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Metagenomics in malaria and non-malarial febrile illnesses

8th ICCMg Conference, Geneva, Switzerland

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17 November 2023

Outline

Malaria

Malaria Genomics

Non-Malaria Febrile Illnesses (NMFIs)

Why is there a need for metagenomics data in malaria endemic settings?

Outlook



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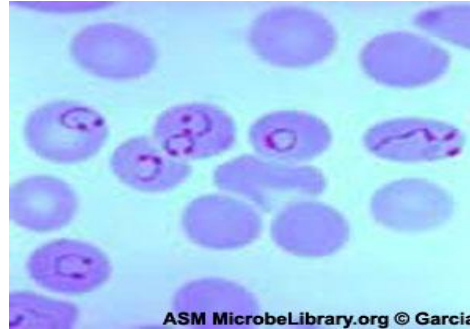
Malaria

Malaria parasite cycle

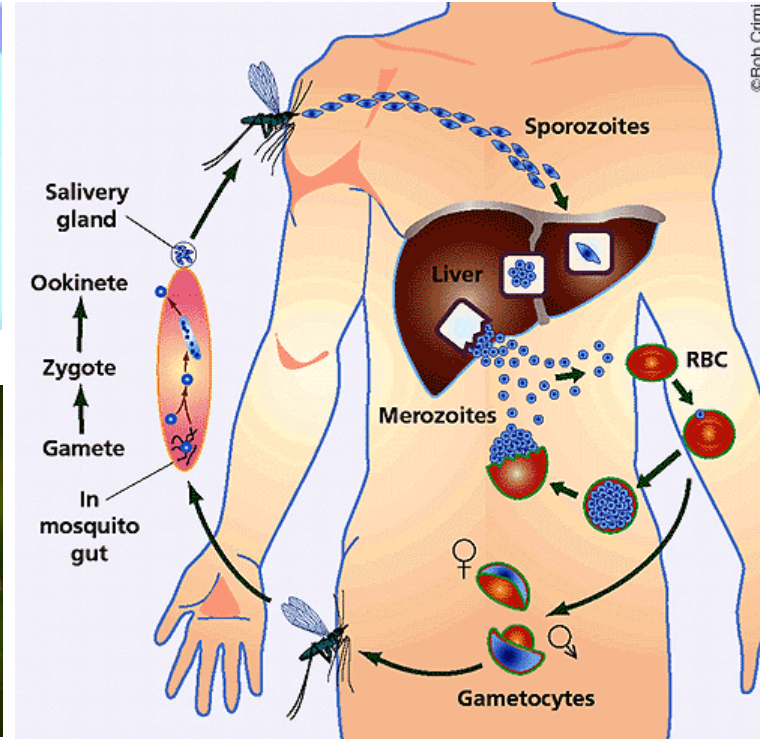
■ Five species

- **Falciparum**
- **Vivax**
- **Ovale**
- **Malariae**
- **Knowlesi** (in Southeast Asia—the monkey malaria parasite)

■ Transmitted by **Anopheline mosquito**



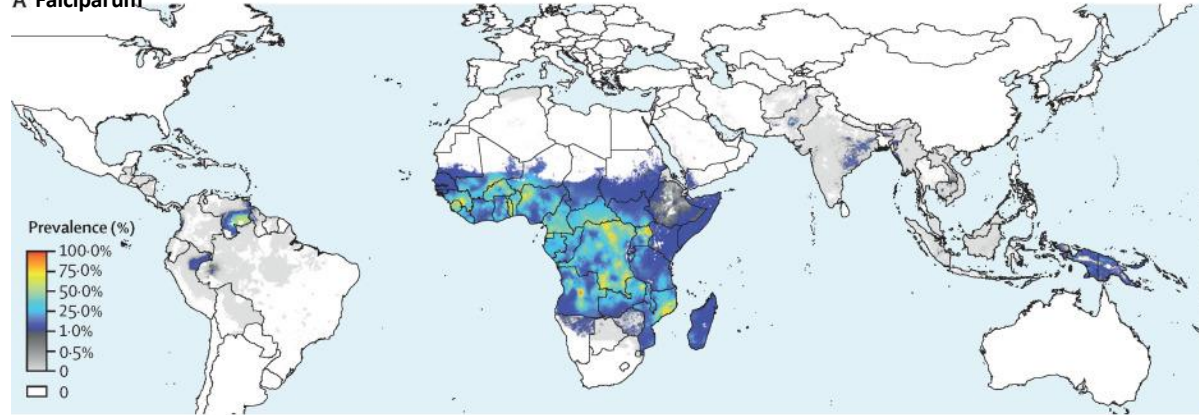
Anopheles freeborni © James Gathany / CDC



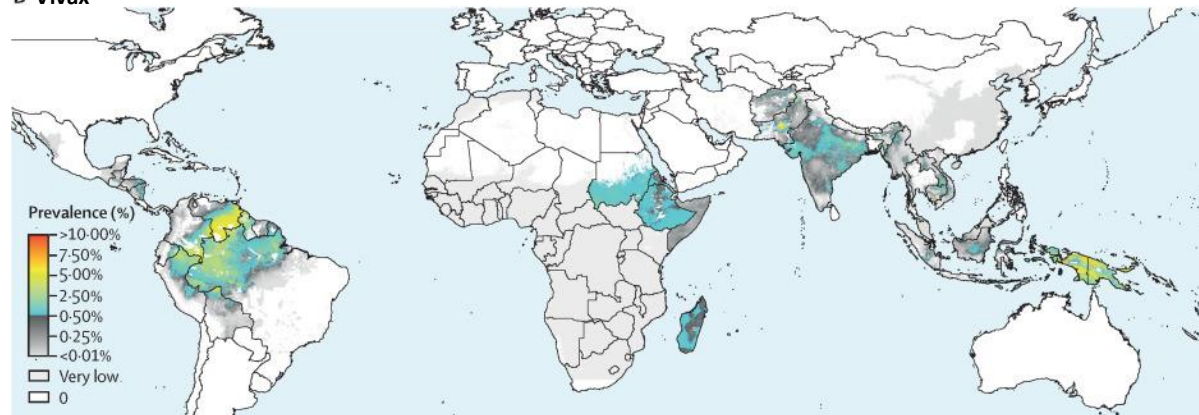
Alan F. Cowman & Brendan S. Crabb. Nature Biotechnology. 2002

