The Epidemiology of *Plasmodium vivax* among Asymptomatic Adults in the Democratic Republic of the Congo

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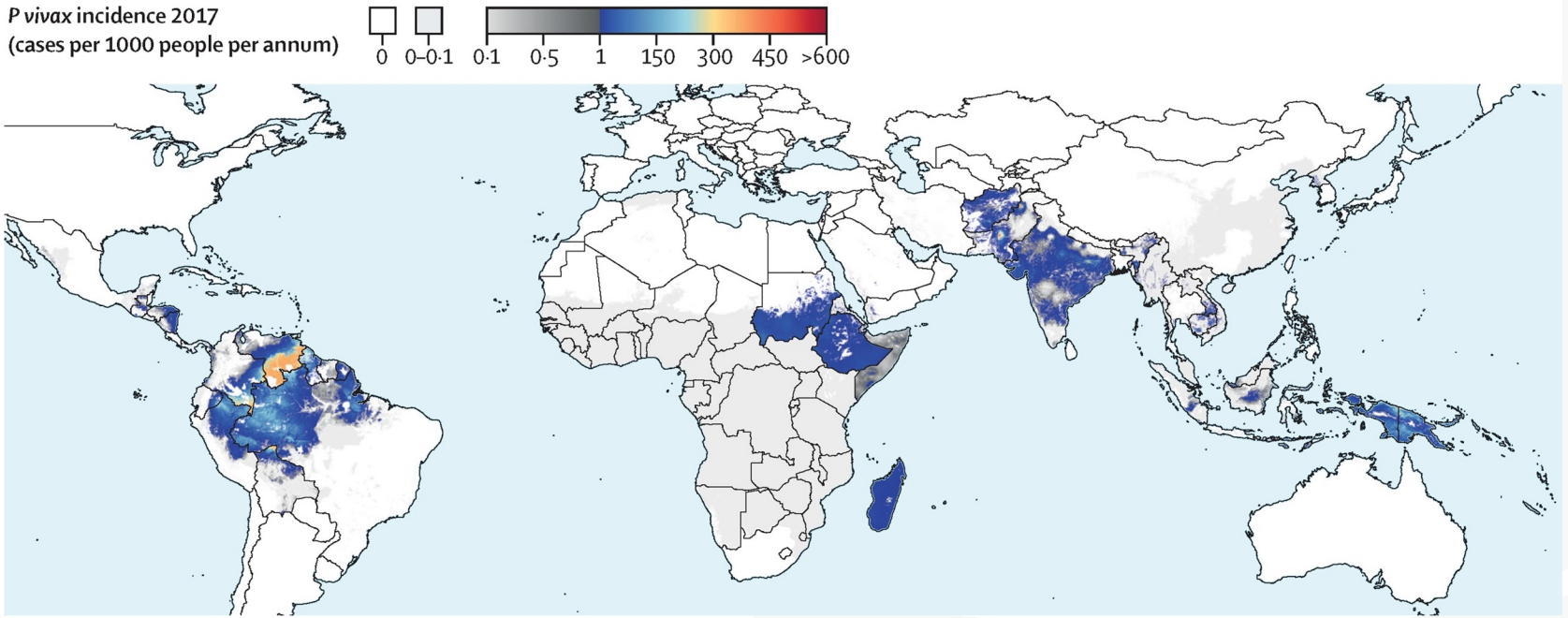
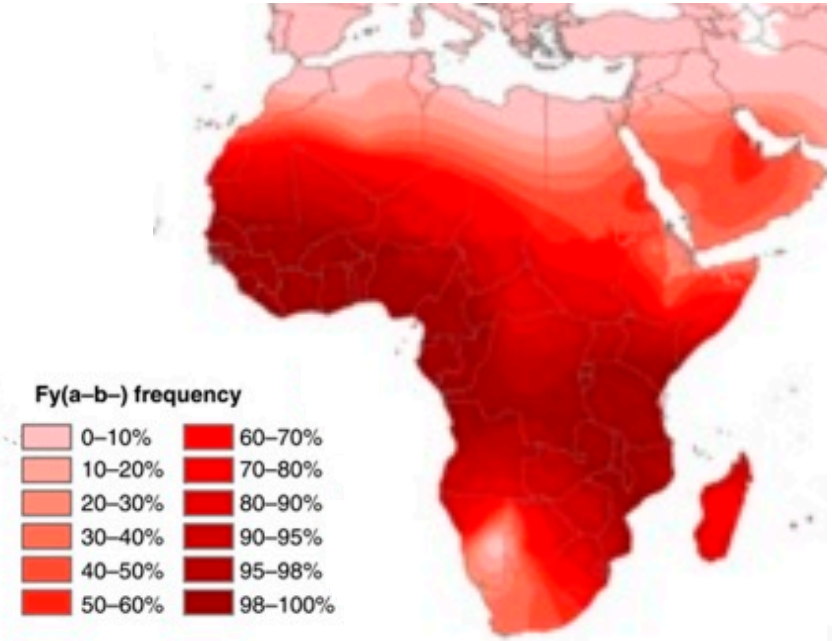
P. vivax Endemicity

