9

IP - 1

DP - 2019 Jun 20

TI - Complement Receptor 1 availability on red blood cell surface modulates

Plasmodium vivax invasion of human reticulocytes.

PG - 8943

LID - 10.1038/s41598-019-45228-6 [doi]

AB - *Plasmodium vivax* parasites preferentially invade reticulocyte cells in a

multistep process that is still poorly understood. In this study, we used

ex vivo invasion assays and population genetic analyses to investigate

the involvement of complement receptor 1 (CR1) in *P. vivax* invasion.

First, we observed that *P. vivax* invasion of reticulocytes was consistently reduced when CR1 surface expression was reduced

through

enzymatic cleavage, in the presence of naturally low-CR1-expressing cells

compared with high-CR1-expressing cells, and with the addition of soluble

CR1, a known inhibitor of *P. falciparum* invasion. Immunoprecipitation

experiments with *P. vivax* Reticulocyte Binding Proteins showed no

evidence of complex formation. In addition, analysis of CR1 genetic data

for worldwide human populations with different exposure to malaria

parasites show significantly higher frequency of CR1 alleles associated

with low receptor expression on the surface of RBCs and higher linkage

disequilibrium in human populations exposed to *P. vivax* malaria compared

with unexposed populations. These results are consistent with a positive

selection of low-CR1-expressing alleles in *vivax*-endemic areas.

Collectively, our findings demonstrate that CR1 availability on the

surface of RBCs modulates *P. vivax* invasion. The identification of new

molecular interactions is crucial to guiding the rational development of

new therapeutic interventions against *vivax* malaria.

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GR - UL1 TR001863/TR/NCATS NIH HHS/United States
PT - Journal Article
PT - Research Support, Non-U.S. Gov't
DEP - 20190620
PL - England
TA - Sci Rep
JT - Scientific reports
JID - 101563288
RN - 0 (Receptors, Complement)
SB - IM
MH - Erythrocyte Membrane/*metabolism
MH - Gene Frequency
MH - Humans
MH - Linkage Disequilibrium
MH - Malaria, Vivax/parasitology/transmission
MH - Plasmodium vivax/*physiology
MH - Receptors, Complement/genetics/*metabolism
MH - Reticulocytes/*parasitology
PMC - PMC6586822
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s41598-019-45228-6.

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OWN - NLM
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LR - 20200327
IS - 1935-2735 (Electronic)
IS - 1935-2727 (Linking)
VI - 13
IP - 5
DP - 2019 May
TI - Malaria vector species in Amazonian Peru co-occur in larval
habitats but
have distinct larval microbial communities.
PG - e0007412
LID - 10.1371/journal.pntd.0007412 [doi]
AB - In Amazonian Peru, the primary malaria vector, Nyssorhynchus

darlingi (formerly *Anopheles darlingi*), is difficult to target using standard vector control methods because it mainly feeds and rests outdoors. Larval source management could be a useful supplementary intervention, but to determine its feasibility, more detailed studies on the larval ecology of *Ny. darlingi* are essential. We conducted a multi-level study of the larval ecology of Anophelinae mosquitoes in the peri-Iquitos region of Amazonian Peru, examining the environmental characteristics of the larval habitats of four species, comparing the larval microbiota among species and habitats, and placing *Ny. darlingi* larval habitats in the context of spatial heterogeneity in human malaria transmission. We collected *Ny. darlingi*, *Nyssorhynchus rangeli* (formerly *Anopheles rangeli*), *Nyssorhynchus triannulatus* s.l. (formerly *Anopheles triannulatus* s.l.), and *Nyssorhynchus* sp. nr. *konderi* (formerly *Anopheles* sp. nr. *konderi*) from natural and artificial water bodies throughout the rainy and dry seasons. We found that, consistent with previous studies in this region and in Brazil, the presence of *Ny. darlingi* was significantly associated with water bodies in landscapes with more recent deforestation and lower light intensity. *Nyssorhynchus darlingi* presence was also significantly associated with a lower vegetation index, other Anophelinae species, and emergent vegetation. Though they were collected in the same water bodies, the microbial communities of *Ny. darlingi* larvae were distinct from those of *Ny. rangeli* and *Ny. triannulatus* s.l., providing evidence either for a species-specific larval microbiome or for segregation of these species in distinct microhabitats within each water body. We demonstrated that houses with more reported malaria cases were located closer to *Ny. darlingi* larval habitats; thus, targeted control of these sites could help ameliorate malaria risk. The co-occurrence of *Ny. darlingi* larvae in

water bodies with other putative malaria vectors increases the potential

impact of larval source management in this region.

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LA - eng
GR - R01 AI110112/AI/NIAID NIH HHS/United States
GR - U19 AI089681/AI/NIAID NIH HHS/United States
GR - UL1 TR001863/TR/NCATS NIH HHS/United States
PT - Journal Article
PT - Research Support, N.I.H., Extramural
PT - Research Support, Non-U.S. Gov't
DEP - 20190515
PL - United States
TA - PLoS Negl Trop Dis
JT - PLoS neglected tropical diseases
JID - 101291488
SB - IM
MH - Animals
MH - Anopheles/classification/*microbiology
MH - Bacteria/classification/genetics/*isolation & purification
MH - Brazil
MH - Ecosystem

MH - Humans
MH - Larva/classification/*microbiology
MH - Malaria/*transmission
MH - *Microbiota
MH - Mosquito Vectors/classification/*microbiology
MH - Peru
PMC - PMC6538195
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AID - 10.1371/journal.pntd.0007412 [doi]
AID - PNTD-D-18-01822 [pii]
PST - epublish
S0 - PLoS Negl Trop Dis. 2019 May 15;13(5):e0007412. doi:
10.1371/journal.pntd.0007412. eCollection 2019 May.

PMID- 30697487
OWN - NLM
STAT- PubMed-not-MEDLINE
LR - 20201001
IS - 2167-8359 (Print)
IS - 2167-8359 (Linking)
VI - 7
DP - 2019
TI - Use of open mobile mapping tool to assess human mobility
traceability in
rural offline populations with contrasting malaria dynamics.
PG - e6298
LID - 10.7717/peerj.6298 [doi]
AB - Infectious disease dynamics are affected by human mobility
more
powerfully than previously thought, and thus reliable
traceability data
are essential. In rural riverine settings, lack of
infrastructure and
dense tree coverage deter the implementation of cutting-edge
technology
to collect human mobility data. To overcome this challenge,
this study
proposed the use of a novel open mobile mapping tool, GeoODK.
This study
consists of a purposive sampling of 33 participants in six
villages with
contrasting patterns of malaria transmission that demonstrates
a feasible
approach to map human mobility. The self-reported traceability
data

allowed the construction of the first human mobility framework in rural riverine villages in the Peruvian Amazon. The mobility spectrum in these areas resulted in travel profiles ranging from 2 hours to 19 days; and distances between 10 to 167 km. Most importantly, occupational-related mobility profiles with the highest displacements (in terms of time and distance) were observed in commercial, logging, and hunting activities.

These data are consistent with malaria transmission studies in the area that show villages in watersheds with higher human movement are concurrently those with greater malaria risk. The approach we describe represents a potential tool to gather critical information that can facilitate malaria control activities.

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LA - eng
SI - figshare/10.6084/m9.figshare.7091075.v1
PT - Journal Article
DEP - 20190122
PL - United States
TA - PeerJ
JT - PeerJ
JID - 101603425
PMC - PMC6346981
OTO - NOTNLM
OT - Amazon
OT - Contact network
OT - Epidemics
OT - Human mobility
OT - Infectious diseases
OT - Malaria
OT - Network
COIS- The authors declare there are no competing interests.
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PMID- 30653491
OWN - NLM
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IS - 1935-2735 (Electronic)
IS - 1935-2727 (Linking)
VI - 13
IP - 1
DP - 2019 Jan
TI - High-accuracy detection of malaria vector larval habitats using drone-based multispectral imagery.
PG - e0007105
LID - 10.1371/journal.pntd.0007105 [doi]
AB - Interest in larval source management (LSM) as an adjunct intervention to control and eliminate malaria transmission has recently increased mainly because long-lasting insecticidal nets (LLINs) and indoor residual spray (IRS) are ineffective against exophagic and exophilic mosquitoes. In Amazonian Peru, the identification of the most productive, positive water bodies would increase the impact of targeted mosquito control on aquatic life stages. The present study explores the use of unmanned aerial vehicles (drones) for identifying *Nyssorhynchus darlingi* (formerly *Anopheles darlingi*) breeding sites with high-resolution imagery (~0.02m/pixel) and their multispectral profile in Amazonian Peru. Our results show that high-resolution multispectral imagery can discriminate a profile of water bodies where *Ny. darlingi* is most likely to breed (overall accuracy 86.73%- 96.98%) with a moderate differentiation of spectral bands. This work provides proof-of-concept of the use of high-resolution images to detect malaria vector breeding sites in Amazonian Peru and such innovative methodology could be crucial for LSM malaria integrated interventions.
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 DEP – 20190117
 PL – United States
 TA – PLoS Negl Trop Dis
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 JID – 101291488
 SB – IM
 MH – Animals
 MH – Anopheles/*growth & development
 MH – *Ecosystem
 MH – Entomology/*methods
 MH – Female
 MH – Image Processing, Computer-Assisted/*methods
 MH – Mosquito Vectors/*growth & development
 MH – Optical Imaging/*methods
 MH – Peru
 MH – Proof of Concept Study
 PMC – PMC6353212

COIS- The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a

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AID - 10.1371/journal.pntd.0007105 [doi]

AID - PNTD-D-18-00902 [pii]

PST - epublish

S0 - PLoS Negl Trop Dis. 2019 Jan 17;13(1):e0007105. doi:

10.1371/journal.pntd.0007105. eCollection 2019 Jan.

PMID- 30517211

OWN - NLM

STAT- MEDLINE

DCOM- 20190206

LR - 20190215

IS - 1678-8060 (Electronic)

IS - 0074-0276 (Linking)

VI - 113

IP - 12

DP - 2018 Dec 3

TI - Nyssorhynchus dunhami: bionomics and natural infection by Plasmodium

falciparum and P. vivax in the Peruvian Amazon.

PG - e180380

LID - S0074-02762018001200300 [pii]

LID - 10.1590/0074-02760180380 [doi]

AB - BACKGROUND Nyssorhynchus dunhami, a member of the Nuneztovari Complex,

has been collected in Brazil, Colombia, and Peru and described as

zoophilic. Although to date Ny. dunhami has not been documented to be

naturally infected by Plasmodium, it is frequently misidentified as other

Oswaldoi subgroup species that are local or regional malaria vectors.

OBJECTIVES The current study seeks to verify the morphological identification of Nuneztovari Complex species collected in the peri-

Iquitos region of Amazonian Peru, to determine their Plasmodium infection

status, and to describe ecological characteristics of their larval

habitats. METHODS We collected Ny. nuneztovari s.l. adults in

2011–2012,
and *Ny. nuneztovari* s.l. larvae and adults in 2016–2017. When possible, samples were identified molecularly using cytochrome c oxidase subunit I (COI) barcode sequencing. Adult *Ny. nuneztovari* s.l. from 2011–2012 were tested for *Plasmodium* using real-time PCR. Environmental characteristics associated with *Ny. nuneztovari* s.l. larvae-positive water bodies were evaluated. FINDINGS We collected 590 *Ny. nuneztovari* s.l. adults and 116 larvae from eight villages in peri-Iquitos. Of these, 191 adults and 111 larvae were identified by COI sequencing; all were *Ny. dunhami*. Three *Ny. dunhami* were infected with *P. falciparum*, and one with *P. vivax*, all collected from one village on one night. *Ny. dunhami* larvae were collected from natural and artificial water bodies, and their presence was positively associated with other Anophelinae larvae and amphibians, and negatively associated with people living within 250m. MAIN CONCLUSIONS Of *Nuneztovari* Complex species, we identified only *Ny. dunhami* across multiple years in eight peri-Iquitos localities. This study is, to our knowledge, the first report of natural infection of molecularly identified *Ny. dunhami* with *Plasmodium*. We advocate the use of molecular identification methods in this region to monitor *Ny. dunhami* and other putative secondary malaria vectors to more precisely evaluate their importance in malaria transmission.

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LA - eng
GR - R01 AI110112/AI/NIAID NIH HHS/United States
GR - U19 AI089681/AI/NIAID NIH HHS/United States
PT - Journal Article
DEP - 20181203
PL - Brazil
TA - Mem Inst Oswaldo Cruz
JT - Memorias do Instituto Oswaldo Cruz
JID - 7502619
SB - IM

MH - Animals
MH - Anopheles/classification/*parasitology
MH - Brazil
MH - Colombia
MH - Ecology
MH - Malaria, Falciparum/transmission
MH - Malaria, Vivax/transmission
MH - Mosquito Vectors/classification/*parasitology
MH - Peru
MH - Plasmodium falciparum/*isolation & purification
MH - Plasmodium vivax/*isolation & purification
PMC - PMC6276023
EDAT- 2018/12/06 06:00
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AID - S0074-02762018001200300 [pii]
AID - 10.1590/0074-02760180380 [doi]
PST - epublish
S0 - Mem Inst Oswaldo Cruz. 2018 Dec 3;113(12):e180380. doi:
10.1590/0074-02760180380.

PMID- 30486449
OWN - NLM
STAT- MEDLINE
DCOM- 20190226
LR - 20200225
IS - 1660-4601 (Electronic)
IS - 1660-4601 (Linking)
VI - 15
IP - 12
DP - 2018 Nov 27
TI - Effectiveness of a Malaria Surveillance Strategy Based on
Active Case
Detection during High Transmission Season in the Peruvian
Amazon.
LID - E2670 [pii]
LID - 10.3390/ijerph15122670 [doi]
AB - Background: Faced with the resurgence of malaria, malaria
surveillance in
the Peruvian Amazon incorporated consecutive active case
detection (ACD)
interventions using light microscopy (LM) as reactive measure
in
communities with an unusual high number of cases during high
transmission
season (HTS). We assessed the effectiveness in malaria
detection of this
local ACD-based strategy. Methods: A cohort study was
conducted in

June(-)July 2015 in Mazan, Loreto. Four consecutive ACD interventions at intervals of 10 days were conducted in four riverine communities (Gamitanacocha, Primero de Enero, Libertad and Urco Mirano). In each intervention, all inhabitants were visited at home, and finger-prick blood samples collected for immediate diagnosis by LM and on filter paper for later analysis by quantitative real-time polymerase chain reaction (qPCR). Effectiveness was calculated by dividing the number of malaria infections detected using LM by the number of malaria infections detected by delayed qPCR. Results: Most community inhabitants (88.1%, 822/933) were present in at least one of the four ACD interventions. A total of 451 infections were detected by qPCR in 446 participants (54.3% of total participants); five individuals had two infections. Plasmodium vivax was the predominant species (79.8%), followed by P. falciparum (15.3%) and P. vivax-P. falciparum co-infections (4.9%). Most qPCR-positive infections were asymptomatic (255/448, 56.9%). The ACD-strategy using LM had an effectiveness of 22.8% (detection of 103 of the total qPCR-positive infections). Children aged 5(-)14 years, and farming as main economic activity were associated with P. vivax infections.

Conclusions: Although the ACD-strategy using LM increased the opportunity of detecting and treating malaria infections during HTS, the number of detected infections was considerably lower than the real burden of infections (those detected by qPCR).

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LA - eng
PT - Journal Article
PT - Research Support, Non-U.S. Gov't
DEP - 20181127
PL - Switzerland
TA - Int J Environ Res Public Health
JT - International journal of environmental research and public
health
JID - 101238455
SB - IM
MH - Adolescent

MH - Adult
MH - Aged
MH - Aged, 80 and over
MH - Child
MH - Child, Preschool
MH - Cohort Studies
MH - Farms/*statistics & numerical data
MH - Female
MH - Humans
MH - Infant
MH - Infant, Newborn
MH - Malaria, Falciparum/*epidemiology
MH - Malaria, Vivax/*epidemiology
MH - Male
MH - Middle Aged
MH - Peru/epidemiology
MH - Plasmodium falciparum/*isolation & purification
MH - Plasmodium vivax/*isolation & purification
MH - Population Surveillance/*methods
MH - *Seasons
MH - Young Adult
PMC - PMC6314008
OTO - NOTNLM
OT - Peru
OT - active case detection
OT - asymptomatic
OT - diagnosis
OT - malaria
EDAT- 2018/11/30 06:00
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PHST- 2018/11/30 06:00 [pubmed]
PHST- 2019/02/27 06:00 [medline]
AID - ijerph15122670 [pii]
AID - 10.3390/ijerph15122670 [doi]
PST - epublish
S0 - Int J Environ Res Public Health. 2018 Nov 27;15(12). pii:
ijerph15122670.
doi: 10.3390/ijerph15122670.

PMID- 30253764
OWN - NLM
STAT- MEDLINE
DCOM- 20181211
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IS - 1475-2875 (Electronic)
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VI - 17
IP - 1
DP - 2018 Sep 25

TI - Automated microscopy for routine malaria diagnosis: a field comparison on Giemsa-stained blood films in Peru.

PG - 339

LID - 10.1186/s12936-018-2493-0 [doi]

AB - BACKGROUND: Microscopic examination of Giemsa-stained blood films remains a major form of diagnosis in malaria case management, and is a reference standard for research. However, as with other visualization-based diagnoses, accuracy depends on individual technician performance, making standardization difficult and reliability poor. Automated image recognition based on machine-learning, utilizing convolutional neural networks, offers potential to overcome these drawbacks. A prototype digital microscope device employing an algorithm based on machine-learning, the Autoscope, was assessed for its potential in malaria microscopy. Autoscope was tested in the Iquitos region of Peru in 2016 at two peripheral health facilities, with routine microscopy and PCR as reference standards. The main outcome measures include sensitivity and specificity of diagnosis of malaria from Giemsa-stained blood films, using PCR as reference. METHODS: A cross-sectional, observational trial was conducted at two peripheral primary health facilities in Peru. 700 participants were enrolled with the criteria: (1) age between 5 and 75 years, (2) history of fever in the last 3 days or elevated temperature on admission, (3) informed consent. The main outcome measures included sensitivity and specificity of diagnosis of malaria from Giemsa-stained blood films, using PCR as reference. RESULTS: At the San Juan clinic, sensitivity of Autoscope for diagnosing malaria was 72% (95% CI 64-80%), and specificity was 85% (95% CI 79-90%). Microscopy performance was similar to Autoscope, with sensitivity 68% (95% CI 59-76%) and specificity 100% (95% CI 98-100%). At San Juan, 85% of prepared slides had a minimum of 600 WBCs imaged, thus meeting Autoscope's design

assumptions. At the second clinic, Santa Clara, the sensitivity of Autoscope was 52% (95% CI 44–60%) and specificity was 70% (95% CI 64–76%). Microscopy performance at Santa Clara was 42% (95% CI 34–51) and specificity was 97% (95% CI 94–99). Only 39% of slides from Santa Clara met Autoscope's design assumptions regarding WBCs imaged.

CONCLUSIONS:

Autoscope's diagnostic performance was on par with routine microscopy when slides had adequate blood volume to meet its design assumptions, as represented by results from the San Juan clinic. Autoscope's diagnostic performance was poorer than routine microscopy on slides from the Santa Clara clinic, which generated slides with lower blood volumes.

Results of the study reflect both the potential for artificial intelligence to perform tasks currently conducted by highly-trained experts, and the challenges of replicating the adaptiveness of human thought processes.

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LA - eng
PT - Comparative Study
PT - Journal Article
DEP - 20180925
PL - England
TA - Malar J
JT - Malaria journal
JID - 101139802
SB - IM
MH - Adolescent

MH - Adult
MH - Aged
MH - Child
MH - Child, Preschool
MH - Cross-Sectional Studies
MH - Diagnostic Tests, Routine/instrumentation/*methods
MH - Humans
MH - Malaria, Falciparum/*diagnosis
MH - Malaria, Vivax/*diagnosis
MH - Microscopy/instrumentation/*methods
MH - Middle Aged
MH - Peru
MH - Plasmodium falciparum/isolation & purification
MH - Plasmodium vivax/isolation & purification
MH - Prospective Studies
MH - Reproducibility of Results
MH - Sensitivity and Specificity
MH - Young Adult
PMC - PMC6157053
OTO - NOTNLM
OT - Artificial intelligence
OT - Convolutional neural networks
OT - Digital microscopy
OT - Malaria
OT - Microscopy
EDAT- 2018/09/27 06:00
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AID - 10.1186/s12936-018-2493-0 [doi]
AID - 10.1186/s12936-018-2493-0 [pii]
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S0 - Malar J. 2018 Sep 25;17(1):339. doi: 10.1186/
s12936-018-2493-0.

PMID- 29703192
OWN - NLM
STAT- MEDLINE
DCOM- 20190110
LR - 20190110
IS - 1475-2875 (Electronic)
IS - 1475-2875 (Linking)
VI - 17
IP - 1
DP - 2018 Apr 27
TI - Acceptability of a herd immunity-focused, transmission-
blocking malaria
vaccine in malaria-endemic communities in the Peruvian Amazon:
an
exploratory study.

PG - 179

LID - 10.1186/s12936-018-2328-z [doi]

AB - BACKGROUND: A transmission-blocking vaccine (TBV) to prevent malaria-

infected humans from infecting mosquitoes has been increasingly

considered as a tool for malaria control and elimination. This study

tested the hypothesis that a malaria TBV would be acceptable among

residents of a malaria-hypoendemic region. METHODS: The study was carried

out in six Spanish-speaking rural villages in the Department of Loreto in

the Peruvian Amazon. These villages comprise a cohort of 430 households

associated with the Peru-Brazil International Centre for Excellence in

Malaria Research. Individuals from one-third (143) of enrolled households

in an ongoing longitudinal, prospective cohort study in 6 communities in

Loreto, Peru, were randomly selected to participate by answering a pre-

validated questionnaire. RESULTS: All 143 participants expressed desire

for a malaria vaccine in general; only 1 (0.7%) expressed unwillingness

to receive a transmission-blocking malaria vaccine. Injection was

considered most acceptable for adults (97.2%); for children drops in the

mouth were preferred (96.8%). Acceptability waned marginally with the

projected prospect of multiple injections (83.8%) and different

efficacies at 70 and 50% (90.1 and 71.8%, respectively). Respondents

demonstrated clear understanding that the vaccine was for community,

rather than personal, protection against malaria infection. DISCUSSION:

In this setting of the Peruvian Amazon, a transmission-blocking malaria

vaccine was found to be almost universally acceptable. This study is the

first to report that residents of a malaria-endemic region have been

queried regarding a malaria vaccine strategy that policy-makers in the

industrialized world often dismiss as altruistic.

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LA - eng

GR - R01 AI067727/AI/NIAID NIH HHS/United States

GR - R01AI067727/National Institutes of Health

GR - U19AI089681/National Institutes of Health

GR - K24AI068903/National Institutes of Health

GR - U19 AI089681/AI/NIAID NIH HHS/United States

GR - D43TW007120/National Institutes of Health

GR - D43 TW007120/TW/FIC NIH HHS/United States

GR - K24 AI068903/AI/NIAID NIH HHS/United States

PT - Journal Article

DEP - 20180427

PL - England

TA - Malar J

JT - Malaria journal

JID - 101139802

RN - 0 (Malaria Vaccines)

SB - IM

MH - Adult

MH - Aged

MH - Female

MH - Humans

MH - *Immunity, Herd

MH - Longitudinal Studies

MH - Malaria Vaccines/*immunology

MH - Malaria, Falciparum/*prevention & control

MH - Malaria, Vivax/*prevention & control

MH - Male

MH - Middle Aged

MH - Plasmodium falciparum/*immunology

MH - Plasmodium vivax/*immunology

MH - Prospective Studies

MH - Young Adult

PMC - PMC5921293

OTO - NOTNLM

OT - Amazon

OT - Malaria

OT - Peru

OT - Social acceptability

OT - Transmission-blocking vaccine (TBV)

EDAT- 2018/04/29 06:00

MHDA- 2019/01/11 06:00

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PHST- 2019/01/11 06:00 [medline]
AID - 10.1186/s12936-018-2328-z [doi]
AID - 10.1186/s12936-018-2328-z [pii]
PST - epublish
S0 - Malar J. 2018 Apr 27;17(1):179. doi: 10.1186/s12936-018-2328-z.

PMID- 29465219

OWN - NLM

STAT- MEDLINE

DCOM- 20190618

LR - 20191228

IS - 2373-8227 (Electronic)

IS - 2373-8227 (Linking)

VI - 4

IP - 4

DP - 2018 Apr 13

TI - Continuous Supply of Plasmodium vivax Sporozoites from Colonized

Anopheles darlingi in the Peruvian Amazon.

PG - 541-548

LID - 10.1021/acsinfecdis.7b00195 [doi]

AB - In vitro culture of Plasmodium vivax liver stages underlies key

understandings of the fundamental biology of this parasite, particularly

the latent, hyponozoite stage, toward drug and vaccine development. Here,

we report systematic production of Plasmodium vivax sporozoites in

colonized Anopheles darlingi mosquitoes in the Peruvian Amazon. Human

subject-derived P. vivax-infected blood was fed to Anopheles darlingi

females using standard membrane feedings assays. Optimizing A. darlingi

infection and sporozoite production included replacement of infected

patient donor serum with naive donor serum, comparing anticoagulants in

processing blood samples, and addition of penicillin-streptomycin and ATP

to infectious blood meals. Replacement of donor serum by naive serum in

the P. vivax donor blood increased oocysts in the mosquito midgut, and

heparin, as anticoagulant, was associated with the highest sporozoite

yields. Maintaining blood-fed mosquitoes on penicillin-streptomycin in

sugar significantly extended mosquito survival which enabled greater

sporozoite yield. In this study, we have shown that a robust P. vivax

sporozoite production is feasible in a malaria-endemic setting where

infected subjects and a stable *A. darlingi* colony are brought together,

with optimized laboratory conditions.