Global malaria distribution

A *Falciparum*



B *Vivax*

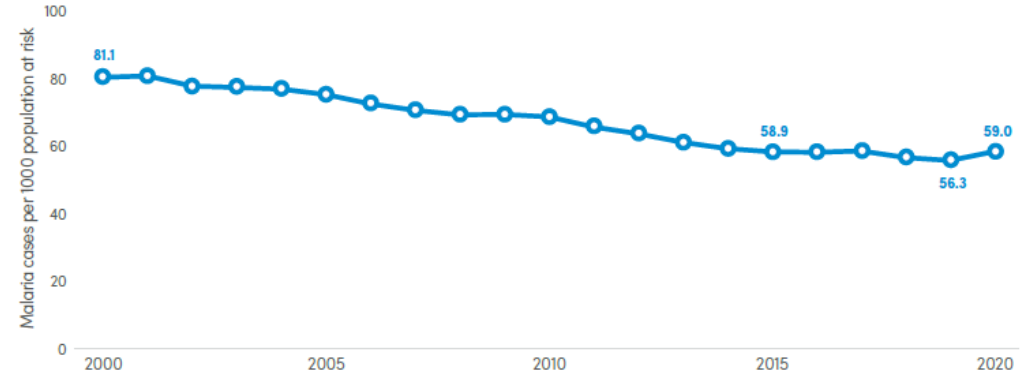


Epidemiology

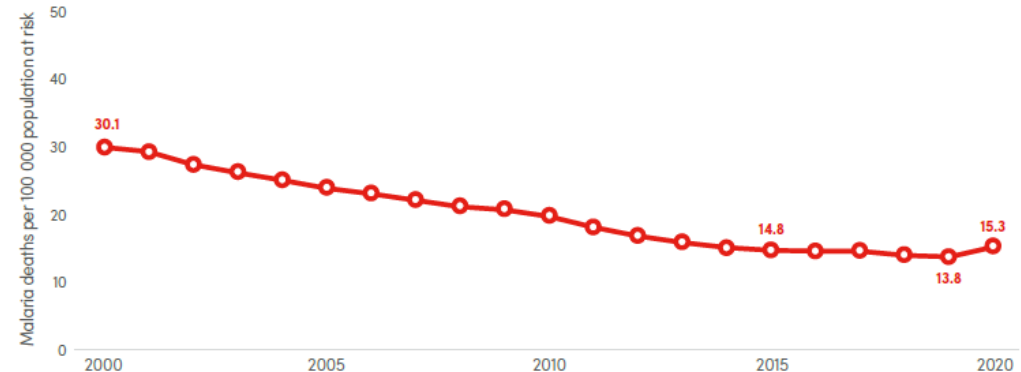
- 249 millions cases in 2020 in 85 countries
- Incidence decreased by 27% between 2010 and 2015 and < 2% between 2015 and 2019
- Increase in number of cases in 2019 due to COVID 19 pandemic
- Twenty nine countries accounted for 95% of malaria cases globally
- Global mortality estimated at 627,000 in 2020
- Increase in number of deaths in 2020 due to COVID 19 pandemic (68%), and new method of calculation (32%)
- Mortality decreased by 50% between 2010 and 2019

World Malaria Report, WHO, 2021

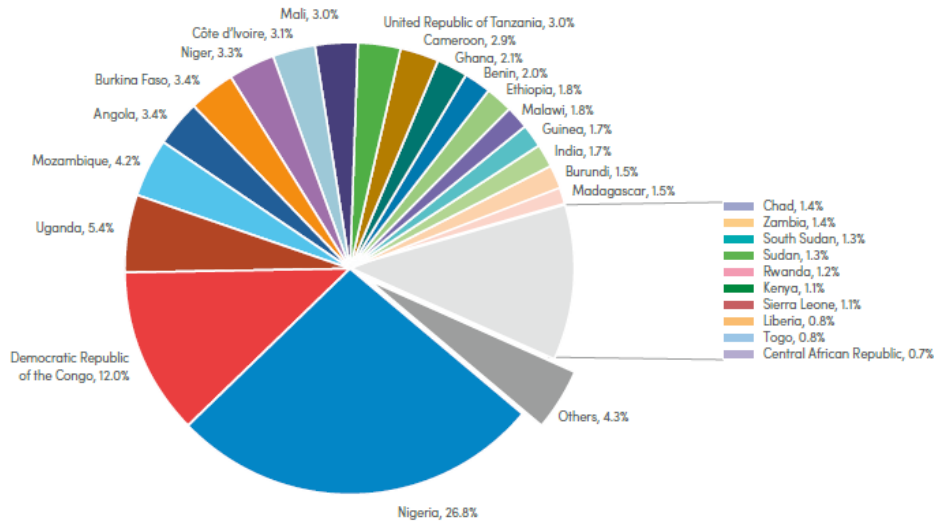
a) Malaria incidence



b) Malaria mortality



Malaria cases & deaths by country

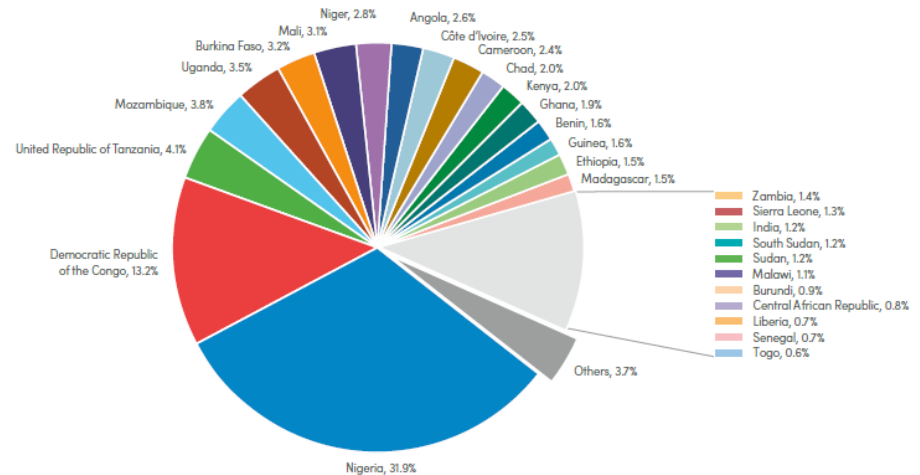


51% of malaria deaths from 4 countries:

- Nigeria: 31.9%
- DRC: 13.2%
- Tanzania: 4.1%
- Mozambique: 3.8%

55% malaria cases from 6 countries:

- Nigeria: 26.8%
- DRC: 12%
- Uganda: 5.4%
- Mozambique: 4.2%
- Angola: 3.4%
- Burkina Faso: 3.4%