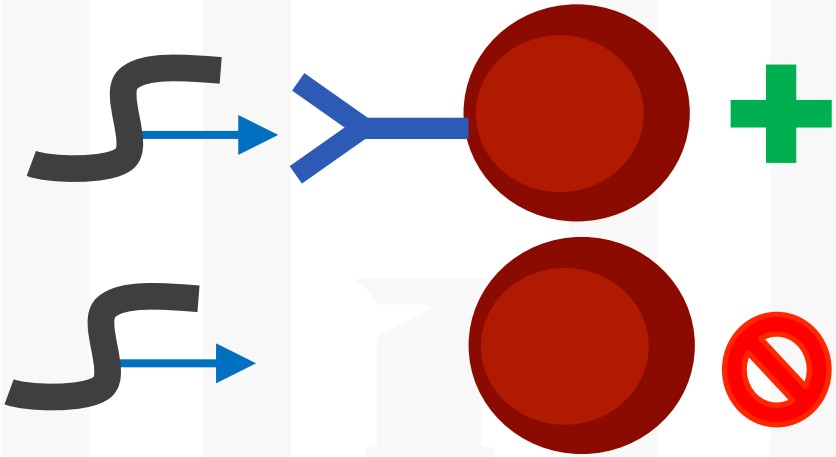


Battle *et al.* 2019, *Lancet*

The Duffy-Negative Phenotype is Common in Sub-Saharan Africa

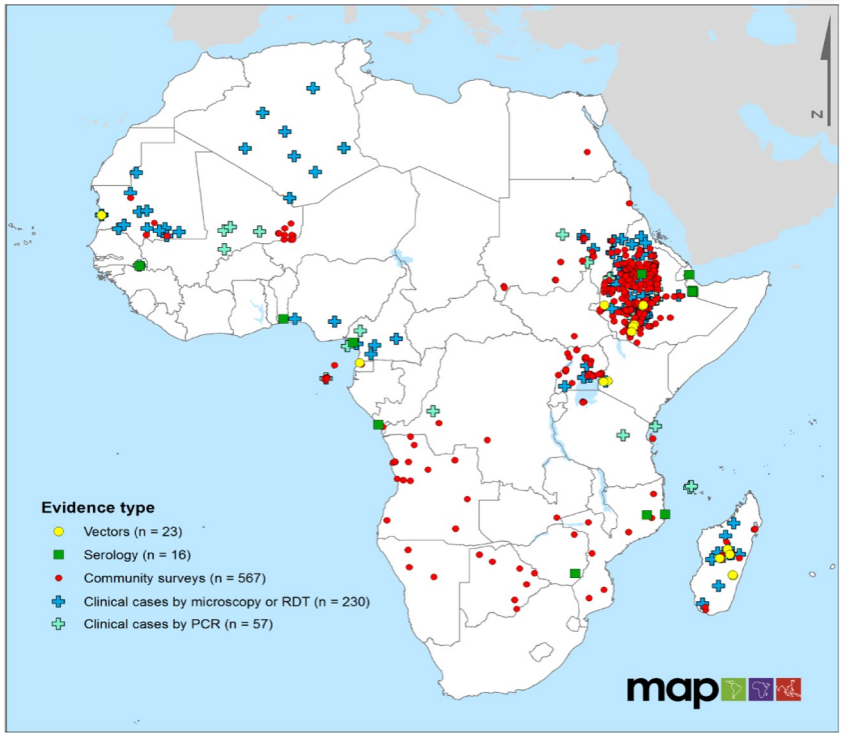


Howes *et al.* 2011, Nat Comms

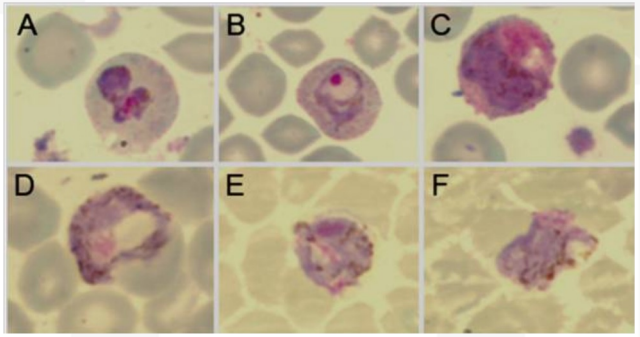


Miller, LH 1976, NEJM
Tournamille, C 1995, Nat Genet
Gunalan *et al.* 2016, PNAS

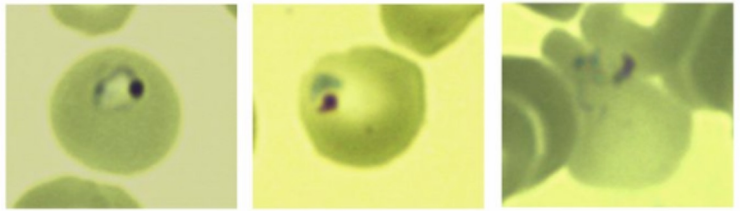
P. Vivax is Prevalent in Africa



Twohig *et al.* 2019, Plos NTD

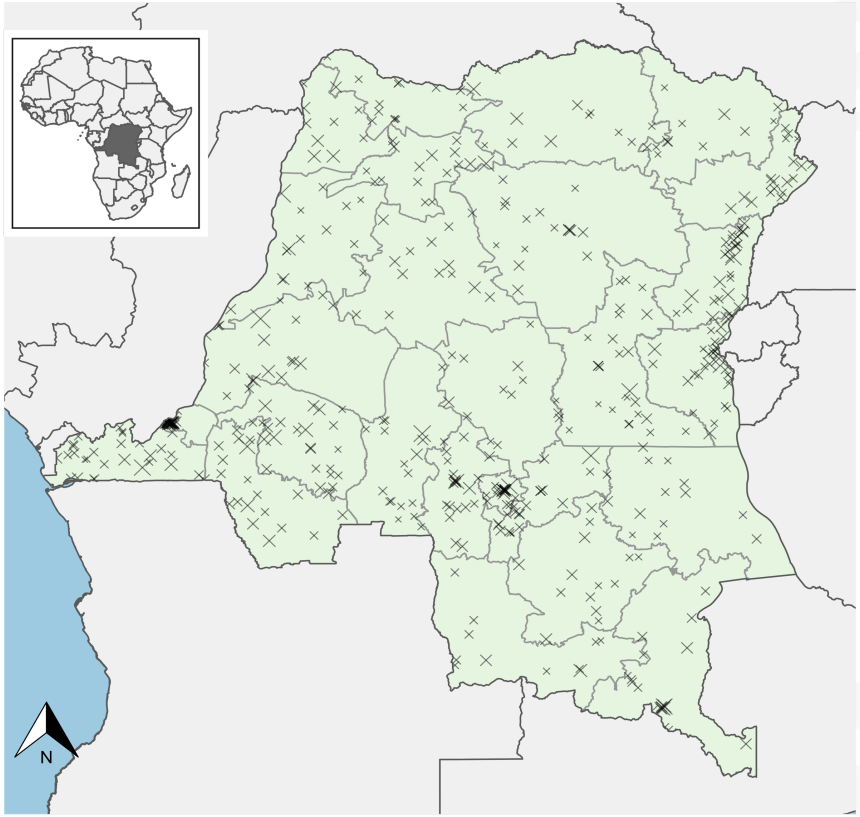


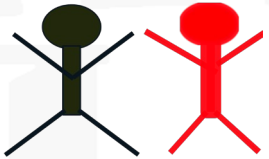