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LA - eng
GR - D43 TW007120/TW/FIC NIH HHS/United States
GR - U19 AI089681/AI/NIAID NIH HHS/United States
PT - Journal Article
PT - Research Support, N.I.H., Extramural
PT - Research Support, Non-U.S. Gov't
DEP - 20180315
PL - United States
TA - ACS Infect Dis
JT - ACS infectious diseases
JID - 101654580
SB - IM
MH - Animals
MH - Anopheles/*parasitology
MH - Female
MH - Gastrointestinal Tract/parasitology
MH - Parasitology/*methods
MH - Peru
MH - Plasmodium vivax/*growth & development/isolation & purification
MH - Sporozoites/*growth & development/isolation & purification
PMC - PMC5902790
OTO - NOTNLM
OT - Anopheles darlingi
OT - Peruvian Amazon
OT - Plasmodium vivax
OT - membrane feeding assays
OT - sporozoite
EDAT- 2018/02/22 06:00
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PHST- 2019/06/19 06:00 [medline]
PHST- 2018/02/22 06:00 [entrez]
AID - 10.1021/acsinfecdis.7b00195 [doi]
PST - ppublish
S0 - ACS Infect Dis. 2018 Apr 13;4(4):541-548. doi:
10.1021/acsinfecdis.7b00195. Epub 2018 Mar 15.

PMID- 29463241
OWN - NLM
STAT- MEDLINE
DCOM- 20181218
LR - 20190124
IS - 1475-2875 (Electronic)
IS - 1475-2875 (Linking)
VI - 17
IP - 1
DP - 2018 Feb 20
TI - Decreasing proportion of Anopheles darlingi biting outdoors
between long-
lasting insecticidal net distributions in peri-Iquitos,
Amazonian Peru.
PG - 86
LID - 10.1186/s12936-018-2234-4 [doi]
AB - BACKGROUND: In Loreto Department, Peru, a successful 2005-2010
malaria
control programme (known as PAMAFRO) included massive
distribution of
long-lasting insecticidal nets (LLINs). Additional local
distribution of
LLINs occurred in individual villages, but not between 2012
and 2015. A
2011-2012 study of the primary regional malaria vector
Anopheles darlingi
detected a trend of increased exophagy compared with pre-
PAMAFRO
behaviour. For the present study, An. darlingi were collected
in three
villages in Loreto in 2013-2015 to test two hypotheses: (1)
that between
LLIN distributions, An. darlingi reverted to pre-intervention
biting
behaviour; and, (2) that there are separate sub-populations of
An.
darlingi in Loreto with distinct biting behaviour. RESULTS: In
2013-2015
An. darlingi were collected by human landing catch during the
rainy and
dry seasons in the villages of Lupuna and Cahuide. The
abundance of An.
darlingi varied substantially across years, villages and time
periods,
and there was a twofold decrease in the ratio of

exophagic:endophagic An.

darlingi over the study period. Unexpectedly, there was evidence of a rainy season population decline in An. darlingi. Plasmodium-infected An. darlingi were detected indoors and outdoors throughout the night, and the monthly An. darlingi human biting rate was correlated with the number of malaria cases. Using nextRAD genotyping-by-sequencing, 162 exophagic and endophagic An. darlingi collected at different times during the night were genotyped at 1021 loci. Based on model-based and non-model-based analyses, all genotyped An. darlingi belonged to a homogeneous population, with no evidence for genetic differentiation by biting location or time. CONCLUSIONS: This study identified a decreasing proportion of exophagic An. darlingi in two villages in the years between LLIN distributions. As there was no evidence for genetic differentiation between endophagic and exophagic An. darlingi, this shift in biting behaviour may be the result of behavioural plasticity in An. darlingi, which shifted towards increased exophagy due to repellence by insecticides used to impregnate LLINs and subsequently reverted to increased endophagy as the nets aged. This study highlights the need to target vector control interventions to the biting behaviour of local vectors, which, like malaria risk, shows high temporal and spatial heterogeneity.

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GR - R01 AI110112/AI/NIAID NIH HHS/United States
GR - T32AI05532901/National Institute of Allergy and Infectious

Diseases

GR - U19 AI089681/AI/NIAID NIH HHS/United States
PT - Journal Article
DEP - 20180220
PL - England
TA - Malar J
JT - Malaria journal
JID - 101139802
SB - IM
MH - Animals
MH - Anopheles/genetics/*physiology
MH - Bites and Stings/*epidemiology
MH - Feeding Behavior
MH - Insecticide-Treated Bednets/*statistics & numerical data
MH - Mosquito Vectors/genetics/*physiology
MH - Peru/epidemiology
PMC - PMC5819687
OTO - NOTNLM
OT - Anopheles darlingi
OT - Biting behaviour
OT - LLINs
OT - NextRAD genotyping
OT - Peruvian Amazon
OT - Population genetic structure
EDAT- 2018/02/22 06:00
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AID - 10.1186/s12936-018-2234-4 [doi]
AID - 10.1186/s12936-018-2234-4 [pii]
PST - epublish
S0 - Malar J. 2018 Feb 20;17(1):86. doi: 10.1186/s12936-018-2234-4.

PMID- 29187975

OWN - NLM

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LR - 20220408

IS - 2045-7758 (Print)

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VI - 7

IP - 22

DP - 2017 Nov

TI - Evolutionary structure of Plasmodium falciparum major variant surface

antigen genes in South America: Implications for epidemic transmission and surveillance.

PG - 9376-9390

LID - 10.1002/ece3.3425 [doi]

AB - Strong founder effects resulting from human migration out of

Africa have led to geographic variation in single nucleotide polymorphisms (SNPs) and microsatellites (MS) of the malaria parasite, Plasmodium falciparum. This is particularly striking in South America where two major founder populations of P. falciparum have been identified that are presumed to have arisen from the transatlantic slave trade. Given the importance of the major variant surface antigen of the blood stages of P. falciparum as both a virulence factor and target of immunity, we decided to investigate the population genetics of the genes encoding "Plasmodium falciparum Erythrocyte Membrane Protein 1" (Pf EMP1) among several countries in South America, in order to evaluate the transmission patterns of malaria in this continent. Deep sequencing of the DBLalpha domain of var genes from 128 P. falciparum isolates from five locations in South America was completed using a 454 high throughput sequencing protocol. Striking geographic variation in var DBLalpha sequences, similar to that seen for SNPs and MS markers, was observed. Colombia and French Guiana had distinct var DBLalpha sequences, whereas Peru and Venezuela showed an admixture. The importance of such geographic variation to herd immunity and malaria vaccination is discussed.

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GR - R01 AI084156/AI/NIAID NIH HHS/United States
PT - Journal Article
DEP - 20171008
PL - England
TA - Ecol Evol
JT - Ecology and evolution
JID - 101566408
PMC - PMC5696401
OTO - NOTNLM
OT - Plasmodium falciparum
OT - Plasmodium falciparum Erythrocyte Membrane Protein 1
OT - evolutionary structure
OT - population genomics
OT - var genes
EDAT- 2017/12/01 06:00
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VI - 16

IP - 1

DP - 2017 Oct 16

TI - High prevalence of very-low Plasmodium falciparum and

Plasmodium vivax

parasitaemia carriers in the Peruvian Amazon: insights into local and occupational mobility-related transmission.

PG - 415

LID - 10.1186/s12936-017-2063-x [doi]

AB - BACKGROUND: The incidence of malaria due both to Plasmodium falciparum

and Plasmodium vivax in the Peruvian Amazon has risen in the past 5

years. This study tested the hypothesis that the maintenance and

emergence of malaria in hypoendemic regions such as Amazonia is

determined by submicroscopic and asymptomatic Plasmodium parasitaemia

carriers. The present study aimed to precisely quantify the rate of very-

low parasitaemia carriers in two sites of the Peruvian Amazon in relation

to transmission patterns of *P. vivax* and *P. falciparum* in this area.

METHODS: This study was carried out within the Amazonian-ICEMR longitudinal cohort. Blood samples were collected for light microscopy

diagnosis and packed red blood cell (PRBC) samples were analysed by qPCR.

Plasma samples were tested for total IgG reactivity against recombinant

PvMSP-10 and PfMSP-10 antigens by ELISA. Occupation and age 10 years and

greater were considered surrogates of occupation-related mobility. Risk

factors for *P. falciparum* and *P. vivax* infections detected by PRBC-qPCR

were assessed by multilevel logistic regression models.

RESULTS: Among

450 subjects, the prevalence of *P. vivax* by PRBC-PCR (25.1%) was sixfold

higher than that determined by microscopy (3.6%). The prevalence of *P.*

falciparum infection was 4.9% by PRBC-PCR and 0.2% by microscopy. More

than 40% of infections had parasitaemia under 5 parasites/ μ L.

Multivariate analysis for infections detected by PRBC-PCR showed that

participants with recent settlement in the study area (AOR 2.1; 95% CI 1.03:4.2), age \geq 30 years (AOR 3.3; 95% CI 1.6:6.9) and seropositivity to *P. vivax* (AOR 1.8; 95% CI 1.0:3.2) had significantly higher likelihood of *P. vivax* infection, while the odds of *P. falciparum* infection was higher for participants between 10 and 29 years (AOR 10.7; 95% CI 1.3:91.1) and with a previous *P. falciparum* infection (AOR 10.4; 95% CI 1.5:71.1). CONCLUSIONS: This study confirms the contrasting transmission patterns of *P. vivax* and *P. falciparum* in the Peruvian Amazon, with stable local transmission for *P. vivax* and the source of *P. falciparum* to the study villages dominated by very low parasitaemia carriers, age 10 years and older, who had travelled away from home for work and brought *P. falciparum* infection with them.

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LA - eng
GR - U19 AI089681/AI/NIAID NIH HHS/United States
PT - Journal Article
PT - Research Support, N.I.H., Extramural
PT - Research Support, Non-U.S. Gov't
DEP - 20171016
PL - England
TA - Malar J
JT - Malaria journal
JID - 101139802
SB - IM
MH - Adolescent
MH - Adult
MH - Asymptomatic Infections/*epidemiology
MH - Child
MH - Cross-Sectional Studies
MH - Female
MH - Humans
MH - Malaria, Falciparum/*epidemiology/parasitology
MH - Malaria, Vivax/*epidemiology/parasitology
MH - Male
MH - Multivariate Analysis
MH - Parasitemia/*epidemiology/parasitology
MH - Peru/epidemiology
MH - Plasmodium falciparum/*isolation & purification
MH - Plasmodium vivax/*isolation & purification
MH - Prevalence
MH - Seroepidemiologic Studies
MH - Young Adult
PMC - PMC5644076
OTO - NOTNLM
OT - Human mobility
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OT - Malaria
OT - Migration
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OT - Plasmodium falciparum
OT - Plasmodium vivax
OT - Sensitivity
OT - Serology
OT - Specificity
OT - Sub-microscopic
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PST - epubliish
S0 - Malar J. 2017 Oct 16;16(1):415. doi: 10.1186/s12936-017-2063-

x.

PMID- 28982155

OWN - NLM

STAT- MEDLINE

DCOM- 20171031

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IS - 1932-6203 (Electronic)

IS - 1932-6203 (Linking)

VI - 12

IP - 10

DP - 2017

TI - Loop-mediated isothermal DNA amplification for asymptomatic malaria

detection in challenging field settings: Technical performance and pilot

implementation in the Peruvian Amazon.

PG - e0185742

LID - 10.1371/journal.pone.0185742 [doi]

AB - BACKGROUND: Loop-mediated isothermal DNA amplification (LAMP) methodology

offers an opportunity for point-of-care (POC) molecular detection of

asymptomatic malaria infections. However, there is still little evidence

on the feasibility of implementing this technique for population

screenings in isolated field settings. METHODS: Overall, we recruited

1167 individuals from terrestrial ('road') and hydric ('riverine')

communities of the Peruvian Amazon for a cross-sectional survey to detect

asymptomatic malaria infections. The technical performance of LAMP was

evaluated in a subgroup of 503 samples, using real-time Polymerase Chain

Reaction (qPCR) as reference standard. The operational feasibility of

introducing LAMP testing in the mobile screening campaigns was assessed

based on field-suitability parameters, along with a pilot POC-LAMP assay

in a riverine community without laboratory infrastructure.

RESULTS: LAMP

had a sensitivity of 91.8% (87.7-94.9) and specificity of 91.9%

(87.8-95.0), and the overall accuracy was significantly better among

samples collected during road screenings than riverine communities

($p < 0.004$). LAMP-based diagnostic strategy was successfully implemented

within the field-team logistics and the POC-LAMP pilot in the

riverine
community allowed for a reduction in the turnaround time for
case
management, from 12–24 hours to less than 5 hours. Specimens
with
haemolytic appearance were regularly observed in riverine
screenings and
could help explaining the hindered performance/interpretation
of the LAMP
reaction in these communities. CONCLUSIONS: LAMP-based
molecular malaria
diagnosis can be deployed outside of reference laboratories,
providing
similar performance as qPCR. However, scale-up in remote field
settings
such as riverine communities needs to consider a number of
logistical
challenges (e.g. environmental conditions, labour-
intensiveness in large
population screenings) that can influence its optimal
implementation.

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LA - eng
PT - Journal Article
DEP - 20171005
PL - United States
TA - PLoS One
JT - PloS one
JID - 101285081
RN - 0 (DNA, Protozoan)
SB - IM
MH - Adolescent
MH - Child
MH - Child, Preschool
MH - DNA, Protozoan/*genetics
MH - Female
MH - Humans
MH - Malaria/*diagnosis/epidemiology/parasitology
MH - Male

MH - Peru/epidemiology
MH - Pilot Projects
MH - Plasmodium/genetics
MH - Prevalence
MH - Real-Time Polymerase Chain Reaction
PMC - PMC5628891
EDAT- 2017/10/06 06:00
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PHST- 2017/11/01 06:00 [medline]
AID - 10.1371/journal.pone.0185742 [doi]
AID - PONE-D-17-20461 [pii]
PST - epublish
S0 - PLoS One. 2017 Oct 5;12(10):e0185742. doi: 10.1371/
journal.pone.0185742.
eCollection 2017.

PMID- 28808240
OWN - NLM
STAT- MEDLINE
DCOM- 20190305
LR - 20200114
IS - 2045-2322 (Electronic)
IS - 2045-2322 (Linking)
VI - 7
IP - 1
DP - 2017 Aug 14
TI - Micro-epidemiology and spatial heterogeneity of *P. vivax*
parasitaemia in
riverine communities of the Peruvian Amazon: A multilevel
analysis.
PG - 8082
LID - 10.1038/s41598-017-07818-0 [doi]
AB - Malaria has steadily increased in the Peruvian Amazon over the
last five
years. This study aimed to determine the parasite prevalence
and micro-
geographical heterogeneity of *Plasmodium vivax* parasitaemia in
communities of the Peruvian Amazon. Four cross-sectional
active case
detection surveys were conducted between May and July 2015 in
four
riverine communities in Mazan district. Analysis of 2785
samples of 820
individuals nested within 154 households for *Plasmodium*
parasitaemia was
carried out using light microscopy and qPCR. The spatio-
temporal
distribution of *Plasmodium* parasitaemia, dominated by *P.*
vivax, was shown

to cluster at both household and community levels. Of enrolled individuals, 47% had at least one *P. vivax* parasitaemia and 10% *P.*

falciparum, by qPCR, both of which were predominantly sub-microscopic and asymptomatic. Spatial analysis detected significant clustering in three communities. Our findings showed that communities at small-to-moderate spatial scales differed in *P. vivax* parasite prevalence, and multilevel Poisson regression models showed that such differences were influenced by factors such as age, education, and location of households within high-risk clusters, as well as factors linked to a local micro-geographic context, such as travel and occupation. Complex transmission patterns were found to be related to human mobility among communities in the same micro-basin.

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GR - D43 TW007120/TW/FIC NIH HHS/United States

GR - D43 TW007393/TW/FIC NIH HHS/United States

GR - U19 AI089681/AI/NIAID NIH HHS/United States

PT - Journal Article

PT - Research Support, Non-U.S. Gov't

DEP - 20170814

PL - England

TA - Sci Rep

JT - Scientific reports

JID - 101563288

SB - IM

MH - Adolescent

MH - Adult

MH - Cluster Analysis

MH - Cross-Sectional Studies

MH - Female

MH - Geography

MH - Humans

MH - Malaria, Falciparum/epidemiology/parasitology

MH - Malaria, Vivax/*epidemiology/*parasitology

MH - Male

MH - Multilevel Analysis

MH - Parasitemia/*epidemiology/*parasitology

MH - Peru/epidemiology

MH - Plasmodium falciparum/isolation & purification

MH - Plasmodium vivax/*isolation & purification

MH - Prevalence

MH - Travel

MH - Young Adult

PMC - PMC5556029

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PST - epublish

S0 - Sci Rep. 2017 Aug 14;7(1):8082. doi: 10.1038/s41598-017-07818-0.

PMID- 28778210

OWN - NLM

STAT- MEDLINE

DCOM- 20180503

LR - 20200114

IS - 1475-2875 (Electronic)

IS - 1475-2875 (Linking)

VI - 16

IP - 1

DP - 2017 Aug 4

TI - Micro-heterogeneity of malaria transmission in the Peruvian

Amazon: a

baseline assessment underlying a population-based cohort study.

PG - 312

LID - 10.1186/s12936-017-1957-y [doi]

AB - BACKGROUND: Understanding the dynamics of malaria transmission in diverse

endemic settings is key for designing and implementing locally adapted

and sustainable control and elimination strategies. A

parasitological and

epidemiological survey was conducted in September–October

2012, as a

baseline underlying a 3-year population-based longitudinal cohort study.

The aim was to characterize malaria transmission patterns in two

contrasting ecological rural sites in the Peruvian Amazon, Lupuna (LUP),

a riverine environment, and Cahuide (CAH), associated with

road-linked

deforestation. METHODS: After a full population census, 1941 individuals

3 years and older (829 in LUP, 1112 in CAH) were interviewed, clinically

examined and had a blood sample taken for the detection of

malaria

parasites by microscopy and PCR. Species-specific parasite

prevalence was

estimated overall and by site. Multivariate logistic

regression models

assessed risk factors for parasite infection by PCR, while

SaTScan

detected spatial clusters of PCR-positive individuals within each site.

In addition, data from routine malaria surveillance in the period

2009–2012 were obtained. RESULTS: Parasite prevalence by PCR was higher

in CAH than in LUP for Plasmodium vivax (6.2% vs. 3.9%) and

for

Plasmodium falciparum (2.6% vs. 1.2%). Among PCR-confirmed

infections,

asymptomatic (Asy) parasite carriers were always more common

than

symptomatic (Sy) infections for P. vivax (Asy/Sy ratio: 2/1 in

LUP and

3.7/1 in CAH) and for P. falciparum (Asy/Sy ratio: 1.3/1 in

LUP and 4/1 in CAH). Sub-patent (Spat) infections also predominated over patent (Pat) infections for both species: *P. vivax* (Spat/Pat ratio: 2.8/1 in LUP and 3.7/1 in CAH) and *P. falciparum* malaria (Spat/Pat ratio: 1.9/1 in LUP and 26/0 in CAH). For CAH, age, gender and living in a household without electricity were significantly associated with *P. vivax* infection, while only age and living in a household with electricity was associated with *P. falciparum* infection. For LUP, only household overcrowding was associated with *P. falciparum* infection. The spatial analysis only identified well-defined clusters of *P. vivax* and *P. falciparum* infected individuals in CAH. Reported malaria incidence indicated that malaria transmission has long occurred in LUP with primarily seasonal patterns, and confirmed a malaria outbreak in CAH since May 2012.

CONCLUSIONS: This parasitological and epidemiological baseline assessment demonstrates that malaria transmission and parasite prevalence is heterogeneous in the Peruvian Amazon, and influenced by local socio-demographics and ecological contexts. Riverine and road construction/deforestation contexts must be taken into account in order to carry out effective anti-malaria control and elimination efforts.

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GR - D43 TW009343/TW/FIC NIH HHS/United States
GR - U19 AI089681/AI/NIAID NIH HHS/United States
PT - Journal Article
PT - Research Support, N.I.H., Extramural
DEP - 20170804
PL - England
TA - Malar J
JT - Malaria journal
JID - 101139802
SB - IM
MH - Adolescent
MH - Adult
MH - Aged
MH - Child
MH - Child, Preschool
MH - Cohort Studies
MH - Ecosystem
MH - Female
MH - Humans
MH - Logistic Models
MH - Malaria, Falciparum/*epidemiology/*transmission
MH - Malaria, Vivax/*epidemiology/*transmission

MH - Male
MH - Middle Aged
MH - Peru/epidemiology
MH - Plasmodium falciparum/physiology
MH - Plasmodium vivax/physiology
MH - Prevalence
MH - Risk Factors
MH - Young Adult
PMC - PMC5544973
OTO - NOTNLM
OT - Heterogeneity
OT - Hotspot
OT - Malaria
OT - PCR
OT - Peruvian Amazon
OT - Transmission
EDAT- 2017/08/06 06:00
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AID - 10.1186/s12936-017-1957-y [doi]
AID - 10.1186/s12936-017-1957-y [pii]
PST - epublish
S0 - Malar J. 2017 Aug 4;16(1):312. doi: 10.1186/s12936-017-1957-y.

PMID- 28671944
OWN - NLM
STAT- MEDLINE
DCOM- 20170726
LR - 20200114
IS - 1935-2735 (Electronic)
IS - 1935-2727 (Linking)
VI - 11
IP - 7
DP - 2017 Jul
TI - Predominance of asymptomatic and sub-microscopic infections characterizes the Plasmodium gametocyte reservoir in the Peruvian Amazon.
PG - e0005674
LID - 10.1371/journal.pntd.0005674 [doi]
AB - Malaria transmission requires that Anopheles mosquitoes ingest Plasmodium gametocyte stages circulating in the human bloodstream. In the context of malaria elimination, understanding the epidemiology of gametocytes relative to all Plasmodium infections and the contribution of asymptomatic and sub-microscopic parasite carriers to the gametocyte reservoir is necessary, especially in low endemic settings

with predominance of *P.vivax*. A 13-month longitudinal study was conducted in two communities (n = 1935 individuals) of Loreto Department, Peru, with five active screenings for Plasmodium infections and gametocyte stages by quantitative real-time PCR (qPCR) and reverse transcription (RT)-qPCR, respectively. Parasite prevalence by qPCR was 7.2% for *P.vivax* (n = 520/7235; range by survey 6.0%–8.1%) and 3.2% for *P.falciparum* (n = 235/7235; range by survey 0.4%–7.7%). Sub-microscopic infections accounted for 73.5% of *P.vivax* (range by survey 60%–89%) and almost the totality of *P.falciparum* cases. Gametocytes were found in 28.4% *P.vivax* infections (range by survey 18.7%–34.1%), with a peak of 61.5% in one community at the start of the transmission season. About 59.8% of all *P.vivax* gametocyte carriers were asymptomatic and 31.9% were sub-microscopic. Age patterns for gametocyte prevalence paralleled asexual stage infections and peaked among >15–25 year old individuals. Asexual parasite density was found to be the strongest predictor for *P.vivax* gametocyte presence in longitudinal multivariate analysis (odds ratio 2.33 [95% confidence interval 1.96, 2.78]; $P < 0.001$). Despite significant differences in seasonality patterns and *P.vivax* prevalence found at the local scale, sub-microscopic and asymptomatic infections predominate and contribute significantly to the gametocyte reservoir in different communities of the Peruvian Amazon. Control and elimination campaigns need sensitive tools to detect all infections that escape routine malaria surveillance, which may contribute to maintain transmission in the region.

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GR - U19 AI089681/AI/NIAID NIH HHS/United States
PT - Journal Article
DEP - 20170703
PL - United States
TA - PLoS Negl Trop Dis
JT - PLoS neglected tropical diseases
JID - 101291488
SB - IM
MH - Adolescent

MH - Adult
MH - Age Distribution
MH - Aged
MH - Aged, 80 and over
MH - Animals
MH - Anopheles
MH - Asymptomatic Infections/*epidemiology
MH - Carrier State/*epidemiology
MH - Child
MH - Child, Preschool
MH - Female
MH - Humans
MH - Infant
MH - Longitudinal Studies
MH - Malaria/*epidemiology/pathology
MH - Male
MH - Middle Aged
MH - Peru/epidemiology
MH - Plasmodium falciparum/genetics/*isolation & purification
MH - Plasmodium vivax/genetics/*isolation & purification
MH - Prospective Studies
MH - Real-Time Polymerase Chain Reaction
MH - Young Adult
PMC - PMC5510906
EDAT- 2017/07/04 06:00
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AID - 10.1371/journal.pntd.0005674 [doi]
AID - PNTD-D-16-02202 [pii]
PST - epublish
S0 - PLoS Negl Trop Dis. 2017 Jul 3;11(7):e0005674. doi:
10.1371/journal.pntd.0005674. eCollection 2017 Jul.

PMID- 28369085
OWN - NLM
STAT- MEDLINE
DCOM- 20170516
LR - 20220331
IS - 1935-2735 (Electronic)
IS - 1935-2727 (Linking)
VI - 11
IP - 4
DP - 2017 Apr
TI - Defining the next generation of Plasmodium vivax diagnostic
tests for
control and elimination: Target product profiles.
PG - e0005516
LID - 10.1371/journal.pntd.0005516 [doi]

AB - The global prevalence of malaria has decreased over the past fifteen years, but similar gains have not been realized against *Plasmodium vivax* because this species is less responsive to conventional malaria control interventions aimed principally at *P. falciparum*. Approximately half of all malaria cases outside of Africa are caused by *P. vivax*. This species places dormant forms in human liver that cause repeated clinical attacks without involving another mosquito bite. The diagnosis of acute patent *P. vivax* malaria relies primarily on light microscopy. Specific rapid diagnostic tests exist but typically perform relatively poorly compared to those for *P. falciparum*. Better diagnostic tests are needed for *P. vivax*. To guide their development, FIND, in collaboration with *P. vivax* experts, identified the specific diagnostic needs associated with this species and defined a series of three distinct target product profiles, each aimed at a particular diagnostic application: (i) point-of-care of acutely ill patients for clinical care purposes; (ii) point-of-care asymptomatic and otherwise sub-patent residents for public health purposes, e.g., mass screen and treat campaigns; and (iii) ultra-sensitive not point-of-care diagnosis for epidemiological research/surveillance purposes. This report presents and discusses the rationale for these *P. vivax*-specific diagnostic target product profiles. These contribute to the rational development of fit-for-purpose diagnostic tests suitable for the clinical management, control and elimination of *P. vivax* malaria.