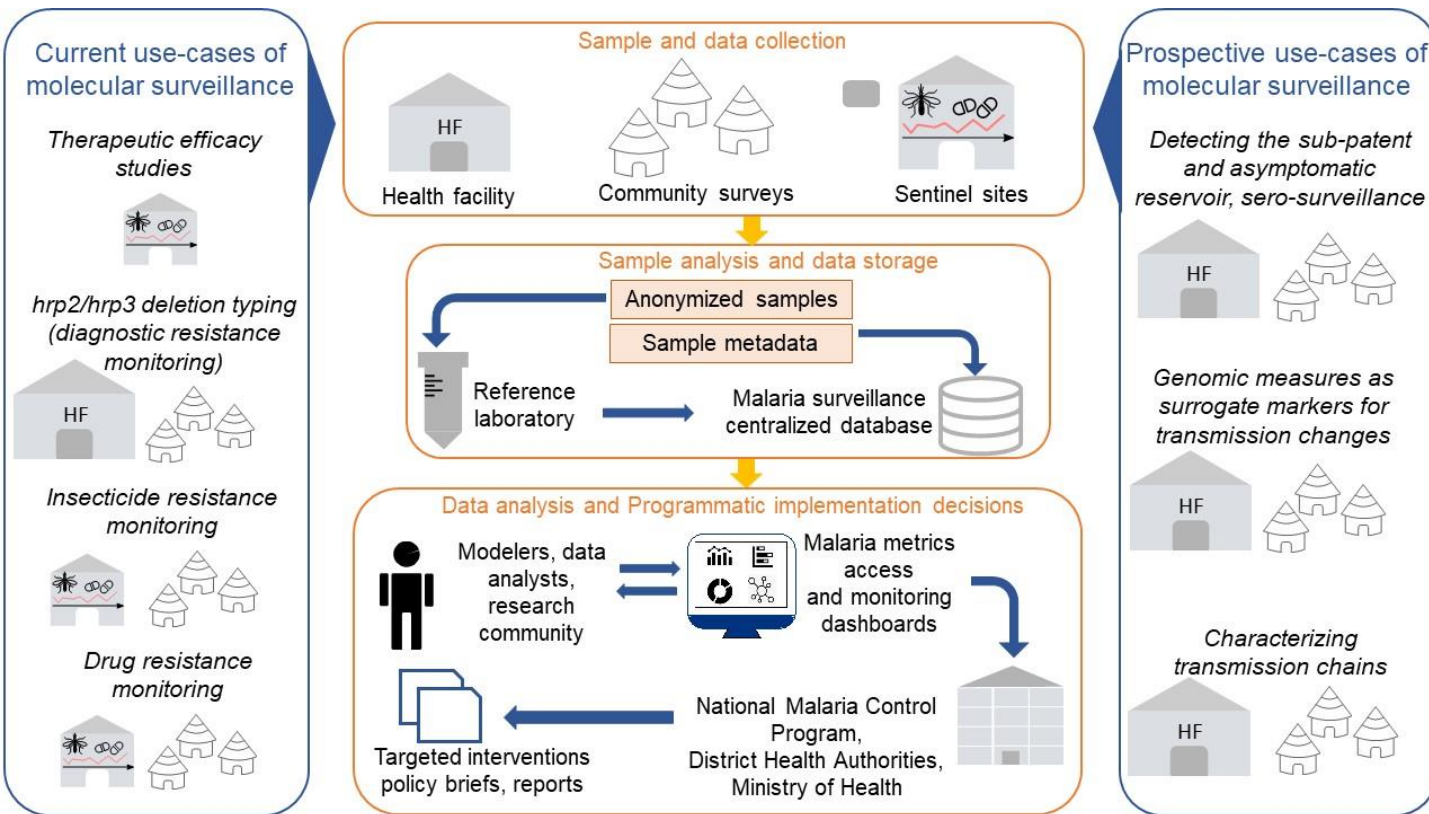


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Malaria genomics

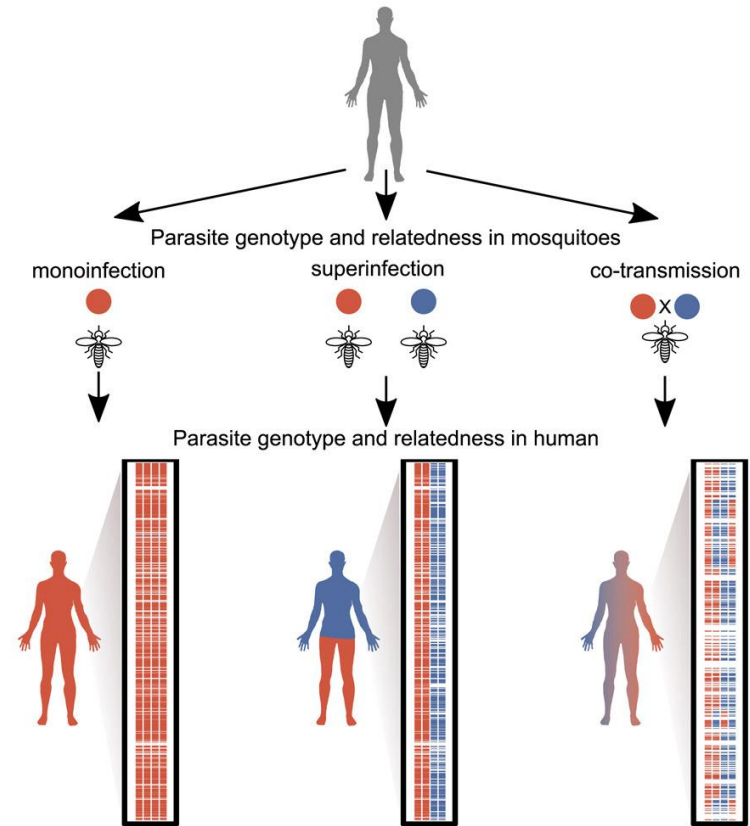
Use cases for malaria genomics



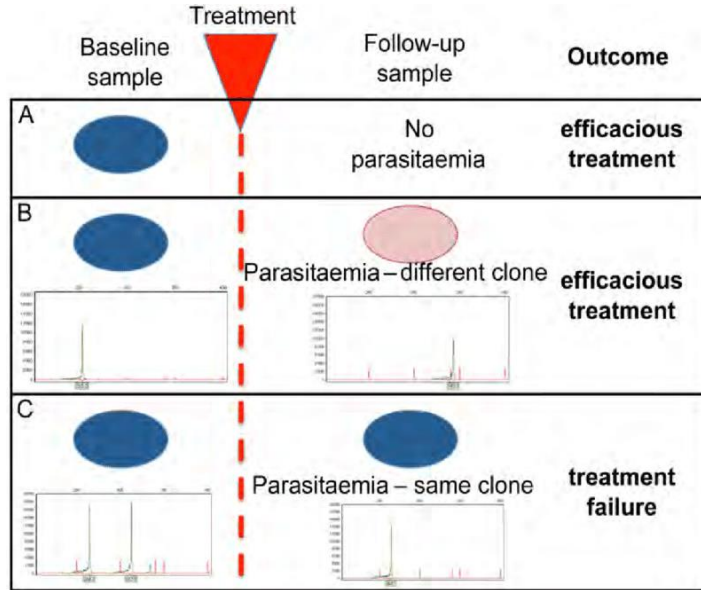
Golumbeanu et al. 2023, AJTMH, in press

Multiplicity of infection (MOI)

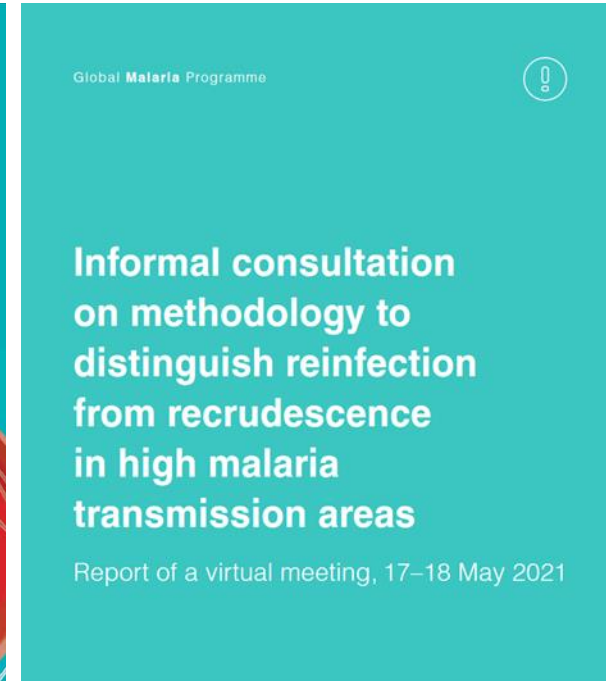
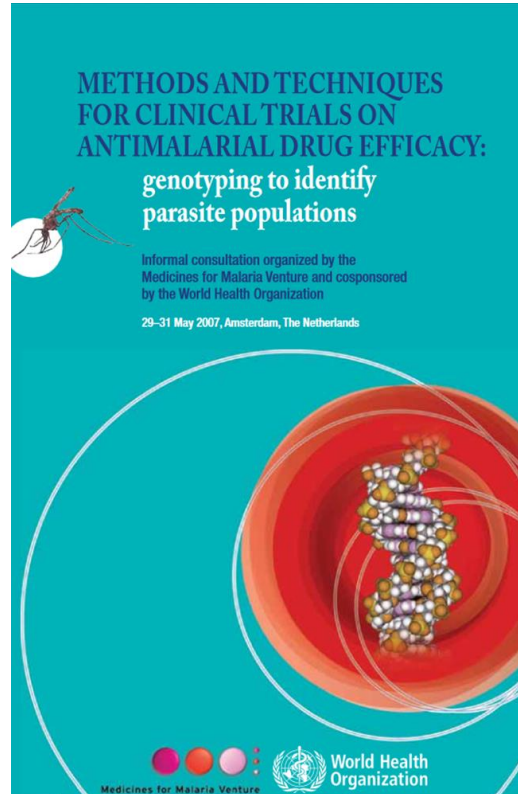
- Higher MOI when using ScSeq compared to bulk sequencing
- Average MOI = 6 compared to 4
- Samples with extremely high MOI: up to 17 different clones
- Need highly diverse markers for routine surveillance with AmpSeq