Plasmodium vivax in a Duffy null individual in Ethiopia



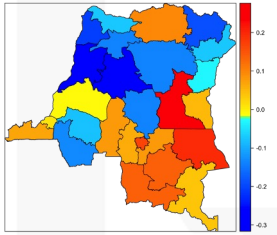
Menard *et al.* 2010, PNAS
Gunalan *et al.* 2016, PNAS

Study Design

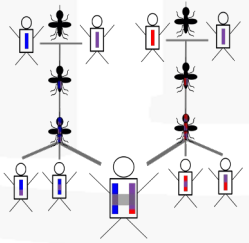




Who



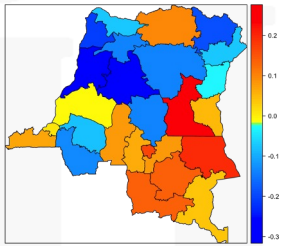
Where



Origin

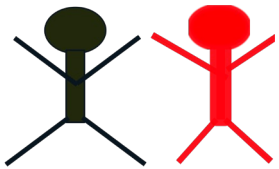
Approach

Quantitative PCR
Speciation PCR



Bayesian Mixed Spatial Models

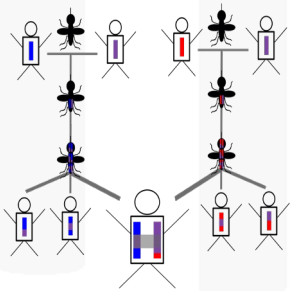
(Province & Cluster)



Odds Ratios
Inverse Prob. Weights

Super Learner Algorithm

(Spatial CV)