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GR - 001/WHO_/World Health Organization/International
GR - U19 AI089702/AI/NIAID NIH HHS/United States
PT - Journal Article
PT - Research Support, Non-U.S. Gov't
DEP - 20170403
PL - United States
TA - PLoS Negl Trop Dis
JT - PLoS neglected tropical diseases
JID - 101291488
SB - IM
MH - Diagnostic Tests, Routine

MH - Humans
MH - Malaria, Falciparum/*diagnosis/parasitology/prevention & control
MH - Malaria, Vivax/*diagnosis/parasitology/prevention & control
MH - Plasmodium falciparum/*isolation & purification
MH - Plasmodium vivax/*isolation & purification
MH - *Point-of-Care Systems
MH - Species Specificity
PMC - PMC5391123
EDAT- 2017/04/04 06:00
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S0 - PLoS Negl Trop Dis. 2017 Apr 3;11(4):e0005516. doi: 10.1371/journal.pntd.0005516. eCollection 2017 Apr.

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OWN - NLM
STAT- MEDLINE
DCOM- 20170606
LR - 20191210
IS - 1475-2875 (Electronic)
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VI - 16
IP - 1
DP - 2017 Mar 24
TI - Analytical sensitivity of current best-in-class malaria rapid diagnostic tests.
PG - 128
LID - 10.1186/s12936-017-1780-5 [doi]
AB - BACKGROUND: Rapid diagnostic tests (RDTs) are today the most widely used method for malaria diagnosis and are recommended, alongside microscopy, for the confirmation of suspected cases before the administration of anti-malarial treatment. The diagnostic performance of RDTs, as compared to microscopy or PCR is well described but the actual analytical sensitivity of current best-in-class tests is poorly documented. This value is however a key performance indicator and a benchmark value needed to developed new RDTs of improved sensitivity. METHODS:

Thirteen RDTs

detecting either the Plasmodium falciparum histidine rich protein 2 (HRP2) or the plasmodial lactate dehydrogenase (pLDH) antigens were

selected from the best performing RDTs according to the WHO-FIND product testing programme. The analytical sensitivity of these products was

evaluated using a range of reference materials including P. falciparum

and Plasmodium vivax whole parasite samples as well as recombinant

proteins. RESULTS: The best performing HRP2-based RDTs could detect all

P. falciparum cultured samples at concentrations as low as 0.8 ng/mL of

HRP2. The limit of detection of the best performing pLDH-based RDT

specifically detecting P. vivax was 25 ng/mL of pLDH.

CONCLUSION: The

analytical sensitivity of P. vivax and Pan pLDH-based RDTs appears to

vary considerably from product to product, and improvement of the limit-

of-detection for P. vivax detecting RDTs is needed to match the

performance of HRP2 and Pf pLDH-based RDTs for P. falciparum. Different

assays using different reference materials produce different values for

antigen concentration in a given specimen, highlighting the need to

establish universal reference assays.

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LA - eng
PT - Comparative Study
PT - Evaluation Study
PT - Journal Article
DEP - 20170324
PL - England
TA - Malar J
JT - Malaria journal
JID - 101139802
RN - 0 (Antigens, Protozoan)
SB - IM
MH - Adult
MH - Antigens, Protozoan/analysis
MH - Chromatography, Affinity/*methods
MH - Diagnostic Tests, Routine/*methods
MH - Humans
MH - Malaria/*diagnosis
MH - Malaria, Falciparum
MH - Malaria, Vivax
MH - Plasmodium falciparum/immunology/isolation & purification
MH - Plasmodium vivax/immunology/*isolation & purification
MH - Sensitivity and Specificity
MH - Time Factors
PMC - PMC5366122
OTO - NOTNLM
OT - Analytical sensitivity
OT - HRP2
OT - Malaria rapid diagnostic test
OT - pLDH
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AID - 10.1186/s12936-017-1780-5 [doi]
AID - 10.1186/s12936-017-1780-5 [pii]
PST - epublish
S0 - Malar J. 2017 Mar 24;16(1):128. doi: 10.1186/
s12936-017-1780-5.

PMID- 28091560
OWN - NLM
STAT- MEDLINE
DCOM- 20181015
LR - 20181113
IS - 2045-2322 (Electronic)
IS - 2045-2322 (Linking)
VI - 7
DP - 2017 Jan 16
TI - Spatio-temporal analysis of malaria incidence in the Peruvian Amazon
Region between 2002 and 2013.
PG - 40350
LID - 10.1038/srep40350 [doi]
AB - Malaria remains a major public health problem in the Peruvian Amazon
where the persistence of high-risk transmission areas (hotspots) challenges the current malaria control strategies. This study aimed at identifying significant space-time clusters of malaria incidence in Loreto region 2002-2013 and to determine significant changes across years in relation to the control measures applied. Poisson regression and purely temporal, spatial, and space-time analyses were conducted. Three significantly different periods in terms of annual incidence rates (AIR) were identified, overlapping respectively with the pre-, during, and post- implementation control activities supported by PAMAFRO project. The most likely space-time clusters of malaria incidence for *P. vivax* and *P. falciparum* corresponded to the pre- and first two years of the PAMAFRO project and were situated in the northern districts of Loreto, while secondary clusters were identified in eastern and southern districts with

the latest onset and the shortest duration of PAMAFRO interventions.
Malaria in Loreto was highly heterogeneous at geographical level and over time. Importantly, the excellent achievements obtained during 5 years of intensified control efforts totally vanished in only 2 to 3 years after the end of the program, calling for sustained political and financial commitment for the success of malaria elimination as ultimate goal.

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PT - Journal Article
PT - Research Support, Non-U.S. Gov't
DEP - 20170116
PL - England
TA - Sci Rep
JT - Scientific reports
JID - 101563288
SB - IM
MH - Cluster Analysis
MH - Geography
MH - Humans
MH - Incidence
MH - Malaria/*epidemiology/parasitology
MH - Malaria, Falciparum/epidemiology/parasitology
MH - Malaria, Vivax/epidemiology/parasitology
MH - Peru/epidemiology
MH - Plasmodium falciparum/physiology
MH - Plasmodium vivax/physiology
MH - *Spatio-Temporal Analysis
PMC - PMC5238441
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AID - 10.1038/srep40350 [doi]
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S0 - Sci Rep. 2017 Jan 16;7:40350. doi: 10.1038/srep40350.

PMID- 27799639

OWN - NLM

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LR - 20190309

IS - 1476-1645 (Electronic)

IS - 0002-9637 (Linking)

VI - 95

IP - 6 Suppl

DP - 2016 Dec 28

TI - Epidemiology of Plasmodium vivax Malaria in Peru.

PG - 133-144

LID - 10.4269/ajtmh.16-0268 [doi]

AB - Malaria in Peru, dominated by Plasmodium vivax, remains a public health

problem. The 1990s saw newly epidemic malaria emerge, primarily in the

Loreto Department in the Amazon region, including areas near to Iquitos,

the capital city, but sporadic malaria transmission also occurred in the

1990s-2000s in both north-coastal Peru and the gold mining regions of

southeastern Peru. Although a Global Fund-supported intervention

(PAMAFRO, 2005-2010) was temporally associated with a decrease of malaria

transmission, from 2012 to the present, both P. vivax and Plasmodium

falciparum malaria cases have rapidly increased. The Peruvian Ministry of

Health continues to provide artemisinin-based combination therapy for

microscopy-confirmed cases of P. falciparum and chloroquine-primaquine

for P. vivax Malaria transmission continues in remote areas nonetheless,

where the mobility of humans and parasites facilitates continued

reintroduction outside of ongoing surveillance activities, which is

critical to address for future malaria control and elimination efforts.

Ongoing P. vivax research gaps in Peru include the following: identification of asymptomatic parasitemics, quantification of

the

contribution of patent and subpatent parasitemics to mosquito transmission, diagnosis of nonparasitemic hypnozoite carriers,

and

implementation of surveillance for potential emergence of

chloroquine-
and 8-aminoquinoline-resistant *P. vivax* Clinical trials of
tafenoquine in
Peru have been promising, and glucose-6-phosphate
dehydrogenase
deficiency in the region has not been observed to be a
limitation to its
use. Larger-scale challenges for *P. vivax* (and malaria in
general) in
Peru include logistical difficulties in accessing remote
riverine
populations, consequences of government policy and poverty
trends, and
obtaining international funding for malaria control and
elimination.

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LA - eng
GR - D43 TW007120/TW/FIC NIH HHS/United States
GR - D43 TW007393/TW/FIC NIH HHS/United States
GR - K24 AI068903/AI/NIAID NIH HHS/United States
GR - U19 AI089681/AI/NIAID NIH HHS/United States
PT - Journal Article
DEP - 20161031
PL - United States
TA - Am J Trop Med Hyg
JT - The American journal of tropical medicine and hygiene
JID - 0370507
RN - 0 (Antimalarials)
SB - IM
MH - Animals
MH - Anopheles/parasitology/physiology
MH - Antimalarials/administration & dosage/therapeutic use
MH - Endemic Diseases
MH - Humans
MH - Incidence
MH - Insect Vectors
MH - Malaria, Vivax/*epidemiology
MH - Peru/epidemiology
MH - Pharmacogenomic Variants
MH - *Plasmodium vivax/genetics
MH - Public Health

MH - Time Factors
PMC - PMC5201219
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AID - 10.4269/ajtmh.16-0268 [doi]
PST - ppublish
S0 - Am J Trop Med Hyg. 2016 Dec 28;95(6 Suppl):133-144. doi:
10.4269/ajtmh.16-0268. Epub 2016 Oct 31.

PMID- 27828953
OWN - NLM
STAT- PubMed-not-MEDLINE
LR - 20191120
IS - 1935-2735 (Electronic)
IS - 1935-2727 (Linking)
VI - 10
IP - 11
DP - 2016 Nov
TI - Correction: Colorimetric Detection of Plasmodium vivax in
Urine Using
MSP10 Oligonucleotides and Gold Nanoparticles.
PG - e0005143
LID - 10.1371/journal.pntd.0005143 [doi]
AB - [This corrects the article DOI: 10.1371/
journal.pntd.0005029.].
FAU - Alnasser, Yossef
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LA - eng
PT - Published Erratum
DEP - 20161109
PL - United States
TA - PLoS Negl Trop Dis
JT - PLoS neglected tropical diseases
JID - 101291488
EFR - PLoS Negl Trop Dis. 2016 Oct 5;10 (10):e0005029. PMID:
27706158
PMC - PMC5102355
EDAT- 2016/11/10 06:00
MHDA- 2016/11/10 06:01
CRDT- 2016/11/10 06:00
PHST- 2016/11/10 06:00 [entrez]
PHST- 2016/11/10 06:00 [pubmed]
PHST- 2016/11/10 06:01 [medline]
AID - 10.1371/journal.pntd.0005143 [doi]
AID - PNTD-D-16-01982 [pii]
PST - epublish
S0 - PLoS Negl Trop Dis. 2016 Nov 9;10(11):e0005143. doi:
10.1371/journal.pntd.0005143. eCollection 2016 Nov.

PMID- 27706158
OWN - NLM
STAT- MEDLINE
DCOM- 20170525
LR - 20210109
IS - 1935-2735 (Electronic)
IS - 1935-2727 (Linking)
VI - 10
IP - 10
DP - 2016 Oct
TI - Colorimetric Detection of Plasmodium vivax in Urine Using
MSP10
Oligonucleotides and Gold Nanoparticles.
PG - e0005029
LID - 10.1371/journal.pntd.0005029 [doi]
AB - Plasmodium vivax is the most prevalent cause of human malaria
in the
world and can lead to severe disease with high potential for
relapse. Its
genetic and geographic diversities make it challenging to
control. P.
vivax is understudied and to achieve control of malaria in
endemic areas,
a rapid, accurate, and simple diagnostic tool is necessary. In
this pilot
study, we found that a colorimetric system using AuNPs and
MSP10 DNA
detection in urine can provide fast, easy, and inexpensive
identification
of P. vivax. The test exhibited promising sensitivity (84%),
high

specificity (97%), and only mild cross-reactivity with *P. falciparum* (21%). It is simple to use, with a visible color change that negates the need for a spectrometer, making it suitable for use in austere conditions. Using urine eliminates the need for finger-prick, increasing both the safety profile and patient acceptance of this model.

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LA - eng
GR - MR/K007467/1/MRC_/Medical Research Council/United Kingdom
GR - U19 AI089681/AI/NIAID NIH HHS/United States
GR - U19 AI089702/AI/NIAID NIH HHS/United States
PT - Journal Article
DEP - 20161005
PL - United States
TA - PLoS Negl Trop Dis
JT - PLoS neglected tropical diseases
JID - 101291488
RN - 0 (Antigens, Protozoan)
RN - 0 (DNA, Protozoan)
RN - 0 (Oligonucleotides)
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RN - 7440-57-5 (Gold)
SB - IM
EIN - PLoS Negl Trop Dis. 2016 Nov 9;10 (11):e0005143. PMID:
27828953
MH - Antigens, Protozoan/genetics
MH - Colorimetry/economics/*methods/standards
MH - Cross Reactions
MH - DNA, Protozoan/urine
MH - Gold
MH - Humans
MH - Malaria, Vivax/*diagnosis/parasitology/urine
MH - Mass Screening
MH - *Metal Nanoparticles
MH - Microscopy
MH - *Oligonucleotides
MH - Parasitemia/diagnosis/parasitology
MH - Pilot Projects
MH - Plasmodium vivax/genetics/*isolation & purification/
ultrastructure
MH - Protozoan Proteins/genetics
MH - Sensitivity and Specificity
MH - Urine/*parasitology
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S0 - PLoS Negl Trop Dis. 2016 Oct 5;10(10):e0005029. doi:
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OWN - NLM
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IS - 1546-1718 (Electronic)
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TI - Population genomics studies identify signatures of global
dispersal and
drug resistance in *Plasmodium vivax*.
PG - 953-8
LID - 10.1038/ng.3588 [doi]
AB - *Plasmodium vivax* is a major public health burden, responsible
for the
majority of malaria infections outside Africa. We explored the
impact of
demographic history and selective pressures on the *P. vivax*
genome by
sequencing 182 clinical isolates sampled from 11 countries
across the
globe, using hybrid selection to overcome human DNA
contamination. We
confirmed previous reports of high genomic diversity in *P.*
vivax relative
to the more virulent *Plasmodium falciparum* species; regional
populations
of *P. vivax* exhibited greater diversity than the global *P.*
falciparum
population, indicating a large and/or stable population.
Signals of
natural selection suggest that *P. vivax* is evolving in
response to
antimalarial drugs and is adapting to regional differences in
the human
host and the mosquito vector. These findings underline the
variable
epidemiology of this parasite species and highlight the
breadth of
approaches that may be required to eliminate *P. vivax*
globally.

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GR - D43 TW007393/TW/FIC NIH HHS/United States
GR - T32 AI007180/AI/NIAID NIH HHS/United States
GR - D43 TW007120/TW/FIC NIH HHS/United States
GR - U19 AI089681/AI/NIAID NIH HHS/United States
GR - U19 AI089686/AI/NIAID NIH HHS/United States
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PT - Journal Article
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TA - Nat Genet
JT - Nature genetics
JID - 9216904
RN - 0 (Antimalarials)
RN - 0 (Genetic Markers)
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CIN - Nat Genet. 2016 Jul 27;48(8):825-6. PMID: 27463397
MH - Antimalarials/pharmacology
MH - Drug Resistance/*genetics
MH - Genetic Markers/*genetics
MH - Humans
MH - Malaria, Vivax/drug therapy/genetics/*parasitology
MH - Metagenomics/*methods
MH - Plasmodium vivax/drug effects/*genetics/pathogenicity
MH - Selection, Genetic/drug effects/*genetics
MH - Transcriptome/*genetics
PMC - PMC5347536
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IS - 1935-2735 (Electronic)
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DP - 2016 Jan
TI - Population Genetics of Plasmodium vivax in the Peruvian
Amazon.
PG - e0004376
LID - 10.1371/journal.pntd.0004376 [doi]
AB - BACKGROUND: Characterizing the parasite dynamics and
population structure
provides useful information to understand the dynamic of
transmission and
to better target control interventions. Despite considerable
efforts for
its control, vivax malaria remains a major health problem in
Peru. In
this study, we have explored the population genetics of
Plasmodium vivax
isolates from Iquitos, the main city in the Peruvian Amazon,
and 25
neighbouring peri-urban as well as rural villages along the
Iquitos-Nauta
Road. METHODOLOGY/ RESULTS: From April to December 2008, 292
P. vivax
isolates were collected and successfully genotyped using 14
neutral
microsatellites. Analysis of the molecular data revealed a
similar
proportion of monoclonal and polyclonal infections in urban
areas, while
in rural areas monoclonal infections were predominant (p =
0.002).
Multiplicity of infection was higher in urban (MOI = 1.5-2)
compared to
rural areas (MOI = 1) (p = 0.003). The level of genetic

diversity was

similar in all areas ($H_e = 0.66-0.76$, $p = 0.32$) though genetic differentiation between areas was substantial ($PHIPT = 0.17$, $p < 0.0001$).

Principal coordinate analysis showed a marked differentiation between

parasites from urban and rural areas. Linkage disequilibrium was detected

in all the areas ($[Formula: see text] = 0.08-0.49$, for all $p < 0.0001$).

Gene flow among the areas was established through Bayesian analysis of migration models. Recent bottleneck events were detected in 4 areas and a

recent parasite expansion in one of the isolated areas. In total, 87

unique haplotypes grouped in 2 or 3 genetic clusters described a sub-

structured parasite population. CONCLUSION/SIGNIFICANCE: Our study shows

a sub-structured parasite population with clonal propagation, with most

of its components recently affected by bottleneck events.

Iquitos city is

the main source of parasite spreading for all the peripheral study areas.

The routes of transmission and gene flow and the reduction of the

parasite population described are important from the public health

perspective as well for the formulation of future control policies.

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PT – Journal Article
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DEP – 20160114
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TA – PLoS Negl Trop Dis
JT – PLoS neglected tropical diseases

JID - 101291488
SB - IM
MH - Genetic Linkage
MH - Genetic Variation
MH - Genotype
MH - Microsatellite Repeats/genetics
MH - Peru
MH - Plasmodium vivax/*genetics
PMC - PMC4713096
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DCOM- 20160523
LR - 20181113
IS - 1932-6203 (Electronic)
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VI - 10
IP - 9
DP - 2015
TI - Hotspots of Malaria Transmission in the Peruvian Amazon: Rapid
Assessment
through a Parasitological and Serological Survey.
PG - e0137458
LID - 10.1371/journal.pone.0137458 [doi]
AB - BACKGROUND: With low and markedly seasonal malaria
transmission,
increasingly sensitive tools for better stratifying the risk
of infection
and targeting control interventions are needed. A cross-
sectional survey
to characterize the current malaria transmission patterns,
identify
hotspots, and detect recent changes using parasitological and
serological
measures was conducted in three sites of the Peruvian Amazon.
MATERIAL
AND METHODS: After full census of the study population, 651
participants
were interviewed, clinically examined and had a blood sample
taken for

the detection of malaria parasites (microscopy and PCR) and antibodies against *P. vivax* (PvMSP119, PvAMA1) and *P. falciparum* (PfGLURP, PfAMA1) antigens by ELISA. Risk factors for malaria infection (positive PCR) and malaria exposure (seropositivity) were assessed by multivariate survey logistic regression models. Age-specific seroprevalence was analyzed using a reversible catalytic conversion model based on maximum likelihood for generating seroconversion rates (SCR, λ). SaTScan was used to detect spatial clusters of serology-positive individuals within each site. RESULTS: The overall parasite prevalence by PCR was low, i.e. 3.9% for *P. vivax* and 6.7% for *P. falciparum*, while the seroprevalence was substantially higher, 33.6% for *P. vivax* and 22.0% for *P. falciparum*, with major differences between study sites. Age and location (site) were significantly associated with *P. vivax* exposure; while location, age and outdoor occupation were associated with *P. falciparum* exposure. *P. falciparum* seroprevalence curves showed a stable transmission throughout time, while for *P. vivax* transmission was better described by a model with two SCRs. The spatial analysis identified well-defined clusters of *P. falciparum* seropositive individuals in two sites, while it detected only a very small cluster of *P. vivax* exposure. CONCLUSION: The use of a single parasitological and serological malaria survey has proven to be an efficient and accurate method to characterize the species specific heterogeneity in malaria transmission at micro-geographical level as well as to identify recent changes in transmission.

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PT - Research Support, Non-U.S. Gov't
DEP - 20150910
PL - United States
TA - PLoS One
JT - PloS one
JID - 101285081
SB - IM
MH - Adolescent
MH - Adult
MH - Child
MH - Factor Analysis, Statistical
MH - Geography
MH - Humans
MH - Incidence
MH - Malaria, Falciparum/*blood/epidemiology/parasitology/
*transmission
MH - Malaria, Vivax/*blood/epidemiology/parasitology/*transmission
MH - Multivariate Analysis
MH - Peru/epidemiology
MH - Plasmodium falciparum
MH - Plasmodium vivax
MH - Prevalence
MH - Risk Factors
MH - Seroepidemiologic Studies
MH - Species Specificity
MH - Young Adult
PMC - PMC4565712
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DCOM- 20151127
LR - 20190309
IS - 1476-1645 (Electronic)
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VI - 93
IP - 3 Suppl
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TI - Malaria Diagnosis Across the International Centers of Excellence for Malaria Research: Platforms, Performance, and Standardization.
PG - 99-109
LID - 10.4269/ajtmh.15-0004 [doi]
AB - Diagnosis is "the act of identifying a disease, illness, or problem by examining someone or something." When an individual with acute fever presents for clinical attention, accurate diagnosis leading to specific, prompt treatment often saves lives. As applied to malaria, not only individual patient diagnosis is important but also assessing population-level malaria prevalence using appropriate diagnostic methods is essential for public health purposes. Similarly, identifying (diagnosing) fake antimalarial medications prevents the use of counterfeit drugs that can have disastrous effects. Therefore, accurate diagnosis in broad areas related to malaria is fundamental to improving health-care delivery, informing funding agencies of current malaria situations, and aiding in the prioritization of regional and national control efforts. The International Centers of Excellence for Malaria Research (ICEMR), supported by the U.S. National Institute of Allergy and Infectious Diseases, has collaborated on global efforts to improve malaria diagnostics by working to harmonize and systematize procedures across different regions where endemicity and financial resources vary. In this article, the different diagnostic methods used across each ICEMR are reviewed and challenges are discussed.
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GR - U19AI089680/AI/NIAID NIH HHS/United States
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GR - U19AI089696/AI/NIAID NIH HHS/United States
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GR - U19AI089681/AI/NIAID NIH HHS/United States
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GR - U19 AI089686/AI/NIAID NIH HHS/United States
GR - U19 AI089688/AI/NIAID NIH HHS/United States
GR - U19 AI089683/AI/NIAID NIH HHS/United States
GR - U19 AI089672/AI/NIAID NIH HHS/United States
GR - U19 AI089702/AI/NIAID NIH HHS/United States
GR - U19AI089686/AI/NIAID NIH HHS/United States
PT - Journal Article
PT - Research Support, N.I.H., Extramural
PT - Review
DEP - 20150810
PL - United States
TA - Am J Trop Med Hyg
JT - The American journal of tropical medicine and hygiene
JID - 0370507
SB - IM
MH - Biomedical Research
MH - Drug Resistance
MH - Humans
MH - International Cooperation
MH - Malaria/*diagnosis
MH - Malaria, Falciparum/diagnosis
MH - Malaria, Vivax/diagnosis
MH - Plasmodium falciparum
MH - Plasmodium vivax
PMC - PMC4574279
EDAT- 2015/08/12 06:00
MHDA- 2015/12/15 06:00

CRDT- 2015/08/12 06:00
PHST- 2015/01/02 00:00 [received]
PHST- 2015/06/23 00:00 [accepted]
PHST- 2015/08/12 06:00 [entrez]
PHST- 2015/08/12 06:00 [pubmed]
PHST- 2015/12/15 06:00 [medline]
AID - 10.4269/ajtmh.15-0004 [doi]
PST - ppublish
S0 - Am J Trop Med Hyg. 2015 Sep;93(3 Suppl):99-109. doi:
10.4269/ajtmh.15-0004. Epub 2015 Aug 10.

PMID- 26259945
OWN - NLM
STAT- MEDLINE
DCOM- 20151127
LR - 20190309
IS - 1476-1645 (Electronic)
IS - 0002-9637 (Linking)
VI - 93
IP - 3 Suppl
DP - 2015 Sep
TI - Malaria Molecular Epidemiology: Lessons from the International
Centers of
Excellence for Malaria Research Network.
PG - 79-86
LID - 10.4269/ajtmh.15-0005 [doi]
AB - Molecular epidemiology leverages genetic information to study
the risk
factors that affect the frequency and distribution of malaria
cases. This
article describes molecular epidemiologic investigations
currently being
carried out by the International Centers of Excellence for
Malaria
Research (ICEMR) network in a variety of malaria-endemic
settings. First,
we discuss various novel approaches to understand malaria
incidence and
gametocytemia, focusing on Plasmodium falciparum and
Plasmodium vivax.
Second, we describe and compare different parasite genotyping
methods
commonly used in malaria epidemiology and population genetics.
Finally,
we discuss potential applications of molecular epidemiological
tools and
methods toward malaria control and elimination efforts.
CI - (c) The American Society of Tropical Medicine and Hygiene.
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GR - U19 AI089676/AI/NIAID NIH HHS/United States
GR - U19 AI089681/AI/NIAID NIH HHS/United States
GR - U19 AI089674/AI/NIAID NIH HHS/United States
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GR - U19 AI089672/AI/NIAID NIH HHS/United States
GR - U19 AI089702/AI/NIAID NIH HHS/United States
PT - Journal Article
PT - Research Support, N.I.H., Extramural
DEP - 20150810
PL - United States
TA - Am J Trop Med Hyg
JT - The American journal of tropical medicine and hygiene
JID - 0370507
SB - IM
MH - Gene Flow/genetics
MH - Genetics, Population
MH - Genotyping Techniques
MH - Humans
MH - International Cooperation
MH - Malaria/*epidemiology/*genetics/prevention & control/
transmission
MH - Malaria, Falciparum/epidemiology/genetics
MH - Malaria, Vivax/epidemiology/genetics
MH - Molecular Epidemiology

MH - Plasmodium/*genetics
MH - Plasmodium falciparum/genetics
MH - Plasmodium vivax/genetics
PMC - PMC4574277
EDAT- 2015/08/12 06:00
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AID - 10.4269/ajtmh.15-0005 [doi]
PST - ppublish
S0 - Am J Trop Med Hyg. 2015 Sep;93(3 Suppl):79-86. doi:
10.4269/ajtmh.15-0005. Epub 2015 Aug 10.