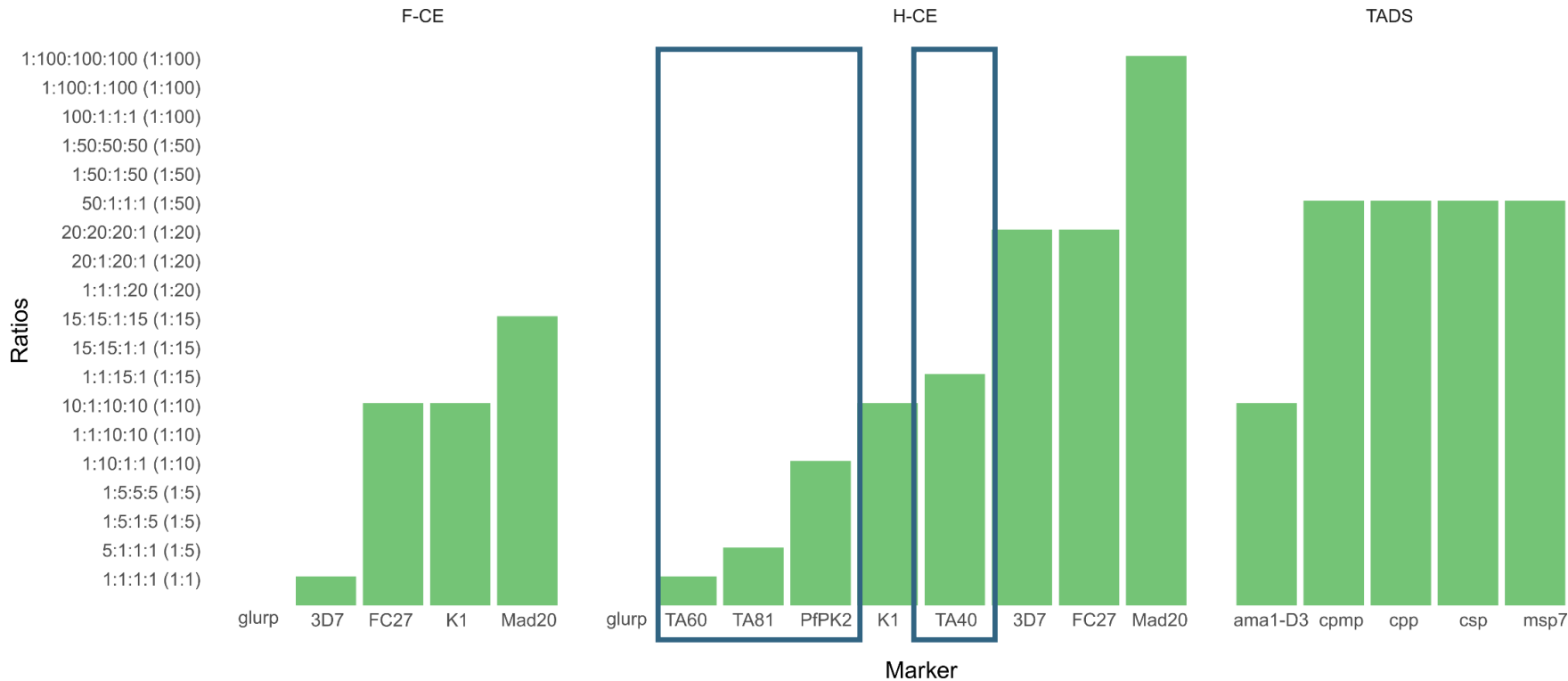
PCR correction



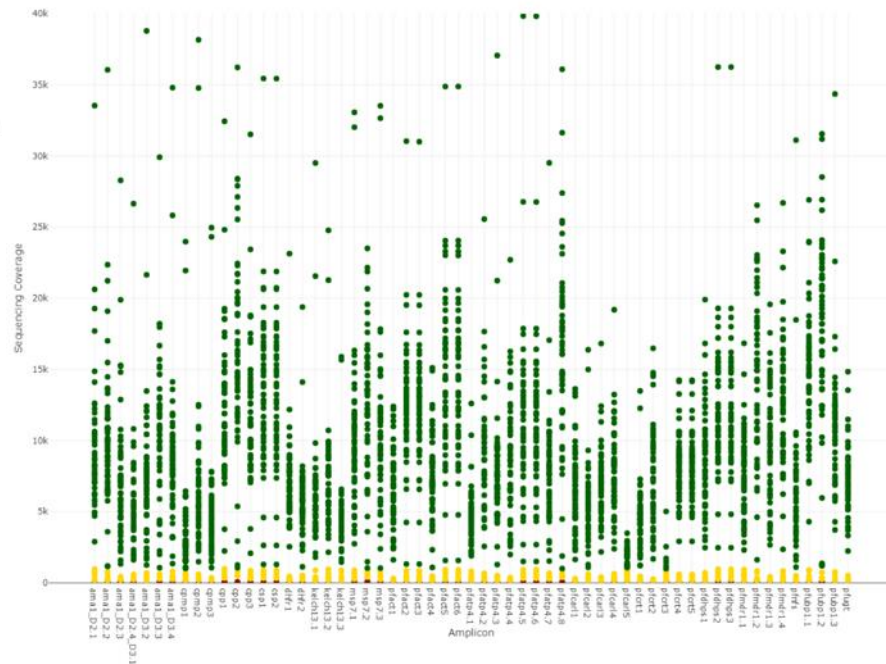
Koepfli et al. 2014; P N G Med J



Analytical sensitivity



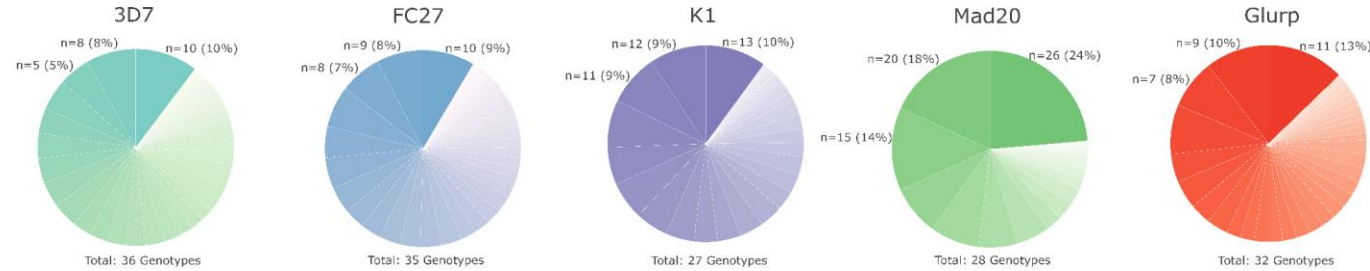
Design molecular markers (Amplicon Sequencing)



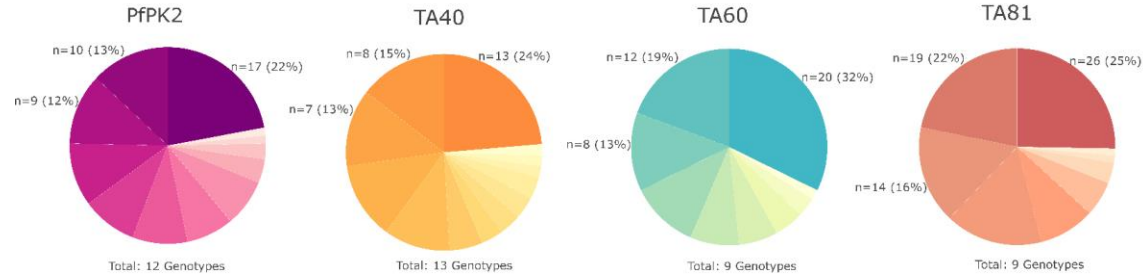
Montero Salas . et al. in development

Select the optimal marker (Amplicon Sequencing)