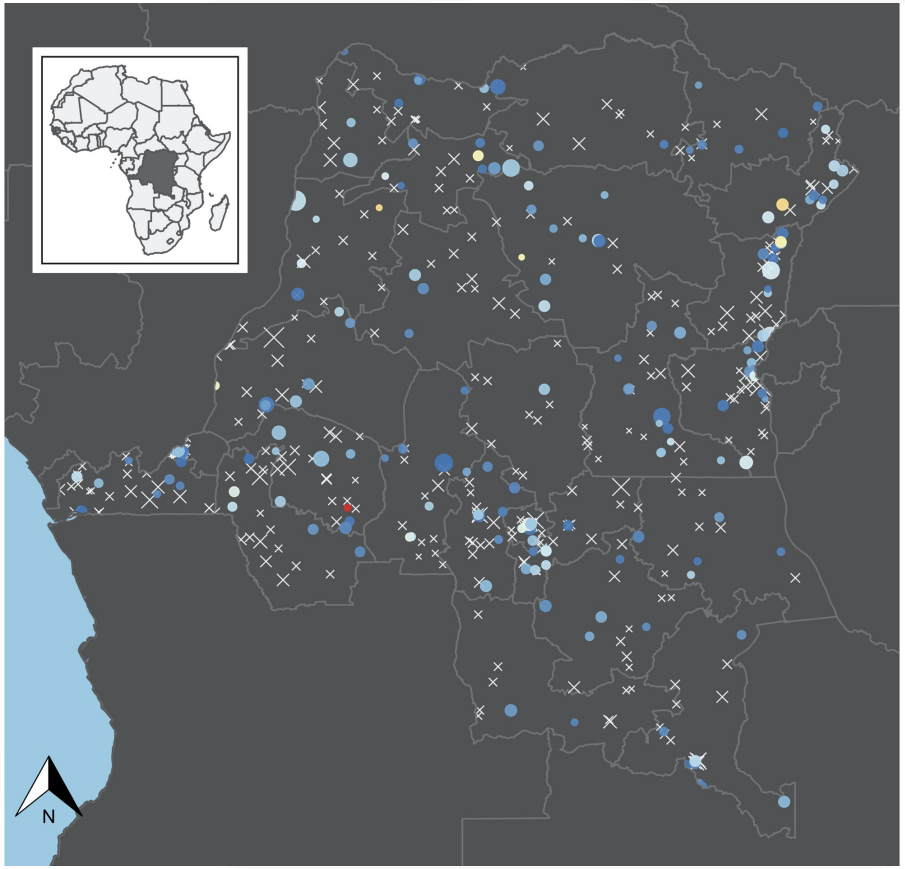
Hybrid Capture
Phylogenetics
Gen Stats

Pv in the DRC was more Common than Expected

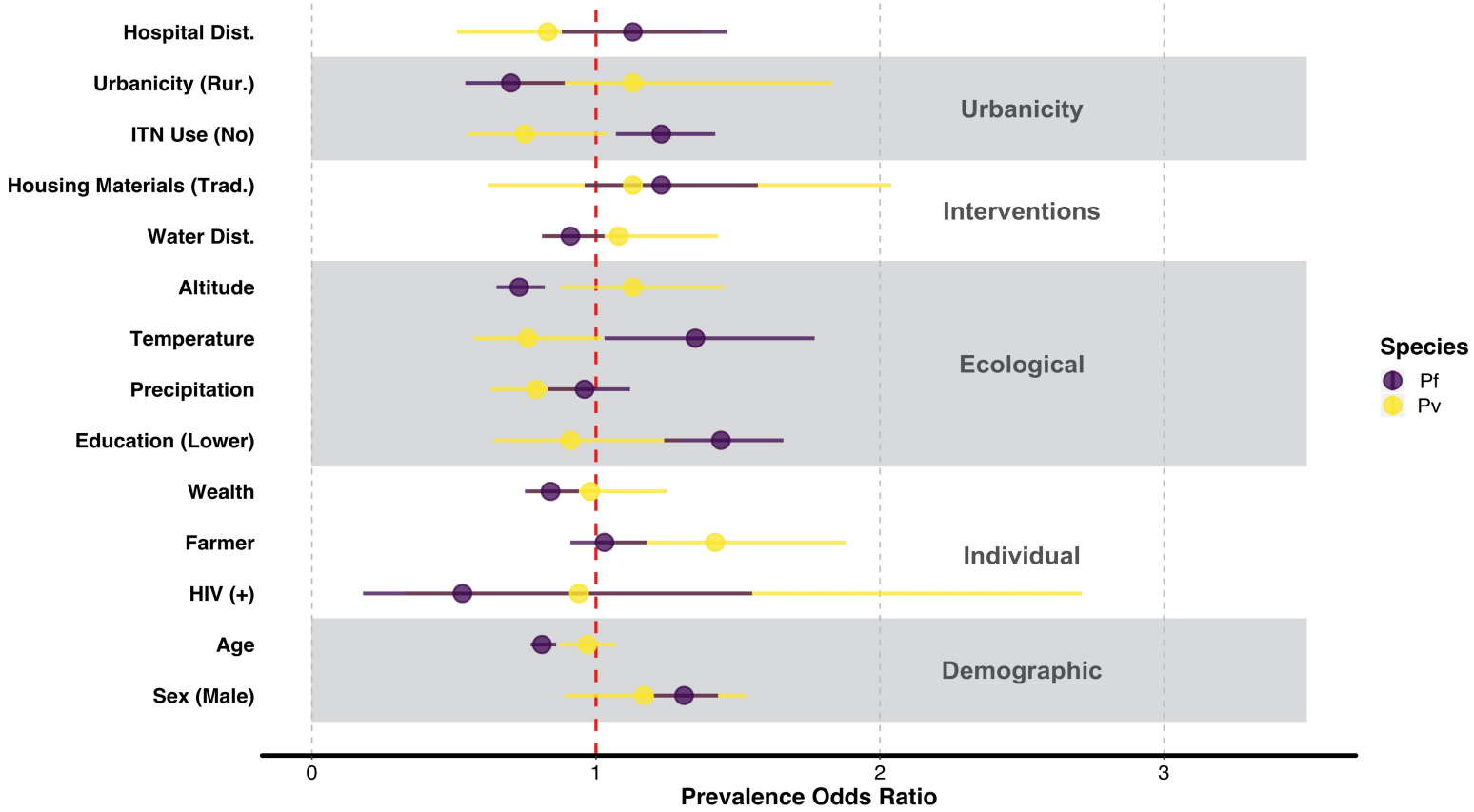
P. vivax Overview

- 540 qPCR-positive samples
- 467 Infections (included in study)
- Prevalence: 2.96% (2.28%, 3.65%)

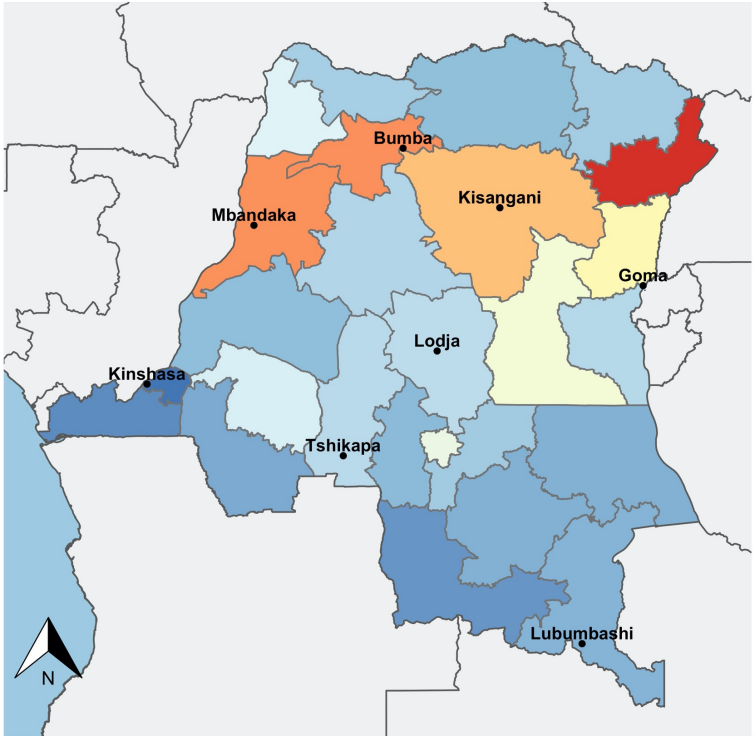
- **Among Clusters**
  - » Cluster-Prev Range: 0 - 46.15%
  - » Infection Range (weighted counts): 0 - 32.51