PMID- 26293655

OWN - NLM

STAT- MEDLINE

DCOM- 20160511

LR - 20220129

IS - 1475-2875 (Electronic)

IS - 1475-2875 (Linking)

VI - 14

DP - 2015 Aug 21

TI - Assessment of an automated capillary system for Plasmodium vivax

microsatellite genotyping.

PG - 326

LID - 10.1186/s12936-015-0842-9 [doi]

AB - BACKGROUND: Several platforms have been used to generate the primary data

for microsatellite analysis of malaria parasite genotypes.

Each has

relative advantages but share a limitation of being time- and cost-

intensive. A commercially available automated capillary gel cartridge

system was assessed in the microsatellite analysis of

Plasmodium vivax

diversity in the Peruvian Amazon. METHODS: The reproducibility and

accuracy of a commercially-available automated capillary system, QIAxcel,

was assessed using a sequenced PCR product of 227 base pairs.

This

product was measured 42 times, then 27 P. vivax samples from Peruvian

Amazon subjects were analyzed with this instrument using five informative

microsatellites. Results from the QIAxcel system were compared with a

Sanger-type sequencing machine, the ABI PRISM((R)) 3100

Genetic Analyzer.

RESULTS: Significant differences were seen between the sequenced amplicons and the results from the QIAxcel instrument. Different runs, plates and cartridges yielded significantly different results. Additionally, allele size decreased with each run by 0.045, or 1 bp, every three plates. QIAxcel and ABI PRISM systems differed in giving different values than those obtained by ABI PRISM, and too many (i.e. inaccurate) alleles per locus were also seen with the automated instrument. CONCLUSIONS: While *P. vivax* diversity could generally be estimated using an automated capillary gel cartridge system, the data demonstrate that this system is not sufficiently precise for reliably identifying parasite strains via microsatellite analysis. This conclusion reached after systematic analysis was due both to inadequate precision and poor reproducibility in measuring PCR product size.

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GR - R01 AI067727/AI/NIAID NIH HHS/United States
GR - D43TW007120/TW/FIC NIH HHS/United States
GR - K24AI068903/AI/NIAID NIH HHS/United States
GR - U19AI089681/AI/NIAID NIH HHS/United States
GR - R01AI067727/AI/NIAID NIH HHS/United States
GR - U19 AI089681/AI/NIAID NIH HHS/United States
GR - D43 TW007120/TW/FIC NIH HHS/United States
GR - K24 AI068903/AI/NIAID NIH HHS/United States
GR - MR/K007467/1/MRC_/Medical Research Council/United Kingdom
PT - Journal Article
PT - Research Support, N.I.H., Extramural
DEP - 20150821
PL - England
TA - Malar J
JT - Malaria journal
JID - 101139802
RN - 0 (DNA, Protozoan)
SB - IM
MH - DNA, Protozoan/genetics
MH - Humans
MH - Malaria, Vivax/epidemiology/*parasitology

MH - Microsatellite Repeats/*genetics
MH - Molecular Epidemiology
MH - Molecular Typing/*methods
MH - Peru/epidemiology
MH - Plasmodium vivax/*genetics
MH - Reproducibility of Results
PMC - PMC4546211
EDAT- 2015/08/22 06:00
MHDA- 2016/05/12 06:00
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PHST- 2015/08/22 06:00 [entrez]
PHST- 2015/08/22 06:00 [pubmed]
PHST- 2016/05/12 06:00 [medline]
AID - 10.1186/s12936-015-0842-9 [doi]
AID - 10.1186/s12936-015-0842-9 [pii]
PST - epublish
S0 - Malar J. 2015 Aug 21;14:326. doi: 10.1186/s12936-015-0842-9.

PMID- 26125189
OWN - NLM
STAT- MEDLINE
DCOM- 20160520
LR - 20210109
IS - 1935-2735 (Electronic)
IS - 1935-2727 (Linking)
VI - 9
IP - 6
DP - 2015
TI - Plasmodium vivax Diversity and Population Structure across
Four
Continents.
PG - e0003872
LID - 10.1371/journal.pntd.0003872 [doi]
AB - Plasmodium vivax is the geographically most widespread human
malaria
parasite. To analyze patterns of microsatellite diversity and
population
structure across countries of different transmission
intensity,
genotyping data from 11 microsatellite markers was either
generated or
compiled from 841 isolates from four continents collected in
1999-2008.
Diversity was highest in South-East Asia (mean allelic
richness
10.0-12.8), intermediate in the South Pacific (8.1-9.9)
Madagascar and
Sudan (7.9-8.4), and lowest in South America and Central Asia
(5.5-7.2).
A reduced panel of only 3 markers was sufficient to identify
approx. 90%
of all haplotypes in South Pacific, African and SE-Asian

populations, but only 60–80% in Latin American populations, suggesting that typing of 2–6 markers, depending on the level of endemicity, is sufficient for epidemiological studies. Clustering analysis showed distinct clusters in Peru and Brazil, but little sub-structuring was observed within Africa, SE-Asia or the South Pacific. Isolates from Uzbekistan were exceptional, as a near-clonal parasite population was observed that was clearly separated from all other populations ($F_{ST} > 0.2$). Outside Central Asia F_{ST} values were highest (0.11–0.16) between South American and all other populations, and lowest (0.04–0.07) between populations from South-East Asia and the South Pacific. These comparisons between *P. vivax* populations from four continents indicated that not only transmission intensity, but also geographical isolation affect diversity and population structure. However, the high effective population size results in slow changes of these parameters. This persistency must be taken into account when assessing the impact of control programs on the genetic structure of parasite populations.

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LA - eng
GR - WT_/Wellcome Trust/United Kingdom
GR - U19 AI089686/AI/NIAID NIH HHS/United States
GR - WT100066MA/WT_/Wellcome Trust/United Kingdom
PT - Journal Article
PT - Research Support, Non-U.S. Gov't
DEP - 20150630
PL - United States
TA - PLoS Negl Trop Dis
JT - PLoS neglected tropical diseases
JID - 101291488
SB - IM
MH - Africa/epidemiology
MH - Alleles
MH - Americas/epidemiology
MH - Asia/epidemiology
MH - Cluster Analysis
MH - Cohort Studies
MH - *Genetic Variation
MH - Genetics, Population
MH - Genotype
MH - Geography
MH - Haplotypes
MH - Humans
MH - Linkage Disequilibrium
MH - Madagascar/epidemiology
MH - Malaria, Vivax/epidemiology/*parasitology/transmission
MH - Microsatellite Repeats/*genetics
MH - Plasmodium vivax/*genetics/isolation & purification
PMC - PMC4488360

EDAT- 2015/07/01 06:00
MHDA- 2016/05/21 06:00
CRDT- 2015/07/01 06:00
PHST- 2014/09/24 00:00 [received]
PHST- 2015/06/02 00:00 [accepted]
PHST- 2015/07/01 06:00 [entrez]
PHST- 2015/07/01 06:00 [pubmed]
PHST- 2016/05/21 06:00 [medline]
AID - 10.1371/journal.pntd.0003872 [doi]
AID - PNTD-D-14-01665 [pii]
PST - epublish
S0 - PLoS Negl Trop Dis. 2015 Jun 30;9(6):e0003872. doi:
10.1371/journal.pntd.0003872. eCollection 2015.

PMID- 25948081
OWN - NLM
STAT- MEDLINE
DCOM- 20160125
LR - 20181113
IS - 1756-3305 (Electronic)
IS - 1756-3305 (Linking)
VI - 8
DP - 2015 May 7
TI - Modelling the potential of focal screening and treatment as
elimination
strategy for Plasmodium falciparum malaria in the Peruvian
Amazon Region.
PG - 261
LID - 10.1186/s13071-015-0868-4 [doi]
AB - BACKGROUND: Focal screening and treatment (FSAT) of malaria
infections
has recently been introduced in Peru to overcome the inherent
limitations
of passive case detection (PCD) and further decrease the
malaria burden.
Here, we used a relatively straightforward mathematical model
to assess
the potential of FSAT as elimination strategy for Plasmodium
falciparum
malaria in the Peruvian Amazon Region. METHODS: A baseline
model was
developed to simulate a scenario with seasonal malaria
transmission and
the effect of PCD and treatment of symptomatic infections on
the P.
falciparum malaria transmission in a low endemic area of the
Peruvian
Amazon. The model was then adjusted to simulate intervention
scenarios
for predicting the long term additional impact of FSAT on P.
falciparum
malaria prevalence and incidence. Model parameterization was
done using
data from a cohort study in a rural Amazonian community as

well as

published transmission parameters from previous studies in similar areas.

The effect of FSAT timing and frequency, using either microscopy or a supposed field PCR, was assessed on both predicted incidence and

prevalence rates. RESULTS: The intervention model indicated that the

addition of FSAT to PCD significantly reduced the predicted *P. falciparum*

incidence and prevalence. The strongest reduction was observed when three

consecutive FSAT were implemented at the beginning of the low transmission season, and if malaria diagnosis was done with PCR. Repeated

interventions for consecutive years (10 years with microscopy or 5 years

with PCR), would allow reaching near to zero incidence and prevalence

rates. CONCLUSIONS: The addition of FSAT interventions to PCD may enable

to reach *P. falciparum* elimination levels in low endemic areas of the

Amazon Region, yet the progression rates to those levels may vary

substantially according to the operational criteria used for the

intervention.

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GR - R01 AI64831/AI/NIAID NIH HHS/United States
PT - Journal Article
PT - Research Support, N.I.H., Extramural
PT - Research Support, Non-U.S. Gov't
DEP - 20150507
PL - England
TA - Parasit Vectors
JT - Parasites & vectors
JID - 101462774
RN - 0 (Antimalarials)
SB - IM
MH - Antimalarials/*therapeutic use
MH - Cohort Studies
MH - Female
MH - Humans
MH - Malaria, Falciparum/drug therapy/epidemiology/parasitology/
*prevention &
control
MH - Male
MH - Models, Theoretical
MH - Peru/epidemiology
MH - Plasmodium falciparum/drug effects/genetics/isolation &
purification/physiology
MH - Rural Population
PMC - PMC4429469
EDAT- 2015/05/08 06:00
MHDA- 2016/01/26 06:00
CRDT- 2015/05/08 06:00
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PHST- 2015/04/21 00:00 [accepted]
PHST- 2015/05/08 06:00 [entrez]
PHST- 2015/05/08 06:00 [pubmed]
PHST- 2016/01/26 06:00 [medline]
AID - 10.1186/s13071-015-0868-4 [doi]
AID - 10.1186/s13071-015-0868-4 [pii]
PST - epublish
S0 - Parasit Vectors. 2015 May 7;8:261. doi: 10.1186/
s13071-015-0868-4.

PMID- 25897626
OWN - NLM
STAT- MEDLINE
DCOM- 20160112
LR - 20181113
IS - 1080-6059 (Electronic)
IS - 1080-6040 (Linking)

VI - 21
IP - 5
DP - 2015 May
TI - Molecular Epidemiology of Plasmodium falciparum Malaria
Outbreak, Tumbes,
Peru, 2010-2012.
PG - 797-803
LID - 10.3201/eid2105.141427 [doi]
AB - During 2010-2012, an outbreak of 210 cases of malaria occurred
in Tumbes,
in the northern coast of Peru, where no Plasmodium falciparum
malaria
case had been reported since 2006. To identify the source of
the parasite
causing this outbreak, we conducted a molecular epidemiology
investigation. Microsatellite typing showed an identical
genotype in all
54 available isolates. This genotype was also identical to
that of
parasites isolated in 2010 in the Loreto region of the
Peruvian Amazon
and closely related to clonot B, a parasite lineage previously
reported
in the Amazon during 1998-2000. These findings are consistent
with travel
history of index case-patients. DNA sequencing revealed
mutations in the
Pfdhfr, Pfdhps, Pfcrt, and Pfmdr1 loci, which are strongly
associated
with resistance to chloroquine and sulfadoxine/pyrimethamine,
and
deletion of the Pfhrp2 gene. These results highlight the need
for timely
molecular epidemiology investigations to trace the parasite
source during
malaria reintroduction events.

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LA - eng
GR - D43 TW007393/TW/FIC NIH HHS/United States
GR - 2D43 TW007393/TW/FIC NIH HHS/United States
PT - Historical Article
PT - Journal Article
PT - Research Support, N.I.H., Extramural
PT - Research Support, U.S. Gov't, Non-P.H.S.
PL - United States
TA - Emerg Infect Dis
JT - Emerging infectious diseases
JID - 9508155
RN - 0 (Antimalarials)
RN - 0 (DNA, Protozoan)
RN - 0 (Protozoan Proteins)
SB - IM
MH - Alleles
MH - Antimalarials/pharmacology
MH - DNA, Protozoan
MH - *Disease Outbreaks
MH - Drug Resistance
MH - Gene Deletion
MH - Genotype
MH - Geography
MH - Haplotypes
MH - History, 21st Century
MH - Humans
MH - Malaria, Falciparum/*epidemiology/history/*parasitology
MH - Microsatellite Repeats
MH - Molecular Epidemiology
MH - Peru/epidemiology
MH - Plasmodium falciparum/drug effects/*genetics
MH - Protozoan Proteins/genetics
PMC - PMC4412223
OTO - NOTNLM
OT - Falciparum malaria
OT - Peru
OT - Plasmodium
OT - malaria
OT - microsatellite markers
OT - parasites
EDAT- 2015/04/22 06:00
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PHST- 2015/04/22 06:00 [pubmed]
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AID - 10.3201/eid2105.141427 [doi]
PST - ppublish
S0 - Emerg Infect Dis. 2015 May;21(5):797-803. doi: 10.3201/
eid2105.141427.

PMID- 25903826
OWN - NLM
STAT- MEDLINE
DCOM- 20160128
LR - 20181113
IS - 1475-2875 (Electronic)
IS - 1475-2875 (Linking)
VI - 14
DP - 2015 Apr 24
TI - Plasmodium vivax malaria at households: spatial clustering and risk factors in a low endemicity urban area of the northwestern Peruvian coast.
PG - 176
LID - 10.1186/s12936-015-0670-y [doi]
AB - BACKGROUND: Peru has presented a decreasing malaria trend during the last decade, particularly in areas on northwestern coast; however, a limited number of cases continues to be reported yearly mainly in malaria hotspots. METHODS: A two-phase study was conducted to identify spatial and temporal clusters of incident Plasmodium vivax malaria, as well as to determine risk factors associated with households (HH) presenting P. vivax malaria episodes in an urban area of the northwestern Peruvian Coast from June 2008 to May 2010. In the first stage, a full census of the study population was conducted, including geo-referencing of reported P. vivax episodes. In the second stage, a population-based case-control study allowed the identification of risk factors associated with HHs reporting episodes. A total of 117 case HHs with reported P. vivax and 117 control HHs without malaria episodes were assessed. A semi-structured questionnaire was used to interview the head of households and to collect data on HH location and structure, availability of public services, preventive malaria measures, family member with outdoor

occupation (farmer, moto-taxi driver), and other HH characteristics. Univariate and multivariate logistic regression analyses were performed to determine case-HH risk factors. SaTScan was used to detect spatial and temporal P. vivax malaria clusters. RESULTS: The most likely spatial cluster of malaria incidence included 1,040 people (22.4% of total population) in 245 HHs (24.6% of total HHs) accounting for 283 malaria episodes (40.1% of total episodes) during the study period (RR = 2.3, $p < 0.001$). A temporal cluster was also identified from April 12, 2009 to July 4, 2009 accounting for 355 malaria episodes (50.4% of total episodes) (RR = 7.2, $p = 0.001$). Factors significantly associated with case HHs compared with control HHs were: proximity to water drain < 200 metres (OR = 2.3, 95% CI: 1.3, 4.0); HH size >5 individuals (OR = 1.8, 95% CI: 1.0, 3.2); lack of potable water (OR = 1.8, 95% CI: 1.1, 3.2); and having domestic and peridomestic animals (OR = 3.6, 95% CI: 1.3, 9.5). CONCLUSION: Plasmodium vivax malaria incidence is highly heterogeneous in space and time in the urban study area with important geographical and housing risk factors associated with symptomatic episodes.

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 GR - R01 AI067727/AI/NIAID NIH HHS/United States
 GR - U19AI089702/AI/NIAID NIH HHS/United States
 GR - D43TW007120/TW/FIC NIH HHS/United States
 GR - R01AI067727/AI/NIAID NIH HHS/United States
 GR - D43 TW007120/TW/FIC NIH HHS/United States
 GR - U19 AI089702/AI/NIAID NIH HHS/United States
 PT - Journal Article
 PT - Research Support, N.I.H., Extramural
 DEP - 20150424
 PL - England
 TA - Malar J
 JT - Malaria journal
 JID - 101139802
 SB - IM
 MH - Case-Control Studies
 MH - Incidence
 MH - Malaria, Vivax/*epidemiology/parasitology
 MH - Peru/epidemiology
 MH - Plasmodium vivax/*physiology
 MH - *Residence Characteristics
 MH - Risk Factors

MH - Spatial Analysis
MH - Urban Population
PMC - PMC4416302
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AID - 10.1186/s12936-015-0670-y [doi]
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S0 - Malar J. 2015 Apr 24;14:176. doi: 10.1186/s12936-015-0670-y.

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OWN - NLM
STAT- MEDLINE
DCOM- 20150522
LR - 20220321
IS - 1537-6613 (Electronic)
IS - 0022-1899 (Linking)
VI - 211
IP - 8
DP - 2015 Apr 15
TI - Genome-level determination of Plasmodium falciparum blood-stage targets of malarial clinical immunity in the Peruvian Amazon.
PG - 1342-51
LID - 10.1093/infdis/jiu614 [doi]
AB - BACKGROUND: Persons with blood-stage Plasmodium falciparum parasitemia in the absence of symptoms are considered to be clinically immune. We hypothesized that asymptomatic subjects with P. falciparum parasitemia would differentially recognize a subset of P. falciparum proteins on a genomic scale. METHODS AND FINDINGS: Compared with symptomatic subjects, sera from clinically immune, asymptotically infected individuals differentially recognized 51 P. falciparum proteins, including the established vaccine candidate PfMSP1. Novel, hitherto unstudied hypothetical proteins and other proteins not previously recognized as potential vaccine candidates were also differentially recognized. Genes encoding the proteins differentially recognized by the Peruvian clinically immune individuals exhibited a significant

enrichment of nonsynonymous nucleotide variation, an observation consistent with these genes undergoing immune selection. CONCLUSIONS: A limited set of *P. falciparum* protein antigens was associated with the development of naturally acquired clinical immunity in the low-transmission setting of the Peruvian Amazon. These results imply that, even in a low-transmission setting, an asexual blood-stage vaccine designed to reduce clinical malaria symptoms will likely need to contain large numbers of often-polymorphic proteins, a finding at odds with many current efforts in the design of vaccines against asexual blood-stage *P. falciparum*.

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GR - R01 AI067727/AI/NIAID NIH HHS/United States
GR - R43 AI075692/AI/NIAID NIH HHS/United States
GR - D43TW007120/TW/FIC NIH HHS/United States
GR - K24AI068903/AI/NIAID NIH HHS/United States
GR - R01AI05759206/AI/NIAID NIH HHS/United States
GR - U19AI089681/AI/NIAID NIH HHS/United States
GR - R01 AI095916/AI/NIAID NIH HHS/United States
GR - R01RHL086488/PHS HHS/United States
GR - AI075692/AI/NIAID NIH HHS/United States
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GR - 1R01AI067727/AI/NIAID NIH HHS/United States
GR - K24 AI068903/AI/NIAID NIH HHS/United States
PT - Journal Article
PT - Research Support, N.I.H., Extramural
DEP - 20141107
PL - United States

TA - J Infect Dis
JT - The Journal of infectious diseases
JID - 0413675
RN - 0 (Antibodies, Protozoan)
RN - 0 (Antigens, Protozoan)
RN - 0 (Malaria Vaccines)
RN - 0 (Protozoan Proteins)
SB - IM
MH - Adolescent
MH - Adult
MH - Antibodies, Protozoan/immunology
MH - Antigens, Protozoan/genetics/immunology
MH - Child
MH - Female
MH - Humans
MH - Malaria Vaccines/immunology
MH - Malaria, Falciparum/*blood/*immunology
MH - Male
MH - Middle Aged
MH - Parasitemia/blood/immunology/parasitology
MH - Plasmodium falciparum/*genetics/*immunology
MH - Protozoan Proteins/*blood/genetics/immunology
MH - Young Adult
PMC - PMC4402338
OTO - NOTNLM
OT - geographic medicine
OT - immunology
OT - malaria
OT - systems biology
EDAT- 2014/11/09 06:00
MHDA- 2015/05/23 06:00
CRDT- 2014/11/09 06:00
PHST- 2014/11/09 06:00 [entrez]
PHST- 2014/11/09 06:00 [pubmed]
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AID - jiu614 [pii]
AID - 10.1093/infdis/jiu614 [doi]
PST - ppublish
S0 - J Infect Dis. 2015 Apr 15;211(8):1342-51. doi: 10.1093/infdis/
jiu614.

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PMID- 24768682
OWN - NLM
STAT- MEDLINE
DCOM- 20150112
LR - 20140602
IS - 1567-7257 (Electronic)
IS - 1567-1348 (Linking)
VI - 25
DP - 2014 Jul
TI - Genetic diversity of VAR2CSA ID1-DBL2Xb in worldwide
Plasmodium
falciparum populations: impact on vaccine design for placental

malaria.

PG - 81-92

LID - 10.1016/j.meegid.2014.04.010 [doi]

LID - S1567-1348(14)00132-4 [pii]

AB - In placental malaria (PM), sequestration of infected erythrocytes in the

placenta is mediated by an interaction between VAR2CSA, a Plasmodium

falciparum protein expressed on erythrocytes, and chondroitin sulfate A

(CSA) on syncytiotrophoblasts. Recent works have identified ID1-DBL2Xb as

the minimal CSA-binding region within VAR2CSA able to induce strong

protective immunity, making it the leading candidate for the development

of a vaccine against PM. Assessing the existence of population differences in the distribution of ID1-DBL2Xb polymorphisms is

of paramount importance to determine whether geographic diversity must be

considered when designing a candidate vaccine based on this fragment. In

this study, we examined patterns of sequence variation of ID1-DBL2Xb in a

large collection of P. falciparum field isolates (n=247) from different

malaria-endemic areas, including Africa (Benin, Senegal, Cameroon and

Madagascar), Asia (Cambodia), Oceania (Papua New Guinea), and Latin

America (Peru). Detection of variants and estimation of their allele

frequencies were performed using next-generation sequencing of DNA pools.

A considerable amount of variation was detected along the whole gene

segment, suggesting that several allelic variants may need to be included

in a candidate vaccine to achieve broad population coverage. However,

most sequence variants were common and extensively shared among worldwide

parasite populations, demonstrating long term persistence of those

polymorphisms, probably maintained through balancing selection.

Therefore, a vaccine mixture including such stable antigen variants will

be putatively applicable and efficacious in all world regions where

malaria occurs. Despite similarity in ID1-DBL2Xb allele repertoire across

geographic areas, several peaks of strong population

differentiation were
observed at specific polymorphic loci, pointing out putative
targets of
humoral immunity subject to positive immune selection.

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PT - Research Support, Non-U.S. Gov't
DEP - 20140421
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TA - Infect Genet Evol
JT - Infection, genetics and evolution : journal of molecular
epidemiology and
evolutionary genetics in infectious diseases
JID - 101084138
RN - 0 (Antigens, Protozoan)
RN - 0 (DNA, Protozoan)

RN - 0 (VAR2CSA protein, Plasmodium falciparum)
RN - 0 (Viral Vaccines)
SB - IM
MH - Adolescent
MH - Adult
MH - Antigenic Variation/immunology
MH - Antigens, Protozoan/*genetics/immunology
MH - DNA, Protozoan/genetics
MH - Female
MH - Gene Frequency
MH - Genetic Variation
MH - Humans
MH - Malaria, Falciparum/epidemiology/immunology/*parasitology
MH - Phylogeography
MH - Placenta/immunology/*parasitology
MH - Plasmodium falciparum/classification/immunology/*isolation & purification/*metabolism
MH - Pregnancy
MH - Pregnancy Complications, Parasitic/immunology/*parasitology
MH - Sequence Analysis, DNA
MH - Viral Vaccines/genetics/immunology
MH - Young Adult
OTO - NOTNLM
OT - Genetic structure
OT - Next-generation sequencing
OT - Plasmodium falciparum
OT - Pregnancy-associated malaria
OT - VAR2CSA
OT - Vaccine
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OWN - NLM
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IS - 1476-1645 (Electronic)
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VI - 90
IP - 4

DP - 2014 Apr
TI - Infection of laboratory-colonized *Anopheles darlingi* mosquitoes by *Plasmodium vivax*.
PG - 612-616
LID - 10.4269/ajtmh.13-0708 [doi]
AB - *Anopheles darlingi* Root is the most important malaria vector in the Amazonia region of South America. However, continuous propagation of *An. darlingi* in the laboratory has been elusive, limiting entomological, genetic/genomic, and vector-pathogen interaction studies of this mosquito species. Here, we report the establishment of an *An. darlingi* colony derived from wild-caught mosquitoes obtained in the northeastern Peruvian Amazon region of Iquitos in the Loreto Department. We show that the numbers of eggs, larvae, pupae, and adults continue to rise at least to the F6 generation. Comparison of feeding *Plasmodium vivax* *ex vivo* of F4 and F5 to F1 generation mosquitoes showed the comparable presence of oocysts and sporozoites, with numbers that corresponded to blood-stage asexual parasitemia and gametocytemia, confirming *P. vivax* vectorial capacity in the colonized mosquitoes. These results provide new avenues for research on *An. darlingi* biology and study of *An. darlingi*-*Plasmodium* interactions.