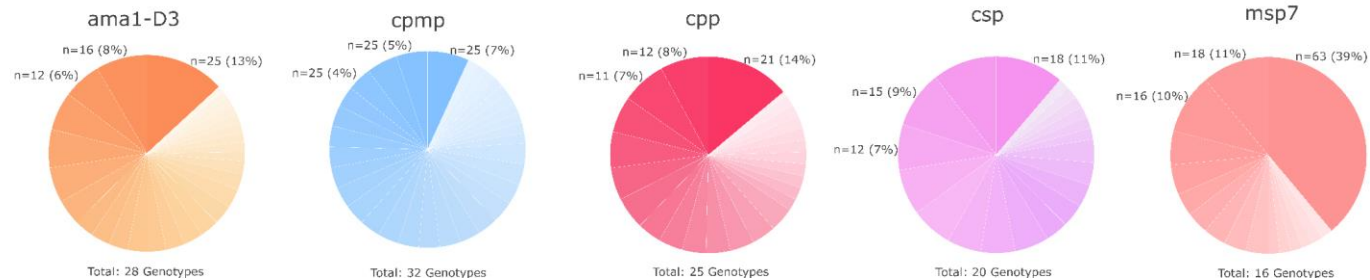
- Length polymorphic genes by CE



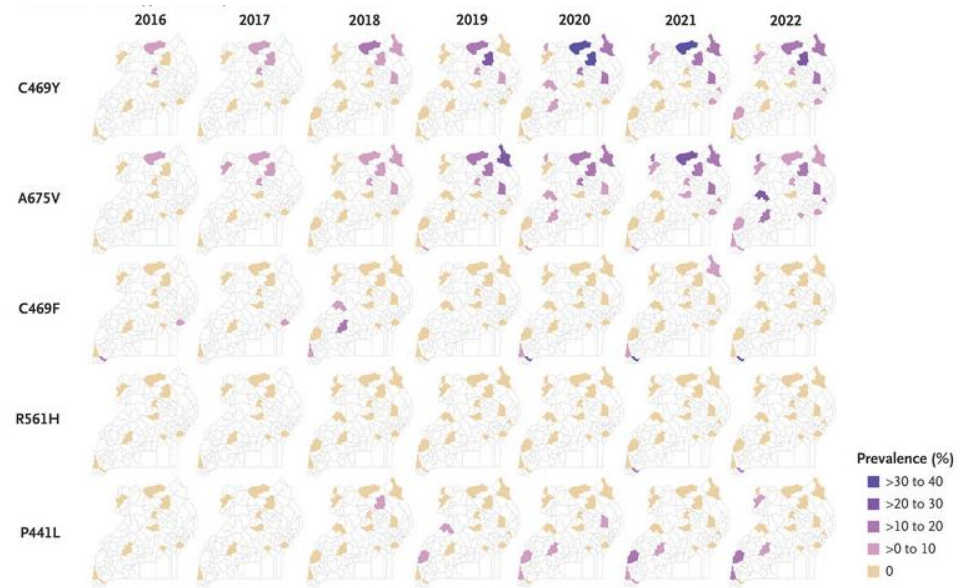
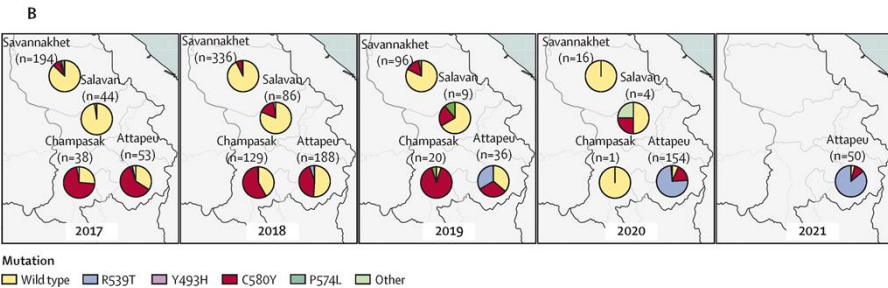
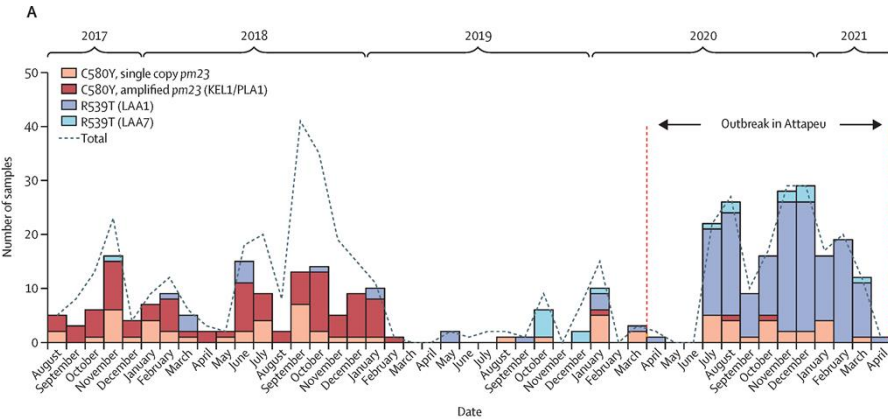
- Microsatellites by CE



- SNP polymorphic genes by TADS



Monitoring the emergence and spread of resistant parasites





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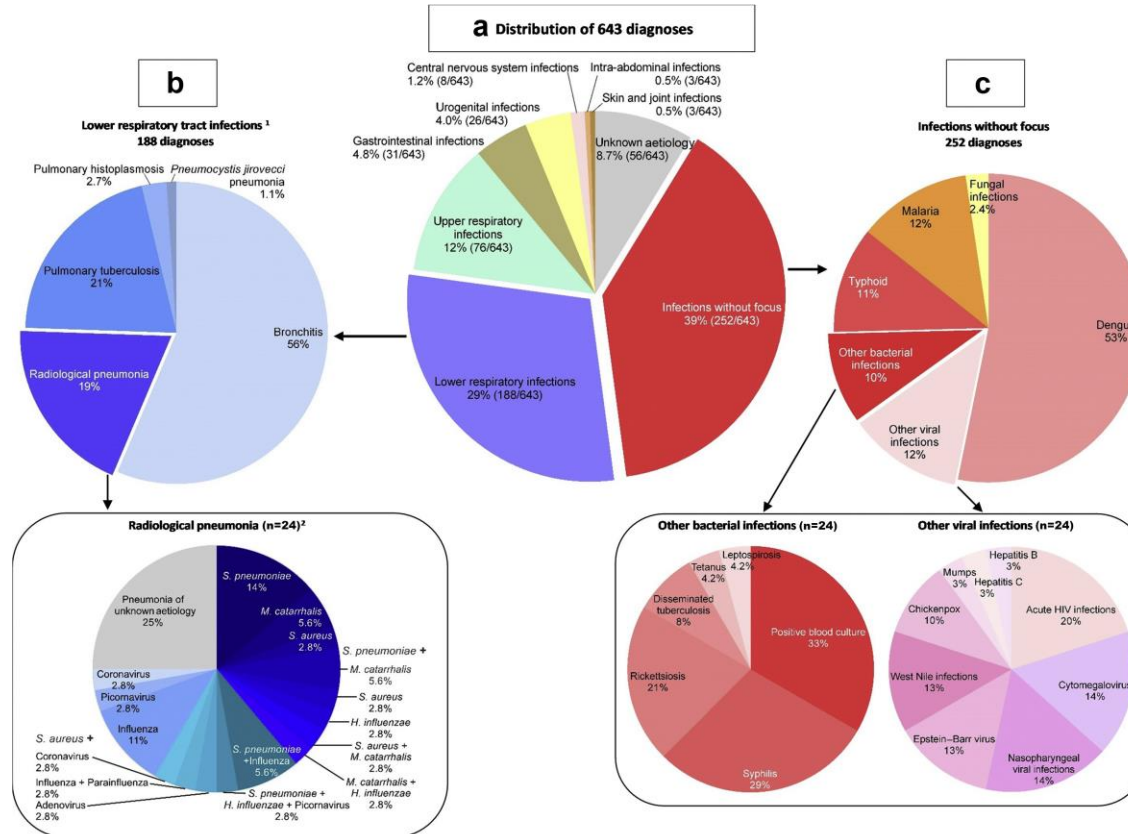
Non-Malarial Febrile Illnesses (NMFIs)