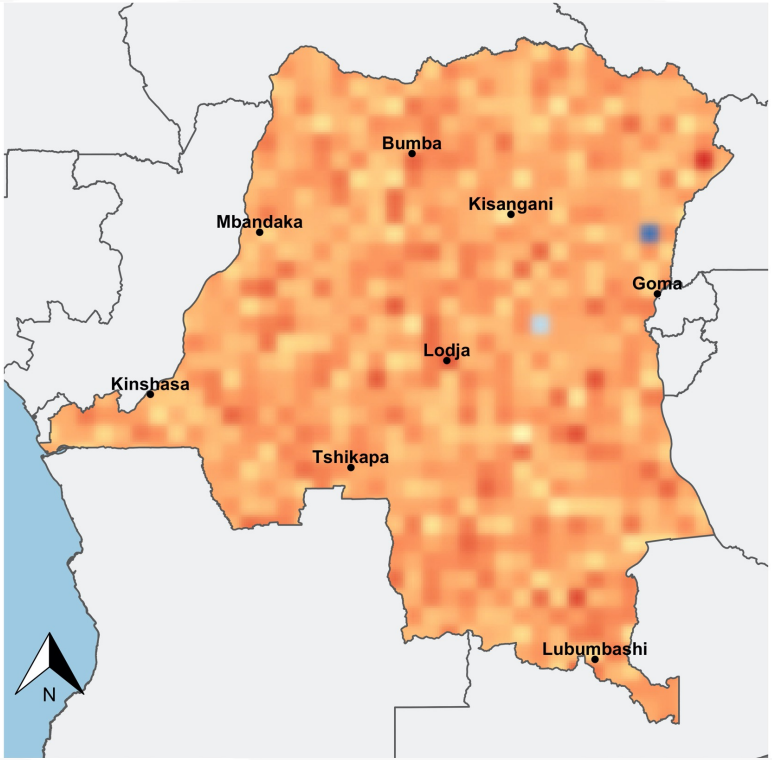


Pv is Not Associated with Many Classic Risk Factors



P. vivax Infections Exhibit Little Spatial Structure

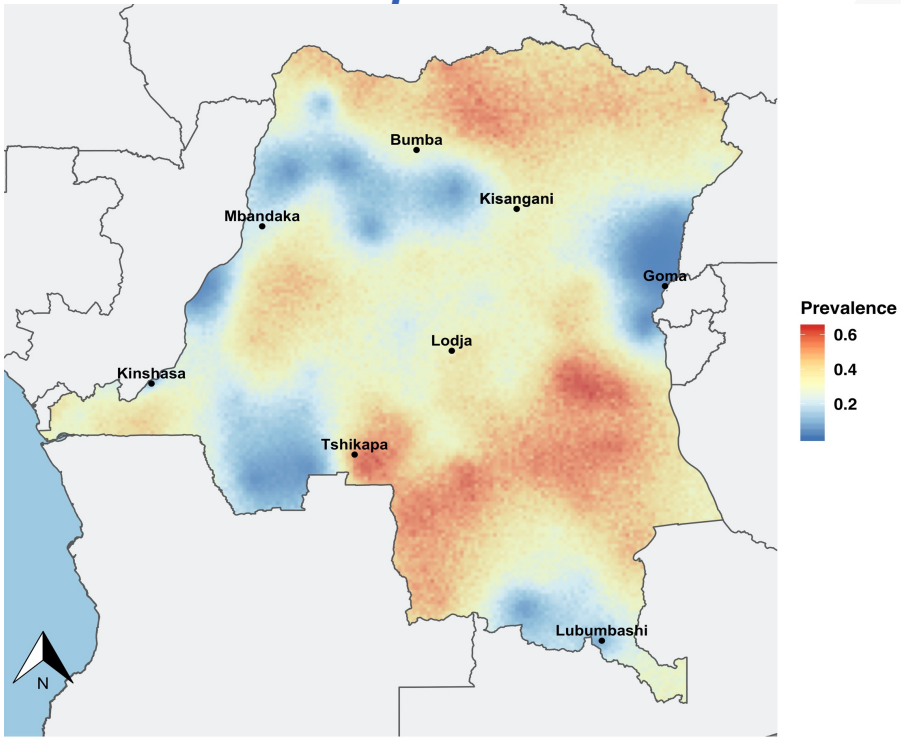




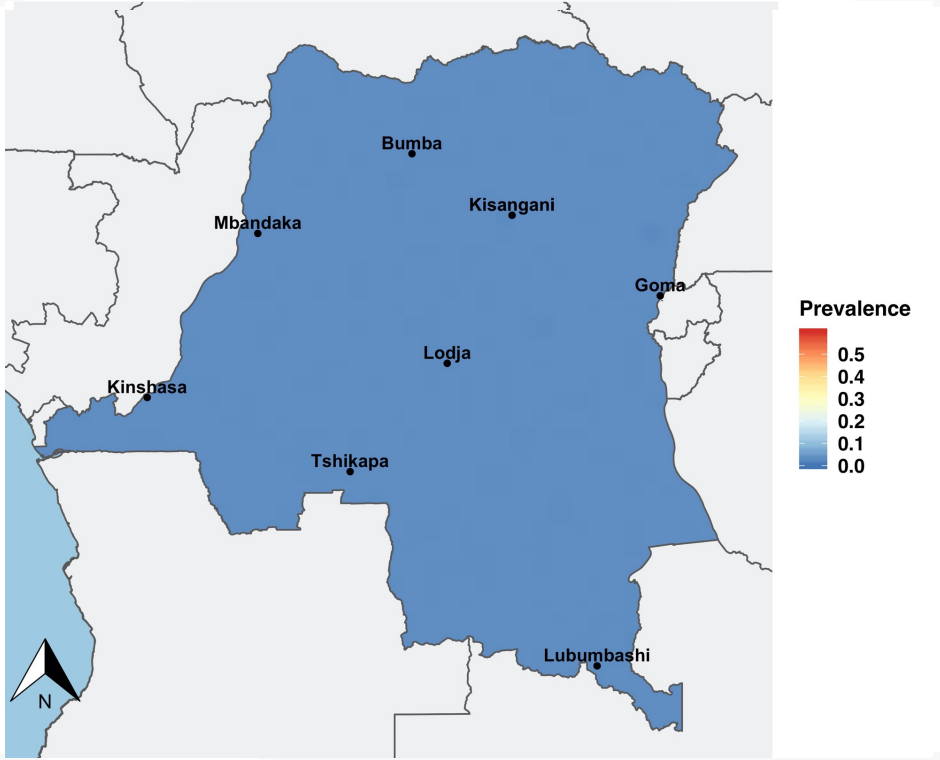
* Incorporates sig. risk factors