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LA - eng
GR - D43 TW009343/TW/FIC NIH HHS/United States
GR - U19 AI089681/AI/NIAID NIH HHS/United States
GR - U19AI089681/AI/NIAID NIH HHS/United States
PT - Journal Article
PT - Research Support, N.I.H., Extramural
PT - Research Support, Non-U.S. Gov't
DEP - 20140217
PL - United States
TA - Am J Trop Med Hyg
JT - The American journal of tropical medicine and hygiene
JID - 0370507
SB - IM
MH - Animals
MH - Anopheles/*parasitology
MH - Female
MH - Insect Vectors/*parasitology
MH - Laboratory Animal Science/methods
MH - Malaria, Vivax/*transmission
MH - Male
MH - Oocysts
MH - *Plasmodium vivax
MH - Sexual Behavior, Animal
MH - Sporozoites
PMC - PMC3973502
EDAT- 2014/02/19 06:00
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AID - 10.4269/ajtmh.13-0708 [doi]
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S0 - Am J Trop Med Hyg. 2014 Apr;90(4):612-616. doi: 10.4269/
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Epub 2014 Feb 17.

PMID- 24834503
OWN - NLM
STAT- MEDLINE
DCOM- 20140626
LR - 20191210
IS - 1365-294X (Electronic)
IS - 0962-1083 (Linking)
VI - 23
IP - 8
DP - 2014 Apr
TI - Patterns of selection on Plasmodium falciparum erythrocyte-
binding

antigens after the colonization of the New World.

PG - 1979-93

AB - Pathogens, which have recently colonized a new host species or new populations of the same host, are interesting models for understanding how populations may evolve in response to novel environments. During its colonization of South America from Africa, *Plasmodium falciparum*, the main agent of malaria, has been exposed to new conditions in distinctive new human populations (Amerindian and populations of mixed origins) that likely exerted new selective pressures on the parasite's genome. Among the genes that might have experienced strong selective pressures in response to these environmental changes, the *eba* genes (erythrocyte-binding antigens genes), which are involved in the invasion of the human red blood cells, constitute good candidates. In this study, we analysed, in South America, the polymorphism of three *eba* genes (*eba-140*, *eba-175*, *eba-181*) and compared it to the polymorphism observed in African populations. The aim was to determine whether these genes faced selective pressures in South America distinct from what they experienced in Africa. Patterns of genetic variability of these genes were compared to the patterns observed at two housekeeping genes (*adsl* and *serca*) and 272 SNPs to separate adaptive effects from demographic effects. We show that, conversely to Africa, *eba-140* seemed to be under stronger diversifying selection in South America than *eba-175*. In contrast, *eba-181* did not show any sign of departure from neutrality. These changes in the patterns of selection on the *eba* genes could be the consequence of changes in the host immune response, the host receptor polymorphisms and/or the ability of the parasite to silence or express differentially its invasion proteins.

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RN - 0 (Carrier Proteins)
RN - 0 (DNA, Protozoan)
RN - 0 (EBA-181 protein, Plasmodium falciparum)
RN - 0 (EBA140 protein, Plasmodium falciparum)
RN - 0 (Membrane Proteins)
RN - 0 (Protozoan Proteins)
RN - 0 (erythrocyte-binding antigen 175, Plasmodium)
SB - IM
MH - Africa
MH - Antigens, Protozoan/*genetics
MH - Carrier Proteins/genetics
MH - DNA, Protozoan/genetics
MH - Erythrocytes/parasitology
MH - Genetics, Population
MH - Humans
MH - Malaria, Falciparum/*parasitology
MH - Membrane Proteins
MH - Molecular Sequence Data
MH - Plasmodium falciparum/*genetics
MH - *Polymorphism, Genetic
MH - Protozoan Proteins/*genetics
MH - *Selection, Genetic
MH - Sequence Analysis, DNA
MH - South America
EDAT- 2014/05/17 06:00
MHDA- 2014/06/27 06:00
CRDT- 2014/05/17 06:00

PHST- 2014/05/17 06:00 [entrez]
PHST- 2014/05/17 06:00 [pubmed]
PHST- 2014/06/27 06:00 [medline]
AID - 10.1111/mec.12696 [doi]
PST - ppublish
S0 - Mol Ecol. 2014 Apr;23(8):1979-93. doi: 10.1111/mec.12696.

PMID- 24642188
OWN - NLM
STAT- MEDLINE
DCOM- 20140915
LR - 20211021
IS - 1475-2875 (Electronic)
IS - 1475-2875 (Linking)
VI - 13
DP - 2014 Mar 19
TI - Relationship of regulatory T cells to Plasmodium falciparum malaria
symptomatology in a hypoendemic region.
PG - 108
LID - 10.1186/1475-2875-13-108 [doi]
AB - BACKGROUND: Previous data have suggested that regulatory T cells (Tregs) balance protective immune responses with immune mediated pathology in malaria. This study aimed to determine to test the hypothesis that Treg proportions or absolute levels are associated with parasitaemia and malaria symptoms. METHODS: Treg cells were quantified by flow cytometry as CD4+ CD25+, Foxp3+, CD127(low) T cells. Three patient groups were assessed: patients with symptomatic Plasmodium falciparum malaria (S), subjects with asymptomatic P. falciparum parasitaemia (AS) and uninfected control individuals (C). RESULTS: S, AS and C groups had similar absolute numbers and percentage of Tregs (3.9%, 3.5% and 3.5% respectively). Levels of parasitaemia were not associated with Treg percentage (p = 0.47). CONCLUSION: Neither relative nor absolute regulatory T cell numbers were found to be associated with malaria-related symptomatology in this study. Immune mechanisms other than Tregs are likely to be responsible for the state of asymptomatic P. falciparum parasitaemia in the Peruvian Amazon; but further study to explore these mechanisms is needed.

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GR - 1K24AI068903/AI/NIAID NIH HHS/United States
GR - 1D43TW007120/TW/FIC NIH HHS/United States
GR - R01AI067727/AI/NIAID NIH HHS/United States
GR - U19 AI089681/AI/NIAID NIH HHS/United States
GR - 1U19AI089681/AI/NIAID NIH HHS/United States
PT - Journal Article
PT - Research Support, N.I.H., Extramural
PT - Research Support, Non-U.S. Gov't
DEP - 20140319
PL - England
TA - Malar J
JT - Malaria journal
JID - 101139802
SB - IM
MH - Adolescent
MH - Adult
MH - Asymptomatic Diseases
MH - Child
MH - Female
MH - Flow Cytometry
MH - Humans
MH - Malaria, Falciparum/*immunology/parasitology
MH - Male
MH - Middle Aged
MH - Parasitemia/*immunology/parasitology
MH - Peru
MH - Plasmodium falciparum/*immunology
MH - T-Lymphocytes, Regulatory/*immunology
MH - Young Adult
PMC - PMC3976150
EDAT- 2014/03/20 06:00
MHDA- 2014/09/16 06:00
CRDT- 2014/03/20 06:00
PHST- 2013/09/16 00:00 [received]
PHST- 2014/03/14 00:00 [accepted]
PHST- 2014/03/20 06:00 [entrez]
PHST- 2014/03/20 06:00 [pubmed]

PHST- 2014/09/16 06:00 [medline]
AID - 1475-2875-13-108 [pii]
AID - 10.1186/1475-2875-13-108 [doi]
PST - epublish
S0 - Malar J. 2014 Mar 19;13:108. doi: 10.1186/1475-2875-13-108.

PMID- 24393454
OWN - NLM
STAT- MEDLINE
DCOM- 20140915
LR - 20211021
IS - 1475-2875 (Electronic)
IS - 1475-2875 (Linking)
VI - 13
DP - 2014 Jan 6
TI - Population structure and spatio-temporal transmission dynamics of

Plasmodium vivax after radical cure treatment in a rural village of the Peruvian Amazon.

PG - 8
LID - 10.1186/1475-2875-13-8 [doi]
AB - BACKGROUND: Despite the large burden of Plasmodium vivax, little is known about its transmission dynamics. This study explored the population structure and spatio-temporal dynamics of P. vivax recurrent infections after radical cure in a two-year cohort study carried out in a rural community of the Peruvian Amazon. METHODS: A total of 37 P. vivax participants recruited in San Carlos community (Peru) between April and December 2008 were treated radically with chloroquine and primaquine and followed up monthly for two years with systematic blood sampling. All samples were screened for malaria parasites and subsequently all P. vivax infections genotyped using 15 microsatellites. Parasite population structure and dynamics were determined by computing different genetic indices and using spatio-temporal statistics. RESULTS: After radical cure, 76% of the study participants experienced one or more recurrent P. vivax infections, most of them sub-patent and asymptomatic. The parasite population displayed limited genetic diversity ($H_e = 0.49$) and clonal structure, with most infections (84%) being monoclonal. Spatio-temporal

clusters of specific haplotypes were found throughout the study and persistence of highly frequent haplotypes were observed over several months within the same participants/households. CONCLUSIONS: In San Carlos community, *P. vivax* recurrences were commonly observed after radical treatment, and characterized by asymptomatic, sub-patent and clustered infections (within and between individuals from a few neighbouring households). Moreover low genetic diversity as well as parasite inbreeding are likely to define a clonal parasite population which has important implications on the malaria epidemiology of the study area.

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LA - eng

PT - Journal Article

PT - Research Support, Non-U.S. Gov't

DEP - 20140106

PL - England

TA - Malar J

JT - Malaria journal

JID - 101139802

RN - 0 (Antimalarials)
RN - 886U3H6UFF (Chloroquine)
RN - MVR3634GX1 (Primaquine)
SB - IM
MH - Adolescent
MH - Adult
MH - Antimalarials/therapeutic use
MH - Child
MH - Child, Preschool
MH - Chloroquine/therapeutic use
MH - Cohort Studies
MH - Female
MH - *Genetic Variation
MH - Haplotypes
MH - Humans
MH - Malaria, Vivax/drug therapy/*epidemiology/parasitology/
*transmission
MH - Male
MH - Middle Aged
MH - Peru/epidemiology
MH - Plasmodium vivax/*genetics
MH - Polymerase Chain Reaction
MH - Primaquine/therapeutic use
MH - Rural Population
MH - Young Adult
PMC - PMC3893378
EDAT- 2014/01/08 06:00
MHDA- 2014/09/16 06:00
CRDT- 2014/01/08 06:00
PHST- 2013/09/04 00:00 [received]
PHST- 2013/12/28 00:00 [accepted]
PHST- 2014/01/08 06:00 [entrez]
PHST- 2014/01/08 06:00 [pubmed]
PHST- 2014/09/16 06:00 [medline]
AID - 1475-2875-13-8 [pii]
AID - 10.1186/1475-2875-13-8 [doi]
PST - epublish
S0 - Malar J. 2014 Jan 6;13:8. doi: 10.1186/1475-2875-13-8.

PMID- 24077522
OWN - NLM
STAT- MEDLINE
DCOM- 20140428
LR - 20211021
IS - 2045-2322 (Electronic)
IS - 2045-2322 (Linking)
VI - 3
DP - 2013 Sep 30
TI - Multiple genetic origins of histidine-rich protein 2 gene
deletion in
Plasmodium falciparum parasites from Peru.
PG - 2797
LID - 10.1038/srep02797 [doi]
AB - The majority of malaria rapid diagnostic tests (RDTs) detect

Plasmodium

falciparum histidine-rich protein 2 (PfHRP2), encoded by the pfhrp2 gene.

Recently, P. falciparum isolates from Peru were found to lack pfhrp2

leading to false-negative RDT results. We hypothesized that pfhrp2-deleted parasites in Peru derived from a single genetic event. We

evaluated the parasite population structure and pfhrp2 haplotype of

samples collected between 1998 and 2005 using seven neutral and seven

chromosome 8 microsatellite markers, respectively. Five distinct pfhrp2

haplotypes, corresponding to five neutral microsatellite-based clonal

lineages, were detected in 1998–2001; pfhrp2 deletions occurred within

four haplotypes. In 2003–2005, outcrossing among the parasite lineages

resulted in eight population clusters that inherited the five pfhrp2

haplotypes seen previously and a new haplotype; pfhrp2 deletions occurred

within four of these haplotypes. These findings indicate that the genetic

origin of pfhrp2 deletion in Peru was not a single event, but likely

occurred multiple times.

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FAU - Udhayakumar, Venkatachalam
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LA - eng
GR - D43 TW007120/TW/FIC NIH HHS/United States
GR - U19 AI089681/AI/NIAID NIH HHS/United States
GR - D43TW007120/TW/FIC NIH HHS/United States
GR - U19AI089681/AI/NIAID NIH HHS/United States
PT - Journal Article
PT - Research Support, N.I.H., Extramural
PT - Research Support, Non-U.S. Gov't
PT - Research Support, U.S. Gov't, Non-P.H.S.
DEP - 20130930
PL - England
TA - Sci Rep
JT - Scientific reports
JID - 101563288
RN - 0 (Antigens, Protozoan)
RN - 0 (HRP-2 antigen, Plasmodium falciparum)
RN - 0 (Protozoan Proteins)
SB - IM
MH - Animals
MH - Antigens, Protozoan/*genetics
MH - Bayes Theorem
MH - Cluster Analysis
MH - *Gene Deletion
MH - Haplotypes/genetics
MH - Humans
MH - Microsatellite Repeats/genetics
MH - Parasites/*genetics
MH - Peru
MH - Phenotype
MH - Plasmodium falciparum/*genetics
MH - Prevalence
MH - Protozoan Proteins/*genetics
PMC - PMC3786299
EDAT- 2013/10/01 06:00
MHDA- 2014/04/29 06:00
CRDT- 2013/10/01 06:00
PHST- 2013/06/18 00:00 [received]
PHST- 2013/09/04 00:00 [accepted]
PHST- 2013/10/01 06:00 [entrez]
PHST- 2013/10/01 06:00 [pubmed]
PHST- 2014/04/29 06:00 [medline]
AID - srep02797 [pii]
AID - 10.1038/srep02797 [doi]
PST - epublish

S0 - Sci Rep. 2013 Sep 30;3:2797. doi: 10.1038/srep02797.

PMID- 24053144

OWN - NLM

STAT- MEDLINE

DCOM- 20140714

LR - 20211021

IS - 1475-2875 (Electronic)

IS - 1475-2875 (Linking)

VI - 12

DP - 2013 Sep 22

TI - Assessing malaria transmission in a low endemicity area of north-western Peru.

PG - 339

LID - 10.1186/1475-2875-12-339 [doi]

AB - BACKGROUND: Where malaria endemicity is low, control programmes need

increasingly sensitive tools for monitoring malaria transmission

intensity (MTI) and to better define health priorities. A cross-sectional

survey was conducted in a low endemicity area of the Peruvian north-

western coast to assess the MTI using both molecular and serological

tools. METHODS: Epidemiological, parasitological and serological data

were collected from 2,667 individuals in three settlements of Bellavista

district, in May 2010. Parasite infection was detected using microscopy

and polymerase chain reaction (PCR). Antibodies to Plasmodium vivax

merozoite surface protein-119 (PvMSP1(1)(9)) and to Plasmodium falciparum

glutamate-rich protein (PfGLURP) were detected by ELISA. Risk factors for

exposure to malaria (seropositivity) were assessed by multivariate survey

logistic regression models. Age-specific antibody prevalence of both P.

falciparum and P. vivax were analysed using a previously published

catalytic conversion model based on maximum likelihood for generating

seroconversion rates (SCR). RESULTS: The overall parasite prevalence by

microscopy and PCR were extremely low: 0.3 and 0.9%, respectively for P.

vivax, and 0 and 0.04%, respectively for P. falciparum, while seroprevalence was much higher, 13.6% for P. vivax and 9.8%

for P.

falciparum. Settlement, age and occupation as moto-taxi driver

during previous year were significantly associated with *P. falciparum* exposure, while age and distance to the water drain were associated with *P. vivax* exposure. Likelihood ratio tests supported age seroprevalence curves with two SCR for both *P. vivax* and *P. falciparum* indicating significant changes in the MTI over time. The SCR for PfGLURP was 19-fold lower after 2002 as compared to before ($\lambda_1 = 0.022$ versus $\lambda_2 = 0.431$), and the SCR for PvMSP1(1)(9) was four-fold higher after 2006 as compared to before ($\lambda_1 = 0.024$ versus $\lambda_2 = 0.006$). CONCLUSION: Combining molecular and serological tools considerably enhanced the capacity of detecting current and past exposure to malaria infections and related risks factors in this very low endemicity area. This allowed for an improved characterization of the current human reservoir of infections, largely hidden and heterogeneous, as well as providing insights into recent changes in species specific MTIs. This approach will be of key importance for evaluating and monitoring future malaria elimination strategies.

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AU - Erhart A
LA - eng
PT - Journal Article
DEP - 20130922
PL - England
TA - Malar J
JT - Malaria journal
JID - 101139802
RN - 0 (Antibodies, Protozoan)
RN - 0 (DNA, Protozoan)
SB - IM
MH - Adolescent
MH - Adult
MH - Aged
MH - Aged, 80 and over
MH - Antibodies, Protozoan/blood
MH - Child
MH - Child, Preschool
MH - Cross-Sectional Studies
MH - DNA, Protozoan/blood/genetics
MH - Enzyme-Linked Immunosorbent Assay
MH - Female
MH - Humans
MH - Infant
MH - Infant, Newborn
MH - Malaria, Falciparum/epidemiology/*transmission
MH - Malaria, Vivax/epidemiology/*transmission
MH - Male
MH - Middle Aged
MH - Peru/epidemiology
MH - Plasmodium falciparum/genetics/immunology/isolation & purification
MH - Plasmodium vivax/genetics/immunology/isolation & purification
MH - Polymerase Chain Reaction
MH - Young Adult
PMC - PMC3849384
EDAT- 2013/09/24 06:00
MHDA- 2014/07/16 06:00
CRDT- 2013/09/24 06:00
PHST- 2013/05/10 00:00 [received]
PHST- 2013/09/16 00:00 [accepted]
PHST- 2013/09/24 06:00 [entrez]
PHST- 2013/09/24 06:00 [pubmed]
PHST- 2014/07/16 06:00 [medline]
AID - 1475-2875-12-339 [pii]
AID - 10.1186/1475-2875-12-339 [doi]

PST - epublish
S0 - Malar J. 2013 Sep 22;12:339. doi: 10.1186/1475-2875-12-339.

PMID- 24001096

OWN - NLM

STAT- MEDLINE

DCOM- 20140714

LR - 20211021

IS - 1475-2875 (Electronic)

IS - 1475-2875 (Linking)

VI - 12

DP - 2013 Aug 30

TI - The history of 20th century malaria control in Peru.

PG - 303

LID - 10.1186/1475-2875-12-303 [doi]

AB - Malaria has been part of Peruvian life since at least the 1500s. While

Peru gave the world quinine, one of the first treatments for malaria, its

history is pockmarked with endemic malaria and occasional epidemics. In

this review, major increases in Peruvian malaria incidence over the past

hundred years are described, as well as the human factors that have

facilitated these events, and concerted private and governmental efforts

to control malaria. Political support for malaria control has varied and

unexpected events like vector and parasite resistance have adversely

impacted morbidity and mortality. Though the ready availability of novel

insecticides like DDT and efficacious medications reduced malaria to very

low levels for a decade after the post eradication era, malaria reemerged

as an important modern day challenge to Peruvian public health. Its

reemergence sparked collaboration between domestic and international

partners towards the elimination of malaria in Peru.

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LA - eng

PT - Historical Article
PT - Journal Article
PT - Research Support, U.S. Gov't, Non-P.H.S.
PT - Research Support, U.S. Gov't, P.H.S.
PT - Review
DEP - 20130830
PL - England
TA - Malar J
JT - Malaria journal
JID - 101139802
RN - 0 (Antimalarials)
RN - A7V27PHC7A (Quinine)
SB - IM
MH - Antimalarials/history/*therapeutic use
MH - Communicable Disease Control/*history/*methods
MH - Drug Therapy/history
MH - Health Policy
MH - History, 20th Century
MH - Humans
MH - Malaria/drug therapy/*epidemiology/*history/prevention & control
MH - Peru/epidemiology
MH - Quinine
PMC - PMC3766208
EDAT- 2013/09/05 06:00
MHDA- 2014/07/16 06:00
CRDT- 2013/09/05 06:00
PHST- 2013/04/29 00:00 [received]
PHST- 2013/08/21 00:00 [accepted]
PHST- 2013/09/05 06:00 [entrez]
PHST- 2013/09/05 06:00 [pubmed]
PHST- 2014/07/16 06:00 [medline]
AID - 1475-2875-12-303 [pii]
AID - 10.1186/1475-2875-12-303 [doi]
PST - epublish
S0 - Malar J. 2013 Aug 30;12:303. doi: 10.1186/1475-2875-12-303.

PMID- 23300943
OWN - NLM
STAT- MEDLINE
DCOM- 20130820
LR - 20211021
IS - 1932-6203 (Electronic)
IS - 1932-6203 (Linking)
VI - 8
IP - 1
DP - 2013
TI - Traditional nets interfere with the uptake of long-lasting insecticidal
nets in the Peruvian Amazon: the relevance of net preference
for
achieving high coverage and use.
PG - e50294
LID - 10.1371/journal.pone.0050294 [doi]

AB - BACKGROUND: While coverage of long-lasting insecticide-treated nets (LLIN) has steadily increased, a growing number of studies report gaps between net ownership and use. We conducted a mixed-methods social science study assessing the importance of net preference and use after Olyset(R) LLINs were distributed through a mass campaign in rural communities surrounding Iquitos, the capital city of the Amazonian region of Peru. METHODS: The study was conducted in the catchment area of the Pajil and Cahide Health Centres (San Juan district) between July 2007 and November 2008. During a first qualitative phase, participant observation and in-depth interviews collected information on key determinants for net preference and use. In a second quantitative phase, a survey among recently confirmed malaria patients evaluated the acceptability and use of both LLINs and traditional nets, and a case control study assessed the association between net preference/use and housing structure (open vs. closed houses). RESULTS: A total of 10 communities were selected for the anthropological fieldwork and 228 households participated in the quantitative studies. In the study area, bed nets are considered part of the housing structure and are therefore required to fulfil specific architectural and social functions, such as providing privacy and shelter, which the newly distributed Olyset(R) LLINs ultimately did not. The LLINs' failure to meet these criteria could mainly be attributed to their large mesh size, transparency and perceived ineffectiveness to protect against mosquitoes and other insects, resulting in 63.3% of households not using any of the distributed LLINs. Notably, LLIN usage was significantly lower in houses with no interior or exterior walls (35.2%) than in those with walls (73.8%) (OR = 5.2, 95CI [2.2; 12.3], $p < 0.001$). CONCLUSION: Net preference can interfere with

optimal LLIN use. In order to improve the number of effective days of

LLIN protection per dollar spent, appropriate quantitative and qualitative methods for collecting information on net

preference should

be developed before any LLIN procurement decision is made.

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LA – eng

GR – U19 AI089681/AI/NIAID NIH HHS/United States

PT – Journal Article

PT – Research Support, Non-U.S. Gov't

DEP – 20130102

PL – United States

TA – PLoS One

JT – PloS one

JID – 101285081

SB – IM

MH – Attitude to Health

MH – Choice Behavior

MH – Climate

MH – Family Characteristics

MH – Housing

MH – Humans

MH – Insecticide-Treated Bednets/*statistics & numerical data

MH – Malaria/*prevention & control

MH – Mosquito Control/*instrumentation/methods

MH – Patient Acceptance of Health Care/statistics & numerical data

MH – Peru

MH - Rural Population
MH - Seasons
MH - Surveys and Questionnaires
PMC - PMC3534704
EDAT- 2013/01/10 06:00
MHDA- 2013/08/21 06:00
CRDT- 2013/01/10 06:00
PHST- 2012/05/02 00:00 [received]
PHST- 2012/10/22 00:00 [accepted]
PHST- 2013/01/10 06:00 [entrez]
PHST- 2013/01/10 06:00 [pubmed]
PHST- 2013/08/21 06:00 [medline]
AID - 10.1371/journal.pone.0050294 [doi]
AID - PONE-D-12-12503 [pii]
PST - ppublsh
S0 - PLoS One. 2013;8(1):e50294. doi: 10.1371/journal.pone.0050294.
Epub 2013
Jan 2.

PMID- 23118907
OWN - NLM
STAT- MEDLINE
DCOM- 20130509
LR - 20211021
IS - 1932-6203 (Electronic)
IS - 1932-6203 (Linking)
VI - 7
IP - 10
DP - 2012
TI - Plasmodium falciparum field isolates from South America use an atypical red blood cell invasion pathway associated with invasion ligand polymorphisms.
PG - e47913
LID - 10.1371/journal.pone.0047913 [doi]
AB - Studies of Plasmodium falciparum invasion pathways in field isolates have been limited. Red blood cell (RBC) invasion is a complex process involving two invasion protein families; Erythrocyte Binding-Like (EBL) and the Reticulocyte Binding-Like (PfRh) proteins, which are polymorphic and not fully characterized in field isolates. To determine the various P. falciparum invasion pathways used by parasite isolates from South America, we studied the invasion phenotypes in three regions: Colombia, Peru and Brazil. Additionally, polymorphisms in three members of the EBL (EBA-181, EBA-175 and EBL-1) and five members of the PfRh (PfRh1, PfRh2a,

PfRh2b, PfRh4, PfRh5) families were determined. We found that most P. falciparum field isolates from Colombia and Peru invade RBCs through an atypical invasion pathway phenotypically characterized as resistant to all enzyme treatments (NrTrCr). Moreover, the invasion pathways and the ligand polymorphisms differed substantially among the Colombian and Brazilian isolates while the Peruvian isolates represent an amalgam of those present in the Colombian and Brazilian field isolates. The NrTrCr invasion profile was associated with the presence of the PfRh2a pepC variant, the PfRh5 variant 1 and EBA-181 RVNKN variant. The ebl and Pfrh expression levels in a field isolate displaying the NrTrCr profile also pointed to PfRh2a, PfRh5 and EBA-181 as being possibly the major players in this invasion pathway. Notably, our studies demonstrate the uniqueness of the Peruvian P. falciparum field isolates in terms of their invasion profiles and ligand polymorphisms, and present a unique opportunity for studying the ability of P. falciparum parasites to expand their invasion repertoire after being reintroduced to human populations. The present study is directly relevant to asexual blood stage vaccine design focused on invasion pathway proteins, suggesting that regional invasion variants and global geographical variation are likely to preclude a simple one size fits all type of vaccine.