Definition

- Non-malarial febrile illnesses (NMFI) are infectious diseases affecting patients who show signs of indistinguishable fever thus necessitate use of malaria diagnostic tests, but these tests turn out to be negative for malaria

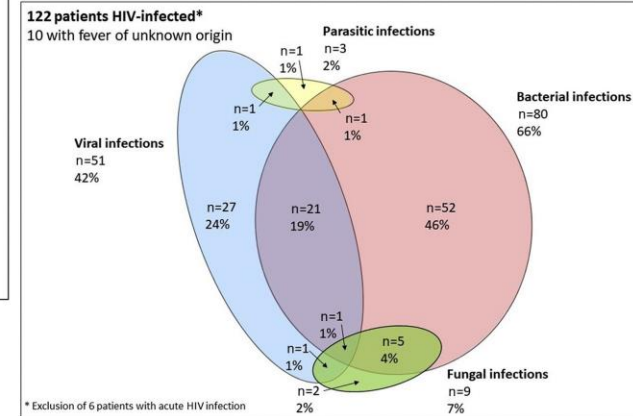
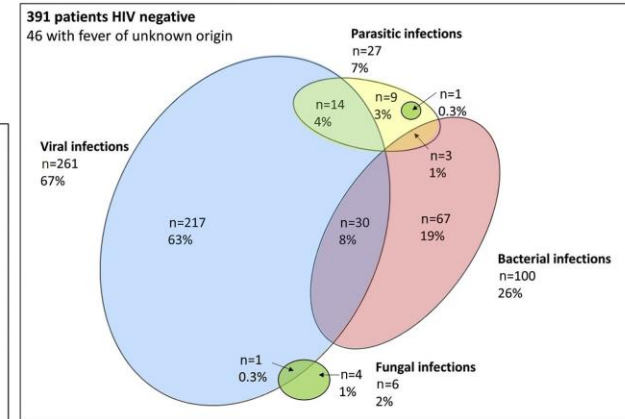
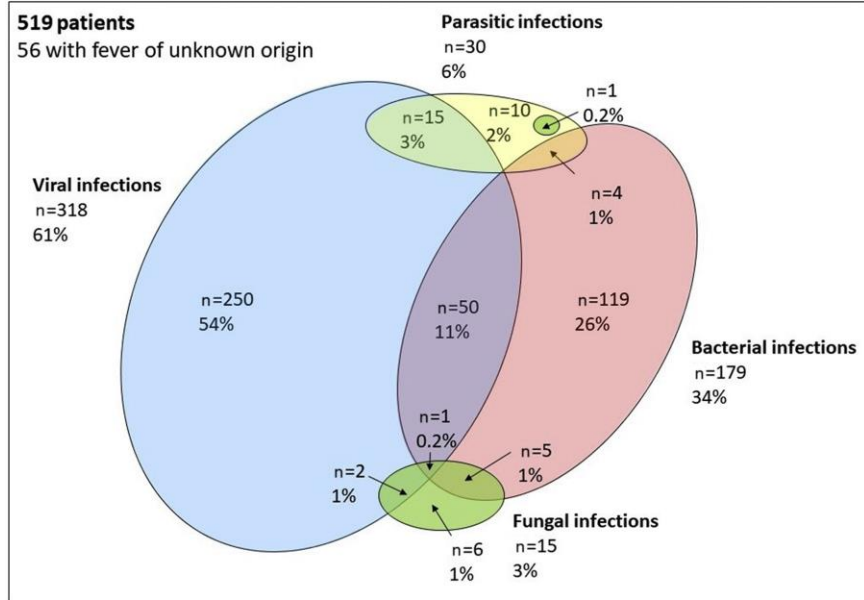
Nyaoke BA. et al. PLoS One. 2019; 14(6): e0217980

Causes of fever in Tanzania



¹ Diagnoses of radiological pneumonia and bronchitis were only considered in patients without pulmonary tuberculosis and/or pneumocystosis.

Causes of fever in Tanzania





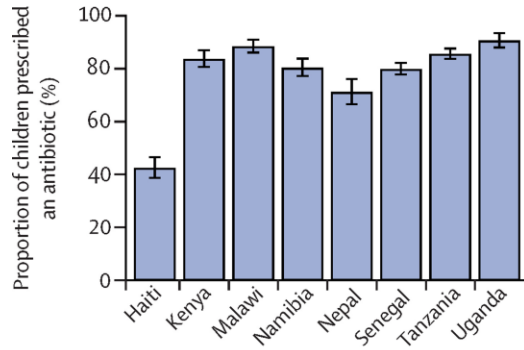
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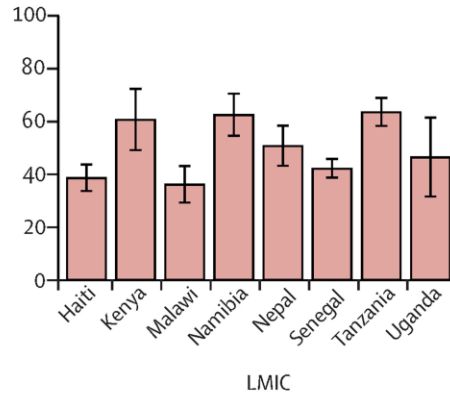
Why is there a need for
metagenomics data in malaria
endemic settings ?

Antibiotic over prescription

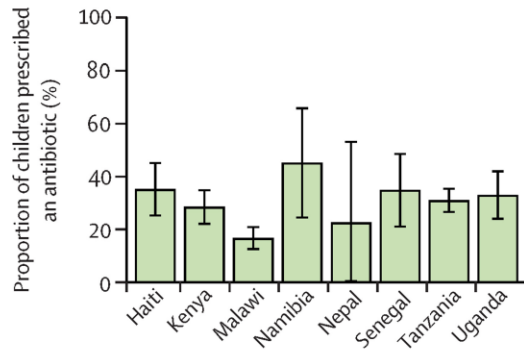
A Respiratory infections



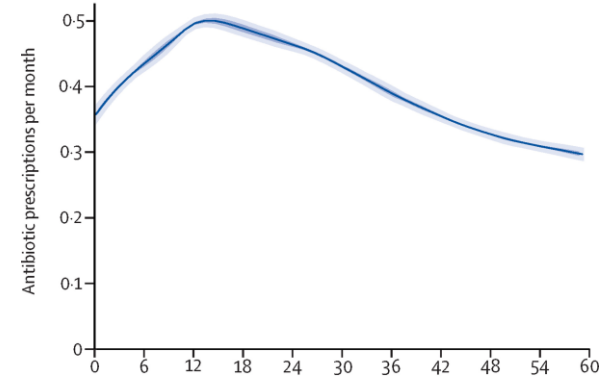
B Diarrhoea



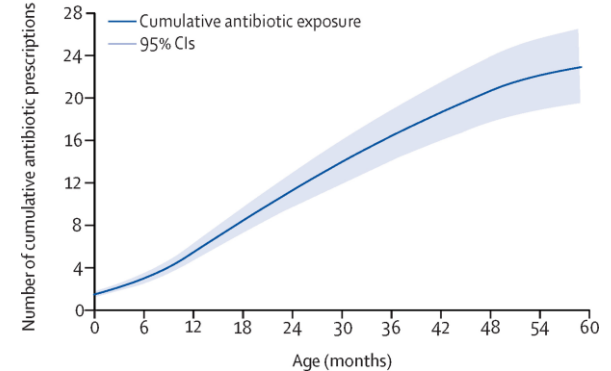
C Malaria



A



B



Limitations of currently used RDTs

Pitfalls and limitations of immunoassay-based RDTs:

Technical

- RDTs based on detection of host antibodies generally have low sensitivity in the first several days of disease – when treatment might be most desirable. Moreover, the accuracy of such tests is affected by host factors and prior infections.
- Despite having a broad range of operating and storage temperatures, antibodies used for RDT assembly may degrade in extreme environments.
- Inherent limits in sensitivity when conventional colorimetric detection is used. Inter-reader variability can be significant, especially for faint test lines.
- May be susceptible to the prozone phenomenon (i.e. falsely negative or borderline results due to an excess of either the antigen or the antibody of interest).
- Specificity may be severely decreased (i.e. false positives) in the presence of concomitant conditions that cause polyclonal hypergammaglobulinaemia.