P. vivax Infections Exhibit Little Spatial Structure

P. falciparum

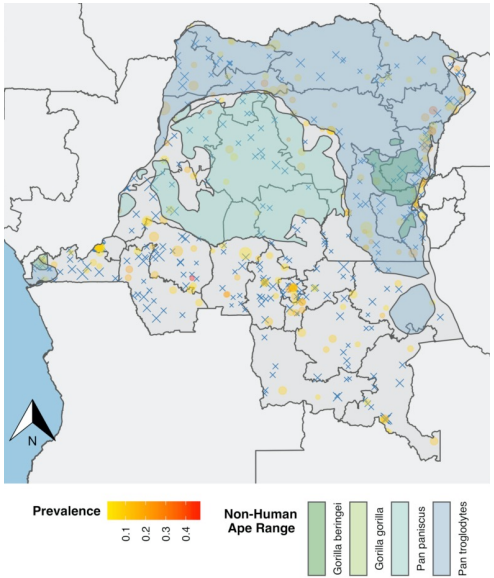


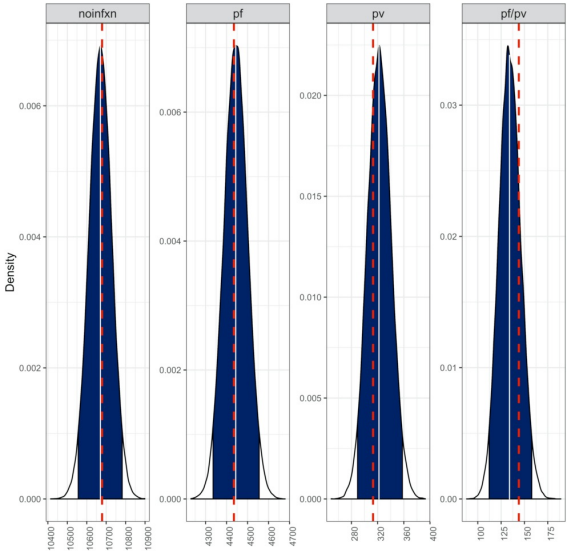
P. vivax

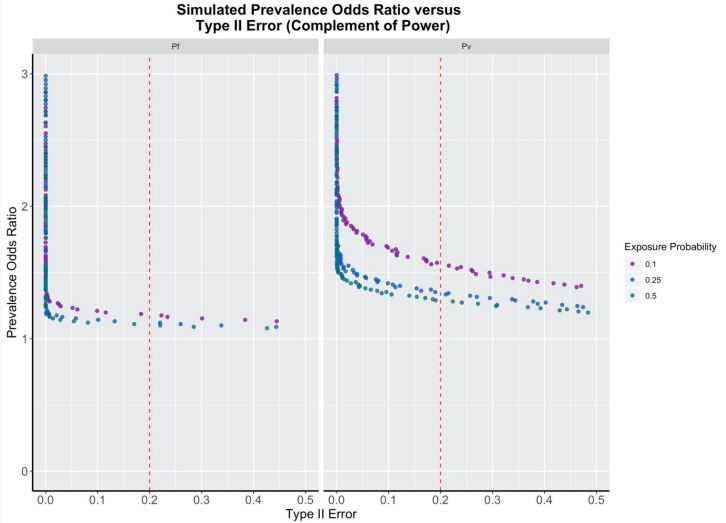


Deutsch-Feldman *et al.* 2019, *In Submission*
Janko *et al.* 2018, Lancet Plan. Health