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GR - R03TW007349/TW/FIC NIH HHS/United States
GR - U19AI089681/AI/NIAID NIH HHS/United States
GR - R03 TW007349/TW/FIC NIH HHS/United States
GR - U19 AI089681/AI/NIAID NIH HHS/United States
GR - K24 AI068903/AI/NIAID NIH HHS/United States
PT - Journal Article
PT - Research Support, N.I.H., Extramural
PT - Research Support, Non-U.S. Gov't
DEP - 20121031
PL - United States
TA - PLoS One
JT - PloS one
JID - 101285081
RN - 0 (Ligands)
RN - 0 (Malaria Vaccines)
RN - 0 (Protozoan Proteins)
SB - IM
MH - Animals
MH - *Erythrocytes/cytology/immunology/parasitology
MH - Humans
MH - Ligands
MH - Malaria Vaccines/immunology
MH - *Malaria, Falciparum/genetics/immunology/metabolism/
parasitology
MH - Phenotype
MH - *Plasmodium falciparum/genetics/immunology/pathogenicity
MH - Polymorphism, Genetic
MH - *Protozoan Proteins/genetics/immunology/metabolism
MH - Reticulocytes/metabolism/parasitology
MH - South America
PMC - PMC3485327
EDAT- 2012/11/03 06:00
MHDA- 2013/05/10 06:00
CRDT- 2012/11/03 06:00
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PHST- 2012/11/03 06:00 [entrez]
PHST- 2012/11/03 06:00 [pubmed]
PHST- 2013/05/10 06:00 [medline]
AID - 10.1371/journal.pone.0047913 [doi]
AID - PONE-D-12-23377 [pii]
PST - ppublish
S0 - PLoS One. 2012;7(10):e47913. doi: 10.1371/
journal.pone.0047913. Epub 2012
Oct 31.

PMID- 23110555
OWN - NLM

STAT- MEDLINE

DCOM- 20130606

LR - 20211021

IS - 1475-2875 (Electronic)

IS - 1475-2875 (Linking)

VI - 11

DP - 2012 Oct 30

TI - Anti-Plasmodium falciparum invasion ligand antibodies in a low malaria transmission region, Loreto, Peru.

PG - 361

LID - 10.1186/1475-2875-11-361 [doi]

AB - BACKGROUND: Erythrocyte invasion by Plasmodium falciparum is a complex

process that involves two families; Erythrocyte Binding-Like (EBL) and

the Reticulocyte Binding-Like (PfRh) proteins. Antibodies that inhibit

merozoite attachment and invasion are believed to be important in

mediating naturally acquired immunity and immunity generated by parasite

blood stage vaccine candidates. The hypotheses tested in this study were

1) that antibody responses against specific P. falciparum invasion

ligands (EBL and PfRh) differ between symptomatic and asymptomatic

individuals living in the low-transmission region of the Peruvian Amazon

and 2), such antibody responses might have an association, either direct

or indirect, with clinical immunity observed in asymptotically

parasitaemic individuals. METHODS: ELISA was used to assess antibody

responses (IgG, IgG1 and IgG3) against recombinant P. falciparum invasion

ligands of the EBL (EBA-175, EBA-181, EBA-140) and PfRh families (PfRh1,

PfRh2a, PfRh2b, PfRh4 and PfRh5) in 45 individuals infected with P.

falciparum from Peruvian Amazon. Individuals were classified as having

symptomatic malaria (N=37) or asymptomatic infection (N=8).

RESULTS:

Antibody responses against both EBL and PfRh family proteins were

significantly higher in asymptomatic compared to symptomatic individuals,

demonstrating an association with clinical immunity.

Significant

differences in the total IgG responses were observed with EBA-175,

EBA-181, PfRh2b, and MSP119 (as a control). IgG1 responses against EBA-181, PfRh2a and PfRh2b were significantly higher in the asymptomatic individuals. Total IgG antibody responses against PfRh1, PfRh2a, PfRh2b, PfRh5, EBA-175, EBA-181 and MSP119 proteins were negatively correlated with level of parasitaemia. IgG1 responses against EBA-181, PfRh2a and PfRh2b and IgG3 response for PfRh2a were also negatively correlated with parasitaemia. CONCLUSIONS: These data suggest that falciparum malaria patients who develop clinical immunity (asymptomatic parasitaemia) in a low transmission setting such as the Peruvian Amazon have antibody responses to defined P. falciparum invasion ligand proteins higher than those found in symptomatic (non-immune) patients. While these findings will have to be confirmed by larger studies, these results are consistent with a potential role for one or more of these invasion ligands as a component of an anti-P. falciparum vaccine in low-transmission malaria-endemic regions.

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GR - D43TW007120/TW/FIC NIH HHS/United States

GR - U19AI089681/AI/NIAID NIH HHS/United States
GR - U19 AI089681/AI/NIAID NIH HHS/United States
GR - D43 TW007120/TW/FIC NIH HHS/United States
GR - K24 AI068903/AI/NIAID NIH HHS/United States
PT - Journal Article
PT - Research Support, N.I.H., Extramural
PT - Research Support, Non-U.S. Gov't
DEP - 20121030
PL - England
TA - Malar J
JT - Malaria journal
JID - 101139802
RN - 0 (Antibodies, Protozoan)
RN - 0 (Immunoglobulin G)
RN - 0 (Ligands)
RN - 0 (Protozoan Proteins)
SB - IM
MH - Adolescent
MH - Adult
MH - Antibodies, Protozoan/*blood
MH - Child
MH - Erythrocytes/parasitology
MH - Female
MH - Humans
MH - Immunoglobulin G/blood
MH - Ligands
MH - Malaria, Falciparum/blood/*immunology/parasitology/
transmission
MH - Male
MH - Middle Aged
MH - Models, Immunological
MH - Parasitemia/blood/immunology/parasitology
MH - Peru
MH - Plasmodium falciparum/*immunology/pathogenicity
MH - Protozoan Proteins/immunology
MH - Young Adult
PMC - PMC3544580
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PHST- 2012/11/01 06:00 [entrez]
PHST- 2012/11/01 06:00 [pubmed]
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AID - 1475-2875-11-361 [pii]
AID - 10.1186/1475-2875-11-361 [doi]
PST - epublish
S0 - Malar J. 2012 Oct 30;11:361. doi: 10.1186/1475-2875-11-361.

PMID- 22952633
OWN - NLM
STAT- MEDLINE
DCOM- 20130219

LR - 20220330
IS - 1932-6203 (Electronic)
IS - 1932-6203 (Linking)
VI - 7
IP - 8
DP - 2012
TI - Rapid diagnostic tests for malaria diagnosis in the Peruvian Amazon:
 impact of p_{fh}rp2 gene deletions and cross-reactions.
PG - e43094
LID - 10.1371/journal.pone.0043094 [doi]
AB - BACKGROUND: In the Peruvian Amazon, Plasmodium falciparum and Plasmodium vivax malaria are endemic in rural areas, where microscopy is not available. Malaria rapid diagnostic tests (RDTs) provide quick and accurate diagnosis. However, p_{fh}rp2 gene deletions may limit the use of histidine-rich protein-2 (PfHRP2) detecting RDTs. Further, cross-reactions of P. falciparum with P. vivax-specific test lines and vice versa may impair diagnostic specificity. METHODS: Thirteen RDT products were evaluated on 179 prospectively collected malaria positive samples. Species diagnosis was performed by microscopy and confirmed by PCR. P_{fh}rp2 gene deletions were assessed by PCR. RESULTS: Sensitivity for P. falciparum diagnosis was lower for PfHRP2 compared to P. falciparum-specific Plasmodium lactate dehydrogenase (Pf-pLDH)-detecting RDTs (71.6% vs. 98.7%, p<0.001). Most (19/21) false negative PfHRP2 results were associated with p_{fh}rp2 gene deletions (25.7% of 74 P. falciparum samples). Diagnostic sensitivity for P. vivax (101 samples) was excellent, except for two products. In 10/12 P. vivax-detecting RDT products, cross-reactions with the PfHRP2 or Pf-pLDH line occurred at a median frequency of 2.5% (range 0%-10.9%) of P. vivax samples assessed. In two RDT products, two and one P. falciparum samples respectively cross-reacted with the Pv-pLDH line. Two Pf-pLDH/pan-pLDH-detecting RDTs showed excellent sensitivity with few (1.0%) cross-reactions but showed faint Pf-pLDH lines in 24.7% and 38.9% of P. falciparum

samples.

CONCLUSION: PfHRP2-detecting RDTs are not suitable in the Peruvian Amazon due to pfhrp2 gene deletions. Two Pf-pLDH-detecting RDTs performed excellently and are promising RDTs for this region although faint test lines are of concern.

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LA - eng

GR - U19 AI089681/AI/NIAID NIH HHS/United States

PT - Journal Article

PT - Research Support, N.I.H., Extramural

PT - Research Support, Non-U.S. Gov't

DEP - 20120828

PL - United States

TA - PLoS One

JT - PloS one

JID - 101285081

RN - 0 (Antigens, Protozoan)

RN - 0 (HRP-2 antigen, Plasmodium falciparum)

RN - 0 (HRP3 protein, Plasmodium falciparum)

RN - 0 (Protozoan Proteins)

SB - IM

MH - Adolescent

MH - Adult

MH - Aged

MH - Antigens, Protozoan/*genetics/metabolism

MH - Child

MH - Child, Preschool

MH - Female

MH - Gene Deletion

MH - Geography

MH - Humans

MH - Infant

MH - Malaria/*diagnosis/*parasitology

MH - Male

MH - Microscopy/methods

MH - Middle Aged
MH - Models, Genetic
MH - Peru
MH - Plasmodium falciparum/*genetics
MH - Plasmodium vivax/*genetics
MH - Polymerase Chain Reaction/methods
MH - Prospective Studies
MH - Protozoan Proteins/*genetics/metabolism
PMC - PMC3429466
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PHST- 2012/09/07 06:00 [pubmed]
PHST- 2013/02/21 06:00 [medline]
AID - 10.1371/journal.pone.0043094 [doi]
AID - PONE-D-12-15357 [pii]
PST - ppublish
S0 - PLoS One. 2012;7(8):e43094. doi: 10.1371/journal.pone.0043094.
Epub 2012
Aug 28.

PMID- 22015425
OWN - NLM
STAT- MEDLINE
DCOM- 20120619
LR - 20220409
IS - 1873-6254 (Electronic)
IS - 0001-706X (Linking)
VI - 121
IP - 3
DP - 2012 Mar
TI - Amazonian malaria: asymptomatic human reservoirs, diagnostic challenges,
environmentally driven changes in mosquito vector populations,
and the
mandate for sustainable control strategies.
PG - 281-91
LID - 10.1016/j.actatropica.2011.10.001 [doi]
AB - Across the Americas and the Caribbean, nearly 561,000 slide-confirmed
malaria infections were reported officially in 2008. The nine Amazonian
countries accounted for 89% of these infections; Brazil and Peru alone
contributed 56% and 7% of them, respectively. Local populations of the
relatively neglected parasite Plasmodium vivax, which currently accounts
for 77% of the regional malaria burden, are extremely diverse genetically
and geographically structured. At a time when malaria

elimination is placed on the public health agenda of several endemic countries, it remains unclear why malaria proved so difficult to control in areas of relatively low levels of transmission such as the Amazon Basin. We hypothesize that asymptomatic parasite carriage and massive environmental changes that affect vector abundance and behavior are major contributors to malaria transmission in epidemiologically diverse areas across the Amazon Basin. Here we review available data supporting this hypothesis and discuss their implications for current and future malaria intervention policies in the region. Given that locally generated scientific evidence is urgently required to support malaria control interventions in Amazonia, we briefly describe the aims of our current field-oriented malaria research in rural villages and gold-mining enclaves in Peru and a recently opened agricultural settlement in Brazil.

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GR - K24 AI068903/AI/NIAID NIH HHS/United States

GR - U19 AI089681/AI/NIAID NIH HHS/United States

GR - U19 AI089681-02/AI/NIAID NIH HHS/United States

PT - Journal Article

PT - Research Support, N.I.H., Extramural

PT - Review

DEP - 20111012

PL - Netherlands

TA - Acta Trop

JT - Acta tropica
JID - 0370374
SB - IM
MH - Animals
MH - Brazil/epidemiology
MH - Carrier State/*diagnosis/parasitology
MH - Communicable Disease Control/methods/organization & administration
MH - Culicidae/drug effects/parasitology/*physiology
MH - Disease Transmission, Infectious/*prevention & control
MH - Disease Vectors
MH - Environment
MH - Health Policy/legislation & jurisprudence
MH - Humans
MH - Insecticide-Treated Bednets
MH - Malaria/*diagnosis/*prevention & control/transmission
MH - Mosquito Control/methods
MH - Peru/epidemiology
MH - Plasmodium/pathogenicity
MH - Population Density
PMC - PMC3308722
MID - NIHMS360788
EDAT- 2011/10/22 06:00
MHDA- 2012/06/20 06:00
CRDT- 2011/10/22 06:00
PHST- 2011/06/08 00:00 [received]
PHST- 2011/09/30 00:00 [revised]
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PHST- 2011/10/22 06:00 [entrez]
PHST- 2011/10/22 06:00 [pubmed]
PHST- 2012/06/20 06:00 [medline]
AID - S0001-706X(11)00286-5 [pii]
AID - 10.1016/j.actatropica.2011.10.001 [doi]
PST - ppublish
S0 - Acta Trop. 2012 Mar;121(3):281-91. doi:
10.1016/j.actatropica.2011.10.001. Epub 2011 Oct 12.

PMID- 22032415
OWN - NLM
STAT- MEDLINE
DCOM- 20121119
LR - 20151119
IS - 1365-3156 (Electronic)
IS - 1360-2276 (Linking)
VI - 17
IP - 2
DP - 2012 Feb
TI - Preliminary enquiry into the availability, price and quality of malaria rapid diagnostic tests in the private health sector of six malaria-endemic countries.
PG - 147-52
LID - 10.1111/j.1365-3156.2011.02904.x [doi]

AB - OBJECTIVES: This enquiry aimed to provide a snap-shot of availability, price and quality of malaria rapid diagnostic tests (RDTs) in private health facilities at selected sites in six malaria-endemic countries in Africa, South East Asia and South America. METHODS: In each study site, data collectors surveyed private healthcare facilities which were selected based on accessibility from their home institution. Using a questionnaire, information was recorded about the facility itself and the malaria RDT(s) available. Where possible, a small number of RDTs were procured and quality control tested using a standardized procedure. RESULTS: Of the 324 private healthcare facilities visited, 35 outlets (mainly private clinics and hospitals) were found to supply 10 different types of RDTs products. RDT prices across the six countries ranged from US\$1.00 to \$16.81. Five of the 14 malaria RDTs collected failed quality control testing. CONCLUSIONS: In the private outlets sampled, the availability of RDTs was limited. Some of the RDTs whose quality we tested demonstrated inadequate sensitivity. This presents a number of risks. Given the more widespread distribution of antimalarials currently planned for private sector facilities, parasite-based diagnosis in this sector will be essential to adhere to the WHO guidelines for effective case management of malaria. Considerable regulation and quality control are also necessary to assure the availability of accurate and reliable RDTs, as well as adequate case management and provider adherence to RDT results. Public sector engagement is likely to be essential in this process.

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FAU - Bennett, J
AU - Bennett J
FAU - Incardona, S
AU - Incardona S
FAU - Lee, E
AU - Lee E
LA - eng
PT - Journal Article
PT - Research Support, Non-U.S. Gov't
DEP - 20111027
PL - England
TA - Trop Med Int Health
JT - Tropical medicine & international health : TM & IH
JID - 9610576
SB - IM
MH - Africa
MH - Ambulatory Care Facilities
MH - Asia, Southeastern
MH - *Commerce
MH - *Diagnostic Tests, Routine/economics/standards
MH - Endemic Diseases
MH - Health Care Surveys
MH - *Health Services/economics/standards
MH - *Health Services Accessibility
MH - Hospitals
MH - Humans
MH - Malaria/*diagnosis/economics/parasitology
MH - Plasmodium falciparum
MH - Plasmodium vivax
MH - *Private Sector/economics/standards
MH - Quality Control
MH - South America
MH - Surveys and Questionnaires
EDAT- 2011/10/29 06:00
MHDA- 2012/12/10 06:00
CRDT- 2011/10/29 06:00
PHST- 2011/10/29 06:00 [entrez]
PHST- 2011/10/29 06:00 [pubmed]
PHST- 2012/12/10 06:00 [medline]
AID - 10.1111/j.1365-3156.2011.02904.x [doi]
PST - ppublish
S0 - Trop Med Int Health. 2012 Feb;17(2):147-52. doi:

10.1111/j.1365-3156.2011.02904.x. Epub 2011 Oct 27.

PMID- 22203975

OWN - NLM

STAT- MEDLINE

DCOM- 20120312

LR - 20220129

IS - 1091-6490 (Electronic)

IS - 0027-8424 (Linking)

VI - 109

IP - 2

DP - 2012 Jan 10

TI - Multiple independent introductions of Plasmodium falciparum in South

America.

PG - 511-6

LID - 10.1073/pnas.1119058109 [doi]

AB - The origin of Plasmodium falciparum in South America is controversial.

Some studies suggest a recent introduction during the European colonizations and the transatlantic slave trade. Other evidence--

archeological and genetic--suggests a much older origin. We collected and

analyzed P. falciparum isolates from different regions of the world,

encompassing the distribution range of the parasite, including populations from sub-Saharan Africa, the Middle East, Southeast Asia, and

South America. Analyses of microsatellite and SNP polymorphisms show that

the populations of P. falciparum in South America are subdivided in two

main genetic clusters (northern and southern). Phylogenetic analyses, as

well as Approximate Bayesian Computation methods suggest independent

introductions of the two clusters from African sources. Our estimates of

divergence time between the South American populations and their likely

sources favor a likely introduction from Africa during the transatlantic

slave trade.

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FAU - Prugnolle, Franck
AU - Prugnolle F
LA - eng
GR - R01 AI067727/AI/NIAID NIH HHS/United States
GR - 1U19AI089681-01/AI/NIAID NIH HHS/United States
GR - 089275/WT_/Wellcome Trust/United Kingdom
GR - BB/H008802/1/BB_/Biotechnology and Biological Sciences
Research
Council/United Kingdom
GR - U19 AI089681/AI/NIAID NIH HHS/United States
PT - Journal Article
PT - Research Support, N.I.H., Extramural
PT - Research Support, Non-U.S. Gov't
DEP - 20111227
PL - United States
TA - Proc Natl Acad Sci U S A
JT - Proceedings of the National Academy of Sciences of the United
States of
America
JID - 7505876
SB - IM
MH - Bayes Theorem
MH - Cluster Analysis
MH - *Demography
MH - *Emigration and Immigration
MH - *Genetic Variation
MH - Genetics, Population
MH - Humans
MH - Logistic Models
MH - Microsatellite Repeats/genetics
MH - Models, Genetic
MH - *Phylogeny
MH - Phylogeography
MH - Plasmodium falciparum/classification/*genetics
MH - Polymorphism, Single Nucleotide/genetics
MH - Principal Component Analysis
MH - South America
PMC - PMC3258587
EDAT- 2011/12/29 06:00
MHDA- 2012/03/13 06:00
CRDT- 2011/12/29 06:00

PHST- 2011/12/29 06:00 [entrez]
PHST- 2011/12/29 06:00 [pubmed]
PHST- 2012/03/13 06:00 [medline]
AID - 1119058109 [pii]
AID - 10.1073/pnas.1119058109 [doi]
PST - ppublish
S0 - Proc Natl Acad Sci U S A. 2012 Jan 10;109(2):511-6. doi:
10.1073/pnas.1119058109. Epub 2011 Dec 27.

PMID- 21364745

OWN - NLM

STAT- MEDLINE

DCOM- 20110901

LR - 20211020

IS - 1932-6203 (Electronic)

IS - 1932-6203 (Linking)

VI - 6

IP - 2

DP - 2011 Feb 18

TI - True versus apparent malaria infection prevalence: the
contribution of a
Bayesian approach.

PG - e16705

LID - 10.1371/journal.pone.0016705 [doi]

AB - AIMS: To present a new approach for estimating the "true
prevalence" of
malaria and apply it to datasets from Peru, Vietnam, and
Cambodia.

METHODS: Bayesian models were developed for estimating both
the malaria
prevalence using different diagnostic tests (microscopy, PCR &
ELISA),
without the need of a gold standard, and the tests'
characteristics.

Several sources of information, i.e. data, expert opinions and
other

sources of knowledge can be integrated into the model. This
approach

resulting in an optimal and harmonized estimate of malaria
infection

prevalence, with no conflict between the different sources of
information, was tested on data from Peru, Vietnam and

Cambodia. RESULTS:

Malaria sero-prevalence was relatively low in all sites, with
ELISA

showing the highest estimates. The sensitivity of microscopy
and ELISA

were statistically lower in Vietnam than in the other sites.
Similarly,

the specificities of microscopy, ELISA and PCR were
significantly lower

in Vietnam than in the other sites. In Vietnam and Peru,
microscopy was

closer to the "true" estimate than the other 2 tests while as

expected

ELISA, with its lower specificity, usually overestimated the prevalence.

CONCLUSIONS: Bayesian methods are useful for analyzing prevalence results

when no gold standard diagnostic test is available. Though some results

are expected, e.g. PCR more sensitive than microscopy, a standardized and

context-independent quantification of the diagnostic tests' characteristics (sensitivity and specificity) and the

underlying malaria

prevalence may be useful for comparing different sites.

Indeed, the use

of a single diagnostic technique could strongly bias the prevalence

estimation. This limitation can be circumvented by using a Bayesian

framework taking into account the imperfect characteristics of the

currently available diagnostic tests. As discussed in the paper, this

approach may further support global malaria burden estimation initiatives.

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AU - Berkvens D
FAU - Erhart, Annette
AU - Erhart A
LA - eng
PT - Evaluation Study
PT - Journal Article
DEP - 20110218
PL - United States
TA - PLoS One
JT - PloS one
JID - 101285081
SB - IM
MH - Adolescent
MH - Adult
MH - Bayes Theorem
MH - Cambodia/epidemiology
MH - Child
MH - Child, Preschool
MH - Diagnosis, Differential
MH - Diagnostic Tests, Routine/standards/statistics & numerical
data
MH - Humans
MH - Infant
MH - Malaria/*diagnosis/*epidemiology
MH - Middle Aged
MH - Peru/epidemiology
MH - Prevalence
MH - Sensitivity and Specificity
MH - Vietnam/epidemiology
MH - Young Adult
PMC - PMC3041757
EDAT- 2011/03/03 06:00
MHDA- 2011/09/02 06:00
CRDT- 2011/03/03 06:00
PHST- 2010/10/13 00:00 [received]
PHST- 2011/01/10 00:00 [accepted]
PHST- 2011/03/03 06:00 [entrez]
PHST- 2011/03/03 06:00 [pubmed]
PHST- 2011/09/02 06:00 [medline]
AID - 10.1371/journal.pone.0016705 [doi]
PST - epublish
S0 - PLoS One. 2011 Feb 18;6(2):e16705. doi: 10.1371/
journal.pone.0016705.

PMID- 21297986
OWN - NLM
STAT- MEDLINE
DCOM- 20110802
LR - 20211020
IS - 1932-6203 (Electronic)
IS - 1932-6203 (Linking)
VI - 6

IP - 1

DP - 2011 Jan 28

TI - Plasmodium vivax sub-patent infections after radical treatment are common

in Peruvian patients: results of a 1-year prospective cohort study.

PG - e16257

LID - 10.1371/journal.pone.0016257 [doi]

AB - BACKGROUND: There is an increasing body of literature reporting treatment

failure of the currently recommended radical treatment of Plasmodium

vivax infections. As P. vivax is the main malaria species outside the

African continent, emerging tolerance to its radical treatment regime

could have major consequences in countries like Peru, where 80% of

malaria cases are due to P. vivax. Here we describe the results of a

1-year longitudinal follow up of 51 confirmed P. vivax patients living

around Iquitos, Peruvian Amazon, and treated according to the Peruvian

national guidelines. METHODOLOGY: Each month a blood sample for

microscopy and later genotyping was systematically collected. Recent

exposure to infection was estimated by detecting antibodies against the

P. vivax circumsporozoite protein (CSP) and all PCR confirmed P. vivax

infections were genotyped with 16 polymorphic microsatellites.

RESULTS:

During a 1-year period, 84 recurrent infections, 22 positive also by

microscopy, were identified, with a median survival time to first

recurrent infection of 203 days. Most of them (71%) were asymptomatic; in

13 patients the infection persisted undetected by microscopy for several

consecutive months. The genotype of mostly recurrent infections differed

from that at day 0 while fewer differences were seen between the

recurrent infections. The average expected heterozygosity was 0.56. There

was strong linkage disequilibrium ($I(A)(s) = 0.29$, $p < 1.10(-4)$) that

remained also when analyzing only the unique haplotypes, suggesting

common inbreeding. CONCLUSION: In Peru, the P. vivax recurrent infections

were common and displayed a high turnover of parasite genotypes compared to day 0. Plasmodium vivax patients, even when treated according to the national guidelines, may still represent an important parasite reservoir that can maintain transmission. Any elimination effort should consider

such a hidden reservoir.
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FAU - D'Alessandro, Umberto

AU - D'Alessandro U

FAU - Erhart, Annette

AU - Erhart A

LA - eng

PT - Journal Article

PT - Research Support, Non-U.S. Gov't

DEP - 20110128

PL - United States

TA - PLoS One

JT - PloS one

JID - 101285081

RN - 0 (Antibodies, Protozoan)

SB - IM

MH - Antibodies, Protozoan/blood

MH - Cohort Studies

MH - Genotype

MH - Humans

MH - Longitudinal Studies

MH - Malaria, Vivax/*epidemiology/*therapy/transmission

MH - Peru/epidemiology

MH - *Plasmodium vivax/genetics

MH - Polymerase Chain Reaction

MH - Prospective Studies

MH - Recurrence

PMC - PMC3030575

EDAT- 2011/02/08 06:00
MHDA- 2011/08/04 06:00
CRDT- 2011/02/08 06:00
PHST- 2010/08/24 00:00 [received]
PHST- 2010/12/20 00:00 [accepted]
PHST- 2011/02/08 06:00 [entrez]
PHST- 2011/02/08 06:00 [pubmed]
PHST- 2011/08/04 06:00 [medline]
AID - 10.1371/journal.pone.0016257 [doi]
PST - epublish
S0 - PLoS One. 2011 Jan 28;6(1):e16257. doi: 10.1371/
journal.pone.0016257.