Operational

- *Training and quality assurance are essential:* even the simplest RDTs can be improperly used or misinterpreted, and inaccurate results can harm patients and undermine their confidence in local medical services.
- *Feasibility at the point-of-care:* unlike conventional laboratory services, health workers using RDTs might assume responsibility for specimen collection *and* testing, as well as for quality control and documentation. This will become an organizational challenge as RDTs for an ever increasing list of diseases become available.
- *User-interpretation of the signal, documentation and archiving of results:* these may be addressed by battery-operated automated RDT readers, which digitally photograph RDT test strips, uniformly interpret the results, and archive standardized photos for subsequent quality assurance.
- *One test = one disease:* while microscopy and bacterial culture have the ability to detect multiple pathogens at once, including unsuspected ones, most existing RDTs only detect a single pathogen. This limits the usefulness of current RDTs in the management of some important clinical syndromes such as sepsis.

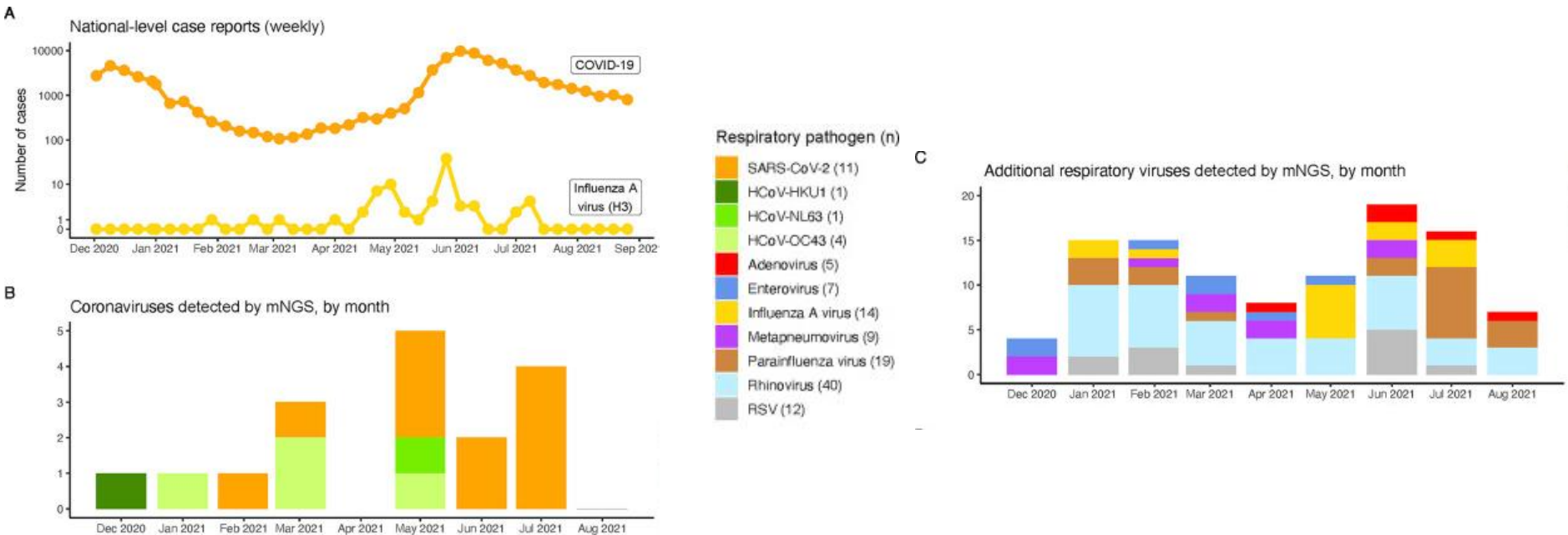
Use of host biomarkers

- CRP can effectively exclude malaria and bacterial infection in febrile children
- Development of CRP/malaria combined RDT

INFECTION	CRP <36.2	CRP ≥36.2
BACTERIAL INFECTION	15 (FN)	34 (TP)
VIRAL INFECTION	122 (TN)	6 (FP)

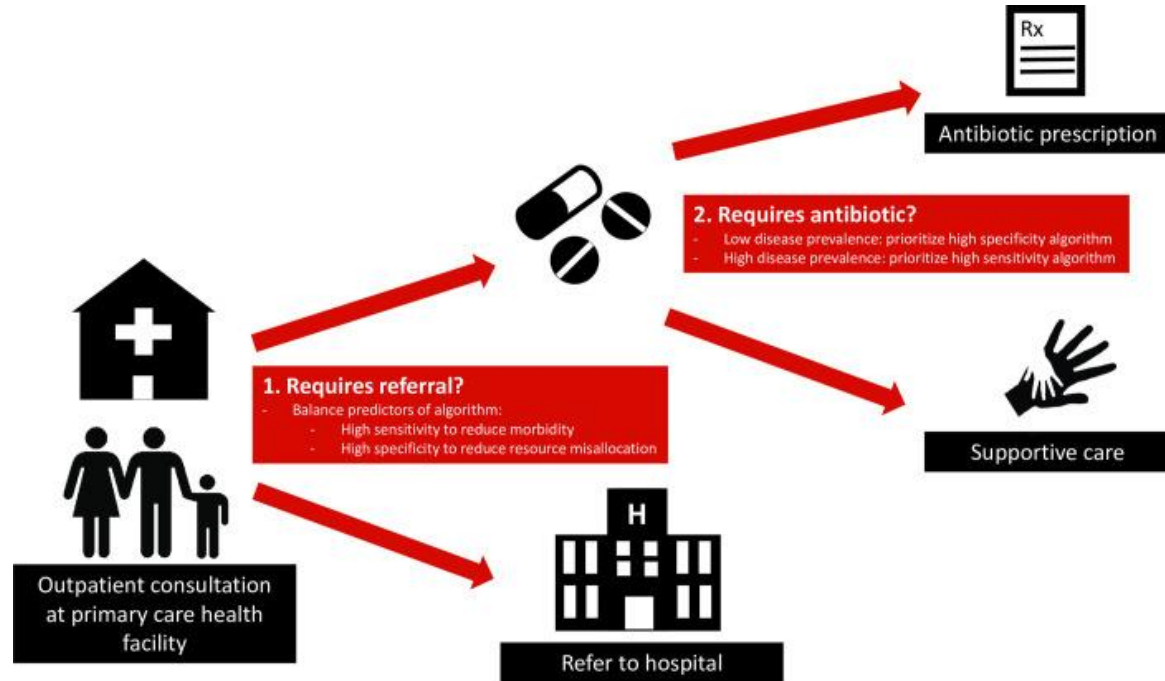
INFECTION	CRP <23.6	CRP ≥23.6
MALARIA	6 (FN)	44 (TP)
VIRAL INFECTION	108 (TN)	20 (FP)

Metagenomics surveillance in LMICs



Use of clinical algorithm assisted with AI

- Most of fevers managed at community level/small health facilities
- Lack of adequate laboratory capacity
- Clinical algorithm for patients triage
 - Clinical symptoms
 - Host biomarkers
 - Genomic surveillance data





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Outlook

COVID-19 as an accelerator ?