Not Due to Non-Human Ape Habitats, *Pv-Pf* Interactions, Power, or Duffy-Negativity,







Duffy Positive: 3/467 (weighted: 1.61/459.18)

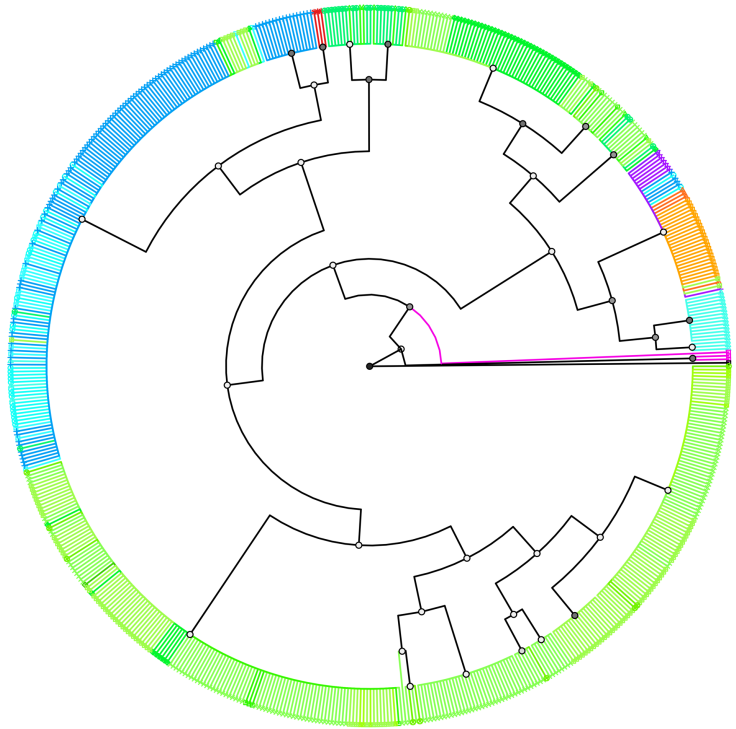
DRC *P. vivax* is Closely Related to South American *Pv*

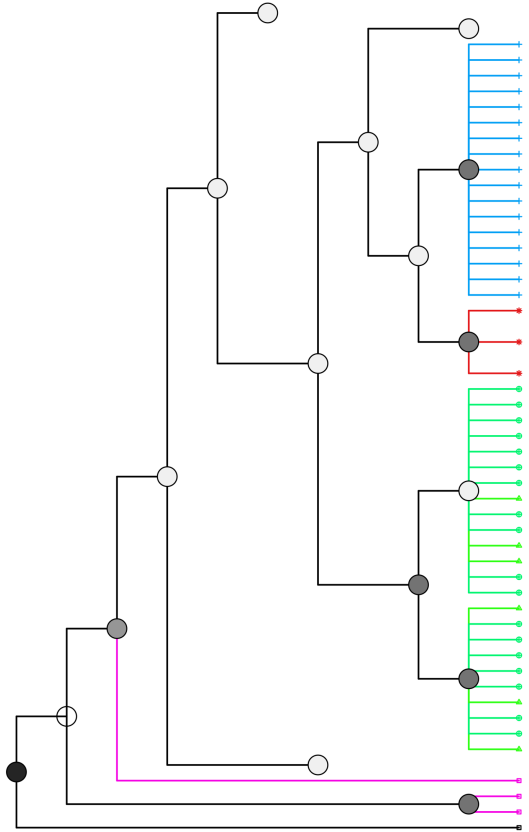
Bootstrap Percentage(BP)

- 60 ≤ BP< 70
- 50 ≤ BP< 60
- 40 ≤ BP< 50
- BP < 40

Country

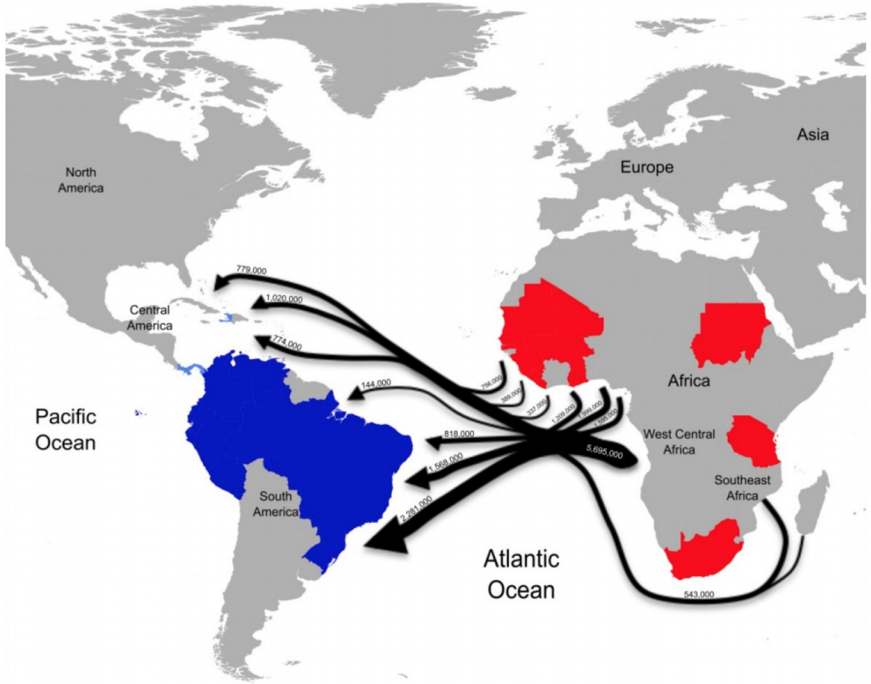
BR	MM
CD	MX
CN	MY
CO	NHA
ET	Pcynomolgi
ID	PE
IN	PG
KH	TH
LA	VN
LK	
MG	