PMID- 21036823
OWN - NLM
STAT- MEDLINE
DCOM- 20101130
LR - 20211020
IS - 1476-1645 (Electronic)
IS - 0002-9637 (Linking)
VI - 83
IP - 5
DP - 2010 Nov
TI - Placental histopathologic changes associated with subclinical
malaria
infection and its impact on the fetal environment.
PG - 973-80
LID - 10.4269/ajtmh.2010.09-0445 [doi]
AB - Microscopic examination of placental tissue can provide an
accurate
assessment of malaria infection during pregnancy. In this
cross-sectional
study of 193 women in Iquitos, Peru, 1.0% and 6.6% had
parasites in the
peripheral blood as detected by microscopy and polymerase
chain reaction,
respectively. However, 22% had placental malaria pigment
indicating past,
subclinical infections. Placental tissues with pigment from 24
cases were
matched by gravidity and month of delivery to 24 controls and
histopathologically examined. Cases had significantly higher
number of
monocytes in the intervillous space (44.7 versus 25.5; P =
0.012).
Pigmented monocytes in fetal vessels were present in 33.3% of
cases. This
study demonstrated that subclinical malarial infection
occurred
frequently in pregnant women and is associated with increased
presence of
monocytes in the placenta. Pigmented monocytes in fetal
vessels suggest
parasites can breach the placental barrier and enter the fetal

circulation.
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LA - eng
GR - R01 AI064831/AI/NIAID NIH HHS/United States
GR - R03 TW008064/TW/FIC NIH HHS/United States
GR - UR3/CCU 418652/PHS HHS/United States
GR - R01AL064831/PHS HHS/United States
PT - Journal Article
PT - Research Support, N.I.H., Extramural
PT - Research Support, Non-U.S. Gov't
PT - Research Support, U.S. Gov't, P.H.S.
PL - United States
TA - Am J Trop Med Hyg
JT - The American journal of tropical medicine and hygiene
JID - 0370507
RN - 0 (Hemeproteins)
RN - 0 (Pigments, Biological)
RN - 39404-00-7 (hemozoin)
SB - IM
MH - Adolescent
MH - Adult
MH - Case-Control Studies
MH - Cross-Sectional Studies
MH - Female
MH - Hemeproteins/analysis
MH - Humans
MH - Malaria, Falciparum/blood/epidemiology/*pathology
MH - Malaria, Vivax/blood/epidemiology/*pathology
MH - Monocytes/pathology
MH - Parasitemia/blood
MH - Peru/epidemiology
MH - Pigments, Biological/analysis
MH - Placenta/chemistry/parasitology/*pathology
MH - Pregnancy
MH - Pregnancy Complications, Parasitic/blood/epidemiology/
*pathology
MH - Young Adult
PMC - PMC2963955
EDAT- 2010/11/03 06:00
MHDA- 2010/12/14 06:00
CRDT- 2010/11/02 06:00
PHST- 2010/11/02 06:00 [entrez]

PHST- 2010/11/03 06:00 [pubmed]
PHST- 2010/12/14 06:00 [medline]
AID - 83/5/973 [pii]
AID - 10.4269/ajtmh.2010.09-0445 [doi]
PST - ppublish
S0 - Am J Trop Med Hyg. 2010 Nov;83(5):973-80. doi:
10.4269/ajtmh.2010.09-0445.

PMID- 21308193
OWN - NLM
STAT- MEDLINE
DCOM- 20110719
LR - 20191112
IS - 1726-4642 (Electronic)
IS - 1726-4634 (Linking)
VI - 27
IP - 4
DP - 2010 Oct-Dec
TI - [Use of standardized blood smear slide sets for competency
assessment in
the malaria microscopic diagnosis in the Peruvian Amazon].
PG - 540-7
LID - S1726-46342010000400008 [pii]
AB - OBJECTIVES: To assess the competency of microscopists for
malaria
diagnosis using standardized slide sets in the Peruvian
Amazon. MATERIAL
AND METHODS: Cross-sectional study carried out in 122 first
level health
facilities of the Peruvian Amazon, between July and September
2007.
Within the frame of the project "Control Malaria in the border
areas of
the Andean Region: A community approach" (PAMAFRO), we
evaluated the
malaria diagnosis performance in 68 microscopists without
expertise (< 1
year of expertise) and 76 microscopists with expertise (> 1
year) using
standardized sets of 20 blood smear slides according to the
World Health
Organization (WHO) recommendations. A correct diagnosis
(correct species
identification) was defined as "agreement", a microscopist was
qualified
as an "expert" if they have an agreement >=90% (>= 18 slides
with
correct diagnosis), as a "referent" with an agreement between
80% and
<90%, "competent" if they are between 70 and <80% and "in
training" if
they have <70%. RESULTS: Microscopists with expertise (68.6%)
had more
agreement than those without expertise (48.2%). The competency

assessment

was acceptable (competent, referent, or experts levels) in 11.8% of the microscopists without expertise and in 52.6% from those with expertise.

The agreement was lower using blood smear slides with *P. falciparum* with low parasitaemia, with *P. malariae* and with mixed infections.

CONCLUSIONS: Is the first assessment, we found only one of three

microscopists from the Peruvian Amazon is competent for malaria diagnosis

according to the WHO standards. From this baseline data, we have to

continue working in order to improve the competency assessment of the

microscopists within the frame of a quality assurance system.

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AU - Aguirre K

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AU - Llanos-Cuentas A

LA - spa

PT - English Abstract

PT - Journal Article

PT - Research Support, Non-U.S. Gov't

TT - Uso de paneles de laminas estandarizadas para la evaluacion de competencias en el diagnostico microscopico de malaria en la

Amazonia

Peruana.

PL - Peru

TA - Rev Peru Med Exp Salud Publica

JT - Revista peruana de medicina experimental y salud publica

JID - 101227566

SB - IM

MH - Clinical Laboratory Techniques/standards

MH - Cross-Sectional Studies

MH - Humans

MH - Malaria/*blood/*diagnosis

MH - Microscopy/standards

MH - Parasitology/standards

MH - Peru

MH - Professional Competence/*standards

EDAT- 2011/02/11 06:00

MHDA- 2011/07/20 06:00
CRDT- 2011/02/11 06:00
PHST- 2011/02/11 06:00 [entrez]
PHST- 2011/02/11 06:00 [pubmed]
PHST- 2011/07/20 06:00 [medline]
AID - S1726-46342010000400008 [pii]
AID - 10.1590/s1726-46342010000400008 [doi]
PST - ppublish
S0 - Rev Peru Med Exp Salud Publica. 2010 Oct-Dec;27(4):540-7. doi:
10.1590/s1726-46342010000400008.

PMID- 20529273
OWN - NLM
STAT- MEDLINE
DCOM- 20101004
LR - 20211020
IS - 1475-2875 (Electronic)
IS - 1475-2875 (Linking)
VI - 9
DP - 2010 Jun 7
TI - Field evaluation of a rapid diagnostic test (Parascreen) for
malaria
diagnosis in the Peruvian Amazon.
PG - 154
LID - 10.1186/1475-2875-9-154 [doi]
AB - BACKGROUND: The rapid diagnostic tests for malaria (RDT)
constitute a
fast and opportune alternative for non-complicated malaria
diagnosis in
areas where microscopy is not available. The objective of this
study was
to validate a RDT named Parascreen under field conditions in
Iquitos,
department of Loreto, Peru. Parascreen is a RDT that detects
the
histidine-rich protein 2 (HRP2) antigen from Plasmodium
falciparum and
lactate deshydrogenase from all Plasmodium species. METHODS:
Parascreen
was compared with microscopy performed by experts (EM) and
polymerase
chain reaction (PCR) using the following indicators:
sensitivity (Se),
specificity (Sp), positive (PV+) and negative predictive
values (PV-),
positive (LR+) and negative likelihood ratio (LR-). RESULTS: 332
patients
with suspected non-complicated malaria who attended to the MOH
health
centres were enrolled between October and December 2006. For
P.
falciparum malaria, Parascreen in comparison with EM, had Se:
53.5%, Sp:
98.7%, PV+: 66.7%, PV-: 97.8%, LR+: 42.27 and LR-: 0.47; and

for non-P.

falciparum malaria, Se: 77.1%, Sp: 97.6%, PV+: 91.4%, PV-: 92.7%, LR+:

32.0 and LR-: 0.22. The comparison of Parascreen with PCR showed, for P.

falciparum malaria, Se: 81.8%, Sp: 99.1%, PV+: 75%, PV-: 99.4, LR+: 87.27

and LR-: 0.18; and for non-P. falciparum malaria Se: 76.1%, Sp: 99.2%,

PV+: 97.1%, PV-: 92.0%, LR+: 92.51 and LR-: 0.24. CONCLUSIONS: The study

results indicate that Parascreen is not a valid and acceptable test for

malaria diagnosis under the field conditions found in the Peruvian

Amazon. The relative proportion of Plasmodium species, in addition to the

genetic characteristics of the parasites in the area, must be considered

before applying any RDT, especially after the finding of P. falciparum

malaria parasites lacking pfhrp2 gene in this region.

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LA - eng

GR - R01 AI067727/AI/NIAID NIH HHS/United States

PT - Evaluation Study

PT - Journal Article

PT - Research Support, N.I.H., Extramural

PT - Research Support, Non-U.S. Gov't

PT - Validation Study

DEP - 20100607

PL - England

TA - Malar J

JT - Malaria journal

JID - 101139802

RN - 0 (Antigens, Protozoan)

RN - 0 (HRP-2 antigen, Plasmodium falciparum)

RN - 0 (Protozoan Proteins)

RN - 0 (Reagent Kits, Diagnostic)
RN - EC 1.1.1.27 (L-Lactate Dehydrogenase)
SB - IM
MH - Adolescent
MH - Adult
MH - Antigens, Protozoan/*blood/genetics/immunology
MH - False Positive Reactions
MH - Female
MH - Humans
MH - Immunoassay/methods/*standards
MH - L-Lactate Dehydrogenase/blood/immunology
MH - Malaria, Falciparum/*diagnosis
MH - Malaria, Vivax/*diagnosis
MH - Male
MH - Microscopy
MH - Middle Aged
MH - Peru
MH - Plasmodium falciparum/genetics/immunology/*isolation & purification
MH - Plasmodium vivax/genetics/immunology/*isolation & purification
MH - Polymerase Chain Reaction
MH - Protozoan Proteins/blood/genetics/immunology
MH - Reagent Kits, Diagnostic
MH - Reproducibility of Results
MH - Sensitivity and Specificity
MH - Young Adult
PMC - PMC2898785
EDAT- 2010/06/10 06:00
MHDA- 2010/10/05 06:00
CRDT- 2010/06/10 06:00
PHST- 2010/02/28 00:00 [received]
PHST- 2010/06/07 00:00 [accepted]
PHST- 2010/06/10 06:00 [entrez]
PHST- 2010/06/10 06:00 [pubmed]
PHST- 2010/10/05 06:00 [medline]
AID - 1475-2875-9-154 [pii]
AID - 10.1186/1475-2875-9-154 [doi]
PST - epublish
S0 - Malar J. 2010 Jun 7;9:154. doi: 10.1186/1475-2875-9-154.

PMID- 20525233
OWN - NLM
STAT- MEDLINE
DCOM- 20101004
LR - 20211020
IS - 1475-2875 (Electronic)
IS - 1475-2875 (Linking)
VI - 9
DP - 2010 Jun 3
TI - Multilocus genotyping reveals high heterogeneity and strong local population structure of the Plasmodium vivax population in the Peruvian Amazon.

PG - 151

LID - 10.1186/1475-2875-9-151 [doi]

AB - BACKGROUND: Peru is one of the Latin American countries with the highest

malaria burden, mainly due to Plasmodium vivax infections.

However,

little is known about P. vivax transmission dynamics in the Peruvian

Amazon, where most malaria cases occur. The genetic diversity and

population structure of P. vivax isolates collected in different

communities around Iquitos city, the capital of the Peruvian Amazon, was

determined. METHODS: Plasmodium vivax population structure was determined

by multilocus genotyping with 16 microsatellites on 159 P. vivax infected

blood samples (mono-infections) collected in four sites around Iquitos

city. The population characteristics were assessed only in samples with

monoclonal infections (n = 94), and the genetic diversity was determined

by calculating the expected heterozygosity and allelic richness. Both

linkage disequilibrium and the genetic differentiation (θ) were

estimated. RESULTS: The proportion of polyclonal infections varied

substantially by site (11% - 70%), with the expected heterozygosity

ranging between 0.44 and 0.69; no haplotypes were shared between the

different populations. Linkage disequilibrium was present in all

populations (IAS 0.14 - 0.61) but was higher in those with fewer

polyclonal infections, suggesting inbreeding and a clonal population

structure. Strong population differentiation ($\theta = 0.45$) was found and

the Bayesian inference cluster analysis identified six clusters based on

distinctive allele frequencies. CONCLUSION: The P. vivax populations

circulating in the Peruvian Amazon basin are genetically diverse,

strongly differentiated and they have a low effective recombination rate.

These results are in line with the low and clustered pattern of malaria

transmission observed in the region around Iquitos city.

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AU - Anne J
FAU - Erhart, Annette
AU - Erhart A
FAU - D'Alessandro, Umberto
AU - D'Alessandro U
LA - eng
PT - Journal Article
PT - Research Support, Non-U.S. Gov't
DEP - 20100603
PL - England
TA - Malar J
JT - Malaria journal
JID - 101139802
RN - 0 (DNA, Protozoan)
SB - IM
MH - DNA, Protozoan/*genetics
MH - Gene Frequency
MH - *Genetic Variation
MH - Genotype
MH - Humans
MH - Linkage Disequilibrium/genetics
MH - Malaria, Vivax/epidemiology/*parasitology/transmission
MH - Microsatellite Repeats/*genetics
MH - Peru/epidemiology
MH - Plasmodium vivax/classification/*genetics/isolation &
purification
MH - Polymerase Chain Reaction
MH - Recombination, Genetic
MH - Retrospective Studies
PMC - PMC2898784
EDAT- 2010/06/08 06:00
MHDA- 2010/10/05 06:00
CRDT- 2010/06/08 06:00

PHST- 2010/03/12 00:00 [received]
PHST- 2010/06/03 00:00 [accepted]
PHST- 2010/06/08 06:00 [entrez]
PHST- 2010/06/08 06:00 [pubmed]
PHST- 2010/10/05 06:00 [medline]
AID - 1475-2875-9-151 [pii]
AID - 10.1186/1475-2875-9-151 [doi]
PST - epublish
S0 - Malar J. 2010 Jun 3;9:151. doi: 10.1186/1475-2875-9-151.

PMID- 20519594
OWN - NLM
STAT- MEDLINE
DCOM- 20100623
LR - 20211020
IS - 1476-1645 (Electronic)
IS - 0002-9637 (Linking)
VI - 82
IP - 6
DP - 2010 Jun
TI - Adherence to 7-day primaquine treatment for the radical cure of *P. vivax* in the Peruvian Amazon.
PG - 1017-23
LID - 10.4269/ajtmh.2010.09-0521 [doi]
AB - Despite being free of charge, treatment adherence to 7-day primaquine for the radical cure of *Plasmodium vivax* was estimated at 62.2% among patients along the Iquitos-Nauta road in the Peruvian Amazon. The principal reason for non-adherence was the perceived adverse effects related to local humoral illness conceptions that hold that malaria produces a hot state of body, which is further aggravated by the characteristically hot medical treatment. Notably, patients were willing to adhere to the first 3 days of treatment during which symptoms are most apparent and include the characteristic chills. Nevertheless, as symptoms abate, the perceived aggravating characteristics of the medication outweigh the perceived advantages of treatment adherence. Improving community awareness about the role of primaquine to prevent further malaria transmission and fostering a realistic system of direct observed treatment intake, organized at community level, can be expected to improve adherence to the radical cure of *P. vivax* in this

area.

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AU - Montalvo TG
FAU - Rodriguez, Hugo
AU - Rodriguez H
FAU - Cuentas, Alejandro Llanos
AU - Cuentas AL
FAU - D'Alessandro, Umberto
AU - D'Alessandro U
FAU - Gamboa, Dionicia
AU - Gamboa D
LA - eng
GR - R01 AI067727/AI/NIAID NIH HHS/United States
GR - R01-AI067727-03/AI/NIAID NIH HHS/United States
PT - Journal Article
PT - Research Support, N.I.H., Extramural
PT - Research Support, Non-U.S. Gov't
PL - United States
TA - Am J Trop Med Hyg
JT - The American journal of tropical medicine and hygiene
JID - 0370507
RN - 0 (Antimalarials)
RN - MVR3634GX1 (Primaquine)
SB - IM
MH - Adolescent
MH - Adult
MH - Aged
MH - Aged, 80 and over
MH - Animals
MH - Antimalarials/*administration & dosage/adverse effects/
*therapeutic use
MH - Child
MH - Child, Preschool
MH - Cultural Characteristics
MH - Directly Observed Therapy
MH - Humans
MH - Infant
MH - Malaria, Vivax/*drug therapy/epidemiology/psychology
MH - Middle Aged

MH - *Patient Compliance/psychology
MH - Peru/epidemiology
MH - Plasmodium vivax/drug effects
MH - Primaquine/*administration & dosage/adverse effects/
*therapeutic use
MH - Young Adult
PMC - PMC2877405
EDAT- 2010/06/04 06:00
MHDA- 2010/06/24 06:00
CRDT- 2010/06/04 06:00
PHST- 2010/06/04 06:00 [entrez]
PHST- 2010/06/04 06:00 [pubmed]
PHST- 2010/06/24 06:00 [medline]
AID - 82/6/1017 [pii]
AID - 10.4269/ajtmh.2010.09-0521 [doi]
PST - ppublish
S0 - Am J Trop Med Hyg. 2010 Jun;82(6):1017-23. doi:
10.4269/ajtmh.2010.09-0521.

PMID- 20470441

OWN - NLM

STAT- MEDLINE

DCOM- 20101004

LR - 20211020

IS - 1475-2875 (Electronic)

IS - 1475-2875 (Linking)

VI - 9

DP - 2010 May 17

TI - Global sequence variation in the histidine-rich proteins 2 and 3 of

Plasmodium falciparum: implications for the performance of malaria rapid diagnostic tests.

PG - 129

LID - 10.1186/1475-2875-9-129 [doi]

AB - BACKGROUND: Accurate diagnosis is essential for prompt and appropriate

treatment of malaria. While rapid diagnostic tests (RDTs) offer great

potential to improve malaria diagnosis, the sensitivity of RDTs has been

reported to be highly variable. One possible factor contributing to

variable test performance is the diversity of parasite antigens. This is

of particular concern for Plasmodium falciparum histidine-rich protein 2

(PfHRP2)-detecting RDTs since PfHRP2 has been reported to be highly

variable in isolates of the Asia-Pacific region. METHODS: The pfhrp2 exon

2 fragment from 458 isolates of P. falciparum collected from 38 countries

was amplified and sequenced. For a subset of 80 isolates, the

exon 2

fragment of histidine-rich protein 3 (pfhrp3) was also amplified and sequenced. DNA sequence and statistical analysis of the variation observed in these genes was conducted. The potential impact of the pfhrp2 variation on RDT detection rates was examined by analysing the relationship between sequence characteristics of this gene and the results of the WHO product testing of malaria RDTs: Round 1 (2008), for 34 PfHRP2-detecting RDTs. RESULTS: Sequence analysis revealed extensive variations in the number and arrangement of various repeats encoded by the genes in parasite populations world-wide. However, no statistically robust correlation between gene structure and RDT detection rate for *P. falciparum* parasites at 200 parasites per microlitre was identified. CONCLUSIONS: The results suggest that despite extreme sequence variation, diversity of PfHRP2 does not appear to be a major cause of RDT sensitivity variation.

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FAU - McCarthy, James
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FAU - Cheng, Qin
AU - Cheng Q
LA - eng
GR - R01 AI067727-03/AI/NIAID NIH HHS/United States
PT - Journal Article
PT - Research Support, N.I.H., Extramural
PT - Research Support, Non-U.S. Gov't
DEP - 20100517
PL - England
TA - Malar J
JT - Malaria journal
JID - 101139802
RN - 0 (Antigens, Protozoan)
RN - 0 (DNA, Protozoan)
RN - 0 (HRP-2 antigen, Plasmodium falciparum)
RN - 0 (Protozoan Proteins)
RN - 0 (Reagent Kits, Diagnostic)
SB - IM
MH - Animals
MH - Antigens, Protozoan/*genetics/immunology
MH - DNA, Protozoan/genetics
MH - Genetic Variation
MH - Humans
MH - Immunoassay/*methods/standards
MH - Malaria, Falciparum/*diagnosis/genetics/parasitology
MH - Plasmodium falciparum/*genetics/immunology/*isolation & purification

MH - Polymerase Chain Reaction
MH - Protozoan Proteins/*genetics/immunology
MH - Reagent Kits, Diagnostic
MH - Sensitivity and Specificity
MH - Sequence Analysis, DNA
PMC - PMC2893195
EDAT- 2010/05/18 06:00
MHDA- 2010/10/05 06:00
CRDT- 2010/05/18 06:00
PHST- 2010/03/08 00:00 [received]
PHST- 2010/05/17 00:00 [accepted]
PHST- 2010/05/18 06:00 [entrez]
PHST- 2010/05/18 06:00 [pubmed]
PHST- 2010/10/05 06:00 [medline]
AID - 1475-2875-9-129 [pii]
AID - 10.1186/1475-2875-9-129 [doi]
PST - epublish
S0 - Malar J. 2010 May 17;9:129. doi: 10.1186/1475-2875-9-129.

PMID- 20111602
OWN - NLM
STAT- MEDLINE
DCOM- 20100520
LR - 20220409
IS - 1932-6203 (Electronic)
IS - 1932-6203 (Linking)
VI - 5
IP - 1
DP - 2010 Jan 25
TI - A large proportion of *P. falciparum* isolates in the Amazon region of Peru lack pfhrp2 and pfhrp3: implications for malaria rapid diagnostic tests.
PG - e8091
LID - 10.1371/journal.pone.0008091 [doi]
AB - BACKGROUND: Malaria rapid diagnostic tests (RDTs) offer significant potential to improve the diagnosis of malaria, and are playing an increasing role in malaria case management, control and elimination. Peru, along with other South American countries, is moving to introduce malaria RDTs as components of malaria control programmes supported by the Global Fund for AIDS, TB and malaria. The selection of the most suitable malaria RDTs is critical to the success of the programmes.
METHODS: Eight of nine microscopy positive *P. falciparum* samples collected in Iquitos, Peru tested negative or weak positive using HRP2-detecting RDTs. These samples were tested for the presence of pfhrp2 and pfhrp3 and

their

flanking genes by PCR, as well as the presence of HRP proteins by ELISA.

To investigate for geographic extent of HRP-deleted parasites and their

temporal occurrence a retrospective study was undertaken on 148

microscopy positive *P. falciparum* samples collected in different areas of

the Amazon region of Peru. FINDINGS: Eight of the nine isolates lacked

the *pfhrp2* and/or *pfhrp3* genes and one or both flanking genes, and the

absence of HRP was confirmed by ELISA. The retrospective study showed

that 61 (41%) and 103 (70%) of the 148 samples lacked the *pfhrp2* or

pfhrp3 genes respectively, with 32 (21.6%) samples lacking both *hrp*

genes. CONCLUSIONS: This is the first documentation of *P. falciparum*

field isolates lacking *pfhrp2* and/or *pfhrp3*. The high frequency and wide

distribution of different parasites lacking *pfhrp2* and/or *pfhrp3* in

widely dispersed areas in the Peruvian Amazon implies that malaria RDTs

targeting HRP2 will fail to detect a high proportion of *P. falciparum* in

malaria-endemic areas of Peru and should not be used. RDTs detecting

parasite LDH or aldolase and quality microscopy should be used for malaria

diagnosis in this region. There is an urgent need for investigation of

the abundance and geographic distribution of these parasites in Peru and

neighbouring countries.

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AU - Cheng Q
LA - eng
GR - R01 AI067727/AI/NIAID NIH HHS/United States
GR - R01 AI067727-03/AI/NIAID NIH HHS/United States
PT - Journal Article
PT - Research Support, N.I.H., Extramural
PT - Research Support, Non-U.S. Gov't
DEP - 20100125
PL - United States
TA - PLoS One
JT - PloS one
JID - 101285081
RN - 0 (Antigens, Protozoan)
RN - 0 (HRP-2 antigen, Plasmodium falciparum)
RN - 0 (Protozoan Proteins)
RN - 0 (Reagent Kits, Diagnostic)
SB - IM
MH - Animals
MH - Antigens, Protozoan/*genetics
MH - Enzyme-Linked Immunosorbent Assay
MH - Malaria, Falciparum/*diagnosis
MH - Plasmodium falciparum/*genetics/isolation & purification
MH - Protozoan Proteins/*genetics
MH - Reagent Kits, Diagnostic
MH - Retrospective Studies
MH - South America
PMC - PMC2810332
EDAT- 2010/01/30 06:00
MHDA- 2010/05/21 06:00
CRDT- 2010/01/30 06:00
PHST- 2009/09/07 00:00 [received]
PHST- 2009/11/06 00:00 [accepted]
PHST- 2010/01/30 06:00 [entrez]
PHST- 2010/01/30 06:00 [pubmed]
PHST- 2010/05/21 06:00 [medline]
AID - 10.1371/journal.pone.0008091 [doi]
PST - epublish
S0 - PLoS One. 2010 Jan 25;5(1):e8091. doi: 10.1371/
journal.pone.0008091.