Africa PGI - Monitoring SARS-CoV-2 Sequencing in Africa

Select a Country
All Countries

Last Updated: 8/17/2023

(Weekly Updates)

143,600

Total SARS-CoV-2 Sequences

53

MS - Omicron (B.1.1.529)

53

MS - Delta (B.1.617.2)

45

MS - Beta (B.1.351)

66,684

Sequences - Omicron

33,986

Sequences - Delta

12,569

Sequences - Beta

50

MS - Alpha (B.1.1.7)

3

MS - Gamma (P.1)

5,103

Sequences - Alpha

3

Sequences - Gamma



Esri, FAO, NOAA, USGS

Powered by Esri

SARS-CoV-2 Sequencing

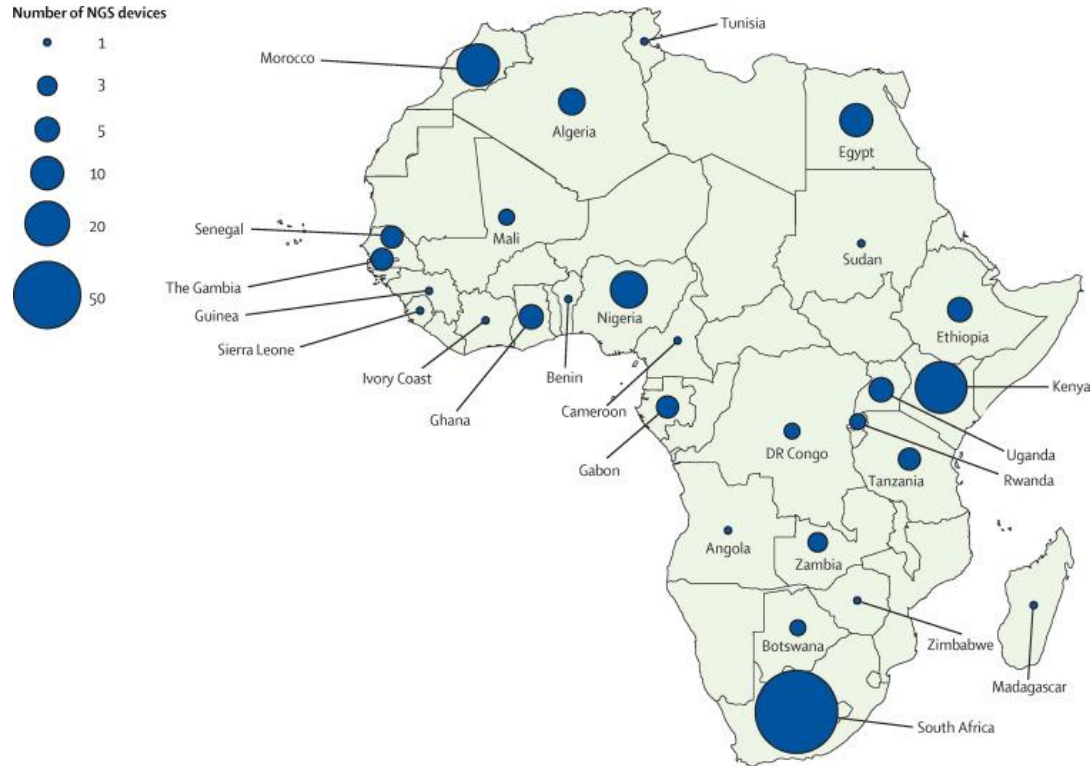
Additional country-specific sequencing info: Move the mouse cursor over the country of interest and click on it. This will display a popup window with additional information.

Data Source: GISAID, Official Regional Collaborating Centre and Member State report, and Official Specialized and Regional Sequencing Hub report. **MS:** Member States.

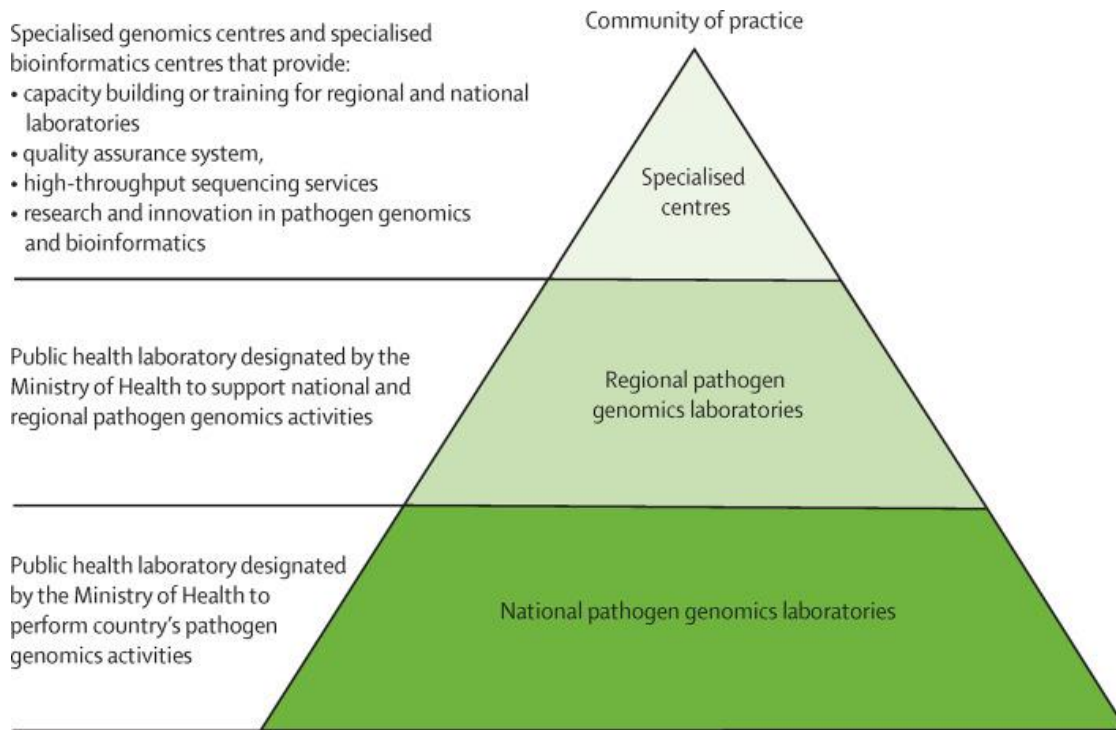
Naming SARS-CoV-2 variants recommended by WHO, [Tracking SARS-CoV-2 variants \(who.int\)](https://www.who.int/tracking-sars-cov-2).

Disclaimer: Data collected from multiple sources and may not reflect the actual figures in country.

NGS capacity in Africa

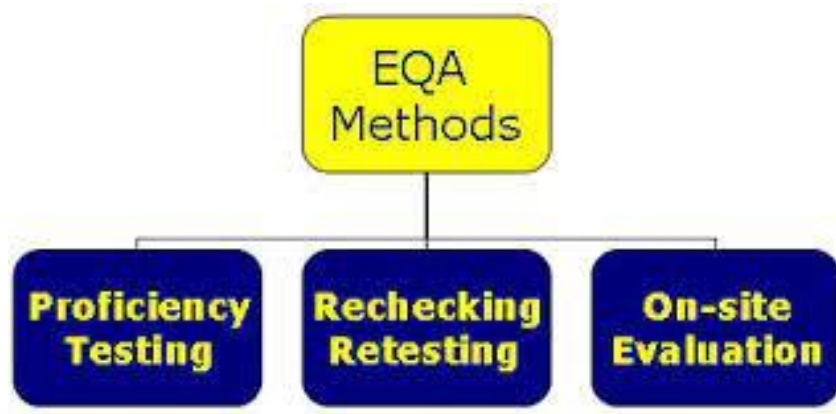


Genomics laboratory and bioinformatics network structure: Africa CDC



Way forward

- Training laboratory staff in genomic analyses
- Training in bioinformatics
- External quality assurance programs
- ISO certification



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Thank you for your attention !

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Department of Medicine
Malaria genotyping group