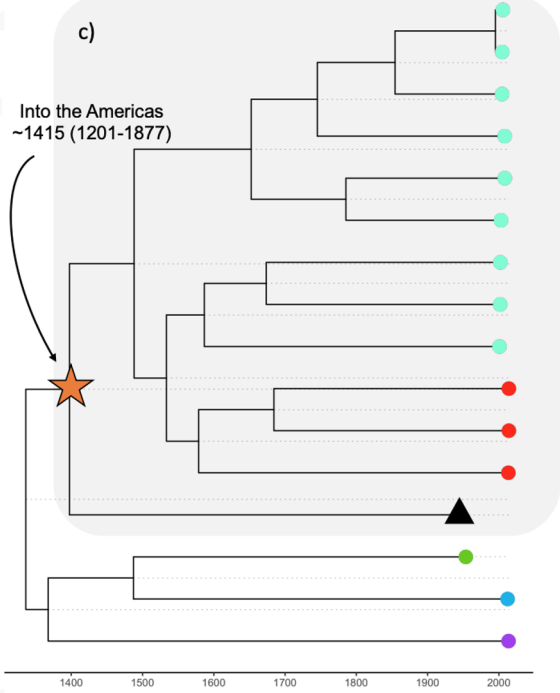


*Mitochondria

DRC *P. vivax* Part of an Older Lineage

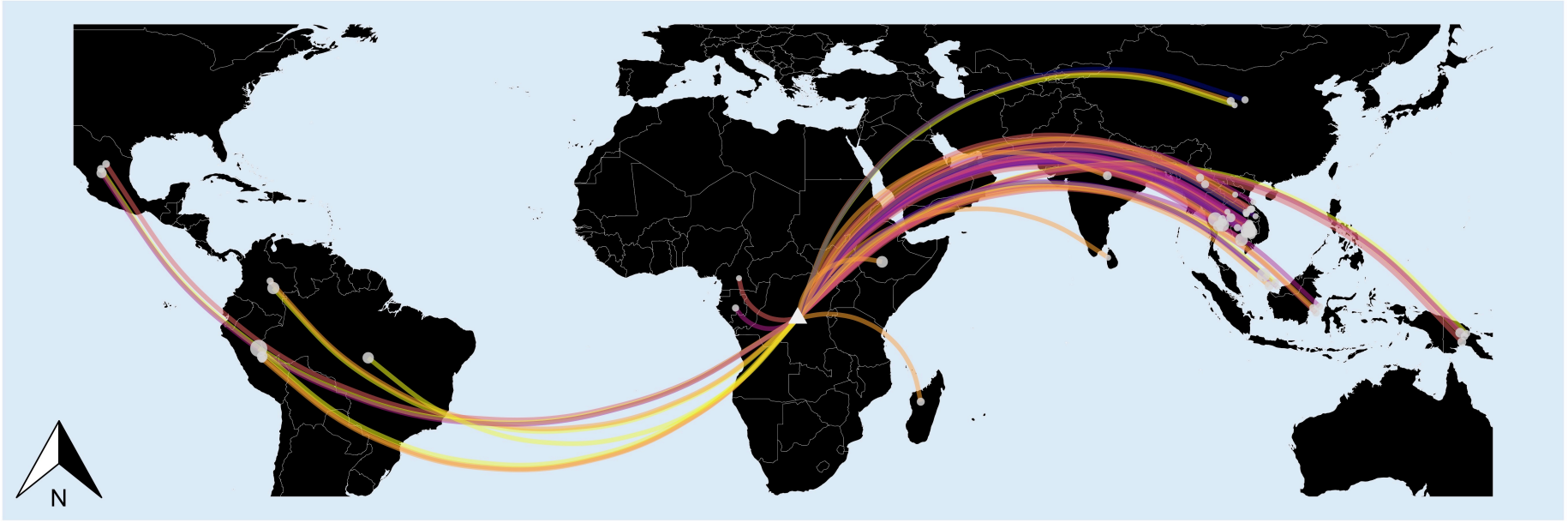


Rodrigues *et al.* 2018



Gelabert *et al.* 2016, PNAS
Dorp & Gelabert, *et al.* 2019, Biorxiv

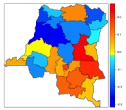
DRC *P. vivax* Shares Characteristics of New World and Old World Isolates

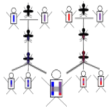


*Mitochondria

Takeaways

Conclusions





- *Pv* was not associated with classic risk factors
- *Pv* maps flat across the DRC (no hotspots)
- DRC *Pv* may represent an older lineage

Interpretation

- Persisted undetected
- DRC *Pv* is an innocuous threat
  - Hiding in the bone marrow?

Limitations

- Cross-sectional
- 3 DRC Mitochondrial Genomes

Strengths

- Spatially rich and large dataset
- DRC is generalizable

Dechavanne *et al.* 2018, bioRxiv

Acknowledgements

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Reproducibility & Data Availability

- Epi analyses: nickbrazeau/VivID_Epi
- NGS analyses: nickbrazeau/VivID_Seq
- NGS Sequences: SRA Pending
- *P. vivax* Infection Data (Upon Request)

GitHub

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