PMID- 19514108
OWN - NLM
STAT- MEDLINE
DCOM- 20091008
LR - 20191210
IS - 1872-7573 (Electronic)

IS - 0378-8741 (Linking)
VI - 123
IP - 3
DP - 2009 Jun 25
TI - Medicinal plants from the Yanasha (Peru): evaluation of the leishmanicidal and antimalarial activity of selected extracts.
PG - 413-22
AB - AIM OF THE STUDY: Ninety-four ethanolic extracts of plants used medicinally by the Yanasha, an Amazonian Peruvian ethnic group, for affections related to leishmaniasis and malaria were screened in vitro against *Leishmania amazonensis* amastigotes and against a *Plasmodium falciparum* chloroquine resistant strain. MATERIALS AND METHODS: The viability of *Leishmania amazonensis* amastigote stages was assessed by the reduction of tetrazolium salt (MTT) while the impact on *Plasmodium falciparum* was determined by measuring the incorporation of radio-labelled hypoxanthine. RESULTS AND CONCLUSIONS: Six plant species displayed good activity against *Plasmodium falciparum* chloroquine resistant strain (IC₅₀ < 10 microg/ml): a Monimiaceae, *Siparuna aspera* (Ruiz & Pavon), A. DC., two Zingiberaceae, *Renealmia thyrsoidea* (Ruiz & Pavon) Poepp. & Endl. and *Renealmia alpinia* (Rottb.), two Piperaceae (*Piper aduncum* L. and *Piper* sp.) and the leaves of *Jacaranda copaia* (Aubl.) D. Don (Bignoniaceae). Eight species displayed interesting leishmanicidal activities (IC₅₀ < 10 microg/ml): *Carica papaya* L. (Caricaceae), *Piper dennisii* Trel (Piperaceae), *Hedychium coronarium* J. Konig (Zingiberaceae), *Cestrum racemosum* Ruiz & Pav. (Solanaceae), *Renealmia alpinia* (Rottb.) Zingiberaceae, *Lantana* sp. (Verbenaceae), *Hyptis lacustris* A. St.-Hil. ex Benth. (Lamiaceae) and *Calea montana* Klat. (Asteraceae). Most of them are used against skin affections by Yanasha people. Results are discussed herein, according to the traditional use of the plants and compared with data obtained from the literature.
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FAU - Bourdy, Genevieve
AU - Bourdy G
LA - eng
PT - Evaluation Study
PT - Journal Article
PT - Research Support, Non-U.S. Gov't
PL - Ireland
TA - J Ethnopharmacol
JT - Journal of ethnopharmacology
JID - 7903310
RN - 0 (Antimalarials)
RN - 0 (Plant Extracts)
RN - 0 (Trypanocidal Agents)
SB - IM
MH - Animals
MH - Antimalarials/*pharmacology
MH - Drug Resistance
MH - Leishmania/*drug effects
MH - Life Cycle Stages
MH - *Magnoliopsida
MH - Medicine, Traditional
MH - Parasitic Sensitivity Tests
MH - Peru
MH - Plant Extracts/*pharmacology
MH - *Plants, Medicinal
MH - Plasmodium falciparum/*drug effects
MH - Trypanocidal Agents/*pharmacology
EDAT- 2009/06/11 09:00
MHDA- 2009/10/09 06:00
CRDT- 2009/06/11 09:00
PHST- 2009/06/11 09:00 [entrez]
PHST- 2009/06/11 09:00 [pubmed]
PHST- 2009/10/09 06:00 [medline]
AID - S0378-8741(09)00189-5 [pii]

AID - 10.1016/j.jep.2009.03.041 [doi]
PST - ppublish
S0 - J Ethnopharmacol. 2009 Jun 25;123(3):413-22. doi:
10.1016/j.jep.2009.03.041.

PMID- 18782451

OWN - NLM

STAT- MEDLINE

DCOM- 20081024

LR - 20211020

IS - 1475-2875 (Electronic)

IS - 1475-2875 (Linking)

VI - 7

DP - 2008 Sep 9

TI - Antibody response dynamics to the Plasmodium falciparum
conserved vaccine

candidate antigen, merozoite surface protein-1 C-terminal 19kD
(MSP1-19kD), in Peruvians exposed to hypoendemic malaria
transmission.

PG - 173

LID - 10.1186/1475-2875-7-173 [doi]

AB - BACKGROUND: In high-transmission areas, developing immunity to
symptomatic Plasmodium falciparum infections requires 2-10
years of

uninterrupted exposure. Delayed malaria-immunity has been
attributed to
difficult-to-develop and then short-lived antibody responses.

METHODS: In

a study area with <0.5 P. falciparum infections/person/year,
antibody

responses to the MSP1-19kD antigen were evaluated and
associations with

P. falciparum infections in children and adults. In months
surrounding

and during the malaria seasons of 2003-2004, 1,772
participants received

> or =6 active visits in one study-year. Community-wide
surveys were

conducted at the beginning and end of each malaria season, and
weekly

active visits were completed for randomly-selected individuals
each

month. There were 79 P. falciparum infections with serum
samples

collected during and approximately one month before and after
infection.

Anti-MSP1-19kD IgG levels were measured by ELISA. RESULTS: The
infection

prevalence during February-July was similar in children
(0.02-0.12

infections/person/month) and adults (0.03-0.14 infections/
person/month)

and was negligible in the four-month dry season. In children
and adults,

the seroprevalence was maintained in the beginning (children = 28.9%, adults = 61.8%) versus ending malaria-season community survey (children = 26.7%, adults = 64.6%). Despite the four-month non-transmission season, the IgG levels in Plasmodium-negative adults were similar to P. falciparum-positive adults. Although children frequently responded upon infection, the transition from a negative/low level before infection to a high level during/after infection was slower in children. Adults and children IgG-positive before infection had reduced symptoms and parasite density. CONCLUSION: Individuals in low transmission areas can rapidly develop and maintain alphaMSP1-19kD IgG responses for >4 months, unlike responses reported in high transmission study areas. A greater immune capacity might contribute to the frequent asymptomatic P. falciparum infections in this Peruvian population.

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FAU - Branch, OraLee H

AU - Branch OH

LA - eng

GR - R01 AI064831/AI/NIAID NIH HHS/United States

PT - Journal Article

PT - Research Support, N.I.H., Extramural

PT - Research Support, Non-U.S. Gov't

DEP - 20080909

PL - England

TA - Malar J

JT - Malaria journal

JID - 101139802

RN - 0 (Antibodies, Protozoan)

RN - 0 (Immunoglobulin G)

RN - 0 (Malaria Vaccines)

RN - 0 (Merozoite Surface Protein 1)

SB - IM
MH - Adolescent
MH - Adult
MH - Aged
MH - Aged, 80 and over
MH - Animals
MH - Antibodies, Protozoan/*blood
MH - Child
MH - Child, Preschool
MH - Endemic Diseases/prevention & control
MH - Enzyme-Linked Immunosorbent Assay
MH - Humans
MH - Immunoglobulin G/blood
MH - Infant
MH - Malaria Vaccines/*immunology
MH - Malaria, Falciparum/epidemiology/*prevention & control/
transmission
MH - Merozoite Surface Protein 1/*immunology
MH - Middle Aged
MH - Peru/epidemiology
MH - Plasmodium falciparum/*immunology
MH - Prevalence
MH - Seroepidemiologic Studies
PMC - PMC2557017
EDAT- 2008/09/11 09:00
MHDA- 2008/10/25 09:00
CRDT- 2008/09/11 09:00
PHST- 2008/03/10 00:00 [received]
PHST- 2008/09/09 00:00 [accepted]
PHST- 2008/09/11 09:00 [pubmed]
PHST- 2008/10/25 09:00 [medline]
PHST- 2008/09/11 09:00 [entrez]
AID - 1475-2875-7-173 [pii]
AID - 10.1186/1475-2875-7-173 [doi]
PST - epublish
S0 - Malar J. 2008 Sep 9;7:173. doi: 10.1186/1475-2875-7-173.

PMID- 17961284
OWN - NLM
STAT- MEDLINE
DCOM- 20080421
LR - 20191210
IS - 1469-8161 (Electronic)
IS - 0031-1820 (Linking)
VI - 135
IP - 3
DP - 2008 Mar
TI - Evaluation of an in vitro and in vivo model for experimental
infection
with Leishmania (Viannia) braziliensis and L. (V.) peruviana.
PG - 319-26
AB - Leishmania (Viannia) braziliensis and L. (V.) peruviana are
two parasite
species characterized by a very different pathogenicity in

humans despite
(V.) a high genetic similarity. We hypothesized previously that L.
peruviana would descend from L. (V.) braziliensis and would
have acquired
its 'peruviana' character during the southward colonization
and
adaptation of the transmission cycle in the Peruvian Andes. In
order to
have a first appreciation of the differences in virulence
between both
species, we evaluated an in vitro and in vivo model for
experimental
infective
stages and the purified metacyclics were used to infect
macrophage cell
lines and golden hamsters. The models were tested with 2
representative
strains of L. (V.) braziliensis from cutaneous and mucosal
origin
respectively and 2 representative strains of L. (V.) peruviana
from
Northern and Southern Peru respectively. Our models were
reproducible and
sensitive enough to detect phenotypic differences among
strains. We
showed in vitro as well as in vivo that the L. (V.)
braziliensis was more
infective than L. (V.) peruviana. Furthermore, we found that
in vitro
infectivity patterns of the 4 strains analysed, were in
agreement with
the geographical structuring of parasite populations
demonstrated in our
previous studies. Further work is needed to confirm our
results with more
strains of different geographical origin and their specific
clinical
outcome. However, our data open new perspectives for
understanding the
process of speciation in Leishmania and its implications in
terms of
pathogenicity.

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FAU - Arevalo, J
AU - Arevalo J
FAU - Dujardin, J-C
AU - Dujardin JC
LA - eng
PT - Comparative Study
PT - Evaluation Study
PT - Journal Article
PT - Research Support, Non-U.S. Gov't
DEP - 20071026
PL - England
TA - Parasitology
JT - Parasitology
JID - 0401121
SB - IM
MH - Adaptation, Biological
MH - Animals
MH - Cell Line
MH - Cricetinae
MH - *Disease Models, Animal
MH - Hydrogen-Ion Concentration
MH - Leishmania braziliensis/genetics/*pathogenicity
MH - Leishmaniasis, Cutaneous/*parasitology
MH - Macrophages/*parasitology
MH - Male
MH - *Mesocricetus
MH - Mice
MH - Peru
MH - Phenotype
MH - Random Allocation
MH - Species Specificity
MH - Time Factors
MH - Virulence
EDAT- 2007/10/27 09:00
MHDA- 2008/04/22 09:00
CRDT- 2007/10/27 09:00
PHST- 2007/10/27 09:00 [pubmed]
PHST- 2008/04/22 09:00 [medline]
PHST- 2007/10/27 09:00 [entrez]
AID - S0031182007003848 [pii]
AID - 10.1017/S0031182007003848 [doi]
PST - ppublish
SO - Parasitology. 2008 Mar;135(3):319-26. doi: 10.1017/
S0031182007003848.
Epub 2007 Oct 26.

PMID- 17897481
OWN - NLM
STAT- MEDLINE
DCOM- 20081105
LR - 20151119
IS - 0031-1820 (Print)
IS - 0031-1820 (Linking)

VI - 134

IP - Pt 12

DP - 2007 Nov

TI - Putative markers of infective life stages in *Leishmania* (*Viannia*)

braziliensis.

PG - 1689-98

AB - Gene expression is known to vary significantly during the *Leishmania*

life-cycle. Its monitoring might allow identification of molecular

changes associated with the infective stages (metacyclics and amastigotes) and contribute to the understanding of the

complex host-

parasite relationships. So far, very few studies have been done on

Leishmania (*Viannia*) *braziliensis*, one of the most pathogenic species.

Such studies require, first of all, reference molecular markers. In the

present work, we applied differential display analysis (DD analysis) in

order to identify transcripts that might be (i) candidate markers of

metacyclics and intracellular amastigotes of *L. (V.) braziliensis* or (ii)

potential controls, i.e. constitutively expressed. In total, 48 DNA

fragments gave reliable sequencing data, 29 of them being potential

markers of infective stages and 12 potential controls. Eight sequences

could be identified with reported genes. Validation of the results of DD

analysis was done for 4 genes (2 differentially expressed and 2 controls)

by quantitative real-time PCR. The infective insect stage-specific

protein (meta 1) was more expressed in metacyclic-enriched preparations.

The oligopeptidase b showed a higher expression in amastigotes. Two

genes, glucose-6-phosphate dehydrogenase and a serine/threonine protein

kinase, were found to be similarly expressed in the different biological

samples.

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FAU - Arevalo, J
AU - Arevalo J
FAU - Dujardin, J-C
AU - Dujardin JC
LA - eng
SI - GENBANK/AM420310
SI - GENBANK/AM420311
SI - GENBANK/AM420312
SI - GENBANK/AM420313
PT - Journal Article
PT - Research Support, Non-U.S. Gov't
DEP - 20070926
PL - England
TA - Parasitology
JT - Parasitology
JID - 0401121
RN - 0 (Biomarkers)
SB - IM
MH - Animals
MH - Base Sequence
MH - Biomarkers/metabolism
MH - Gene Expression Profiling
MH - *Gene Expression Regulation
MH - Genes, Protozoan/*genetics
MH - Humans
MH - Leishmania braziliensis/*genetics/*metabolism
MH - Leishmaniasis, Cutaneous/*parasitology
MH - Molecular Sequence Data
MH - Reproducibility of Results
MH - Reverse Transcriptase Polymerase Chain Reaction
EDAT- 2007/09/28 09:00
MHDA- 2008/11/06 09:00
CRDT- 2007/09/28 09:00
PHST- 2007/09/28 09:00 [pubmed]
PHST- 2008/11/06 09:00 [medline]
PHST- 2007/09/28 09:00 [entrez]
AID - S003118200700306X [pii]
AID - 10.1017/S003118200700306X [doi]
PST - ppublish
S0 - Parasitology. 2007 Nov;134(Pt 12):1689-98. doi:
10.1017/S003118200700306X. Epub 2007 Sep 26.

PMID- 17971864
OWN - NLM
STAT- MEDLINE
DCOM- 20080715
LR - 20211020
IS - 1932-6203 (Electronic)

IS - 1932-6203 (Linking)

VI - 2

IP - 10

DP - 2007 Oct 31

TI - A randomised controlled trial to assess the efficacy of dihydroartemisinin-piperaquine for the treatment of uncomplicated

falciparum malaria in Peru.

PG - e1101

AB - BACKGROUND: Multi-drug resistant falciparum malaria is an important

health problem in the Peruvian Amazon region. We carried out a randomised

open label clinical trial comparing mefloquine-artesunate, the current

first line treatment in this region, with dihydroartemisinin-piperaquine.

METHODS AND FINDINGS: Between July 2003 and July 2005, 522 patients with

P. falciparum uncomplicated malaria were recruited, randomized (260 with

mefloquine-artesunate and 262 with dihydroartemisinin-piperaquine),

treated and followed up for 63 days. PCR-adjusted adequate clinical and

parasitological response, estimated by Kaplan Meier survival and Per

Protocol analysis, was extremely high for both drugs (99.6% for

mefloquine-artesunate and 98.4% and for dihydroartemisinin-piperaquine)

(RR: 0.99, 95%CI [0.97-1.01], Fisher Exact $p = 0.21$). All recrudescences

were late parasitological failures. Overall, gametocytes were cleared

faster in the mefloquine-artesunate group (28 vs 35 days) and new

gametocytes tended to appear more frequently in patients treated with

dihydroartemisinin-piperaquine (day 7: 8 (3.6%) vs 2 (0.9%), RR: 3.84,

95%CI [0.82-17.87]). Adverse events such as anxiety and insomnia were

significantly more frequent in the mefloquine-artesunate group, both in

adults and children. CONCLUSION: Dihydroartemisinin-piperaquine is as

effective as mefloquine-artesunate in treating uncomplicated *P.*

falciparum malaria but it is better tolerated and more affordable than

mefloquine-artesunate (US\$1.0 versus US\$18.65 on the local market).

Therefore, it should be considered as a potential candidate

for the first

line treatment of *P. falciparum* malaria in Peru. TRIAL
REGISTRATION:

ClinicalTrials.gov NCT00373607.

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AU - D'Alessandro U

LA - eng

SI - ClinicalTrials.gov/NCT00373607

PT - Journal Article

PT - Randomized Controlled Trial

PT - Research Support, Non-U.S. Gov't

DEP - 20071031

PL - United States

TA - PLoS One

JT - PloS one

JID - 101285081

RN - 0 (Antimalarials)

RN - 0 (Artemisininins)

RN - 0 (Quinolines)

RN - 0 (Sesquiterpenes)

RN - 60W3249T9M (Artesunate)

RN - 6A9050735X (artenimol)

RN - A0HV2Q956Y (piperaquine)

RN - TML814419R (Mefloquine)

SB - IM

MH - Adolescent

MH - Adult

MH - Antimalarials/*pharmacology

MH - Artemisininins/*administration & dosage

MH - Artesunate

MH - Child

MH - Child, Preschool

MH - Female

MH - Humans
MH - Malaria, Falciparum/*drug therapy
MH - Male
MH - Mefloquine/administration & dosage
MH - Middle Aged
MH - Peru
MH - Quinolines/*administration & dosage
MH - Sesquiterpenes/*administration & dosage
PMC - PMC2040506
EDAT- 2007/11/01 09:00
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PHST- 2007/11/01 09:00 [pubmed]
PHST- 2008/07/17 09:00 [medline]
PHST- 2007/11/01 09:00 [entrez]
AID - 10.1371/journal.pone.0001101 [doi]
PST - epublish
S0 - PLoS One. 2007 Oct 31;2(10):e1101. doi: 10.1371/
journal.pone.0001101.

PMID- 17710315

OWN - NLM

STAT- MEDLINE

DCOM- 20080417

LR - 20190606

IS - 0074-0276 (Print)

IS - 0074-0276 (Linking)

VI - 102

IP - 5

DP - 2007 Aug

TI - Isolation and molecular identification of *Leishmania (Viannia) peruviana*

from naturally infected *Lutzomyia peruensis* (Diptera: Psychodidae) in the Peruvian Andes.

PG - 655-8

AB - *Leishmania (Viannia) peruviana* was isolated from 1/75 *Lutzomyia peruensis*

captured during May 2006 in an endemic cutaneous leishmaniasis region of

the Peruvian Andes (Chaute, Huarochiri, Lima, Peru). Sand fly gut with

promastigotes was inoculated into a hamster and the remaining body was

fixed in ethanol. *L. (Viannia) sp.* was determined by polymerase chain

reaction (PCR), and *Leishmania* species through molecular genotyping by

PCR-restriction fragment length polymorphism analyses targeting the genes

cpb and hsp70, resulting *L. (V.) peruviana*. The infected sand fly

appeared 15 days after the rains finished, time expected and useful real

time data for interventions when transmission is occurring.

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FAU - Arevalo, Jorge

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LA - eng

PT - Journal Article

PL - Brazil

TA - Mem Inst Oswaldo Cruz

JT - Memorias do Instituto Oswaldo Cruz

JID - 7502619

RN - 0 (DNA, Protozoan)

SB - IM

MH - Animals

MH - Cricetinae

MH - DNA, Protozoan/*analysis

MH - Female

MH - Genotype

MH - Leishmania braziliensis/genetics/*isolation & purification

MH - Male

MH - Peru

MH - Polymerase Chain Reaction

MH - Polymorphism, Restriction Fragment Length

MH - Psychodidae/*parasitology

EDAT- 2007/08/22 09:00

MHDA- 2008/04/18 09:00

CRDT- 2007/08/22 09:00

PHST- 2007/02/13 00:00 [received]

PHST- 2007/07/02 00:00 [accepted]

PHST- 2007/08/22 09:00 [pubmed]

PHST- 2008/04/18 09:00 [medline]

PHST- 2007/08/22 09:00 [entrez]

AID - S0074-02762007000500020 [pii]

AID - 10.1590/s0074-02762007000500077 [doi]

PST - ppublish

SO - Mem Inst Oswaldo Cruz. 2007 Aug;102(5):655-8. doi:

10.1590/s0074-02762007000500077.

PMID- 15975146

OWN - NLM

STAT- MEDLINE

DCOM- 20061026

LR - 20181113

IS - 1475-2875 (Electronic)

IS - 1475-2875 (Linking)

VI - 4

DP - 2005 Jun 23

TI - Clustered local transmission and asymptomatic Plasmodium falciparum and

Plasmodium vivax malaria infections in a recently emerged, hypoendemic

Peruvian Amazon community.

PG - 27

AB - BACKGROUND: There is a low incidence of malaria in Iquitos, Peru, suburbs

detected by passive case-detection. This low incidence might be

attributable to infections clustered in some households/ regions and/or

undetected asymptomatic infections. METHODS: Passive case-detection (PCD)

during the malaria season (February-July) and an active case-detection

(ACD) community-wide survey (March) surveyed 1,907 persons.

Each month,

April-July, 100-metre at-risk zones were defined by location of

Plasmodium falciparum infections in the previous month.

Longitudinal ACD

and PCD (ACP+PCD) occurred within at-risk zones, where 137 houses (573

persons) were randomly selected as sentinels, each with one month of

weekly active sampling. Entomological captures were conducted in the

sentinel houses. RESULTS: The PCD incidence was 0.03 P. falciparum and

0.22 Plasmodium vivax infections/person/malaria-season.

However, the

ACD+PCD prevalence was 0.13 and 0.39, respectively. One explanation for

this 4.33 and 1.77-fold increase, respectively, was infection clustering

within at-risk zones and contiguous households. Clustering makes PCD,

generalized to the entire population, artificially low.

Another

attributable-factor was that only 41% and 24% of the P. falciparum and P.

vivax infections were associated with fever and 80% of the asymptomatic

infections had low-density or absent parasitaemias the following week.

After accounting for asymptomatic infections, a 2.6-fold increase in ACD+PCD versus PCD was attributable to clustered transmission in at-risk zones. CONCLUSION: Even in low transmission, there are frequent highly-clustered asymptomatic infections, making PCD an inadequate measure of incidence. These findings support a strategy of concentrating ACD and insecticide campaigns in houses adjacent to houses where malaria was detected one month prior.

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AU – Gotuzzo E

LA – eng

GR – R01 AI064831/AI/NIAID NIH HHS/United States

GR – R03 TW008064/TW/FIC NIH HHS/United States

PT – Journal Article

PT – Research Support, N.I.H., Extramural

PT – Research Support, U.S. Gov't, P.H.S.

DEP – 20050623

PL – England

TA – Malar J

JT – Malaria journal

JID – 101139802

RN – 0 (Antimalarials)

SB – IM

MH – Adolescent

MH – Adult

MH – Aged

MH - Aged, 80 and over
MH - Animals
MH - Anopheles/parasitology
MH - Antimalarials/therapeutic use
MH - Child
MH - Child, Preschool
MH - Female
MH - Humans
MH - Incidence
MH - Infant
MH - Malaria, Falciparum/diagnosis/drug therapy/*epidemiology/
*transmission
MH - Malaria, Vivax/*diagnosis/drug therapy/*epidemiology/
*transmission
MH - Male
MH - Middle Aged
MH - Peru/epidemiology
MH - Plasmodium falciparum/isolation & purification
MH - Plasmodium vivax/isolation & purification
MH - Prevalence
MH - Suburban Population
MH - Time Factors
PMC - PMC1190209
EDAT- 2005/06/25 09:00
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PHST- 2005/06/23 00:00 [accepted]
PHST- 2005/06/25 09:00 [pubmed]
PHST- 2006/10/27 09:00 [medline]
PHST- 2005/06/25 09:00 [entrez]
AID - 1475-2875-4-27 [pii]
AID - 10.1186/1475-2875-4-27 [doi]
PST - epublish
S0 - Malar J. 2005 Jun 23;4:27. doi: 10.1186/1475-2875-4-27.

PMID- 10904411
OWN - NLM
STAT- MEDLINE
DCOM- 20000829
LR - 20190605
IS - 0074-0276 (Print)
IS - 0074-0276 (Linking)
VI - 95
IP - 4
DP - 2000 Jul-Aug
TI - Genomic rearrangements in trypanosomatids: an alternative to
the "one
gene" evolutionary hypotheses?
PG - 527-34
AB - Most molecular trees of trypanosomatids are based on point
mutations
within DNA sequences. In contrast, there are very few
evolutionary

studies considering DNA (re) arrangement as genetic characters. Waiting for the completion of the various parasite genome projects, first information may already be obtained from chromosome size-polymorphism, using the appropriate algorithms for data processing. Three illustrative models are presented here. First, the case of *Leishmania (Viannia) braziliensis/L. (V.) peruviana* is described. Thanks to a fast evolution rate (due essentially to amplification/deletion of tandemly repeated genes), molecular karyotyping seems particularly appropriate for studying recent evolutionary divergence, including eco-geographical diversification. Secondly, karyotype evolution is considered at the level of whole genus *Leishmania*. Despite the fast chromosome evolution rate, there is qualitative congruence with MLEE- and RAPD-based evolutionary hypotheses. Significant differences may be observed between major lineages, likely corresponding to major and less frequent rearrangements (fusion/fission, translocation). Thirdly, comparison is made with *Trypanosoma cruzi*. Again congruence is observed with other hypotheses and major lineages are delineated by significant chromosome rearrangements. The level of karyotype polymorphism within that "species" is similar to the one observed in "genus" *Leishmania*. The relativity of the species concept among these two groups of parasites is discussed.

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FAU - Le Ray, D

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LA - eng
PT - Journal Article
PT - Research Support, Non-U.S. Gov't
PL - Brazil
TA - Mem Inst Oswaldo Cruz
JT - Memorias do Instituto Oswaldo Cruz
JID - 7502619
SB - IM
MH - Animals
MH - *Evolution, Molecular
MH - *Gene Rearrangement
MH - *Genome, Protozoan
MH - Karyotyping
MH - Leishmania braziliensis/cytology/genetics
MH - Polymorphism, Genetic
MH - Trypanosoma cruzi/cytology/genetics
MH - Trypanosomatina/*genetics
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CRDT- 2000/07/25 11:00
PHST- 2000/07/25 11:00 [pubmed]
PHST- 2000/09/02 11:01 [medline]
PHST- 2000/07/25 11:00 [entrez]
AID - S0074-02762000000400015 [pii]
AID - 10.1590/s0074-02762000000400015 [doi]
PST - ppublish
SO - Mem Inst Oswaldo Cruz. 2000 Jul-Aug;95(4):527-34. doi:
10.1590/s0074-02762000000400015.