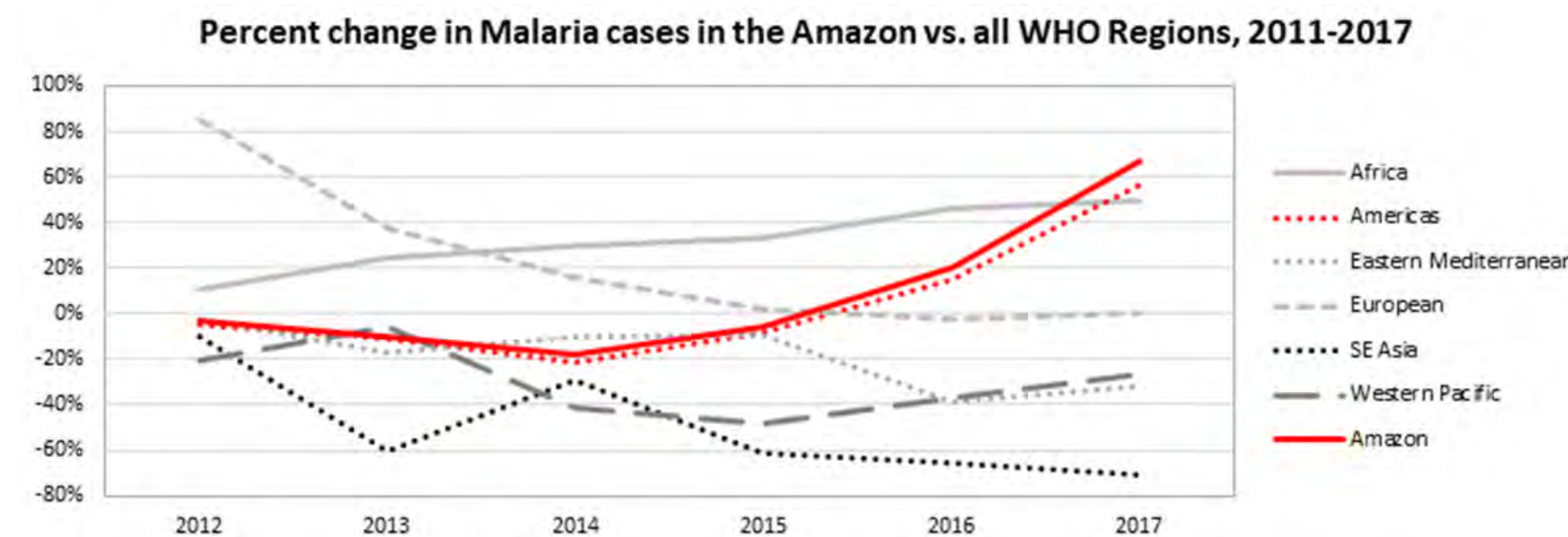


Studying Malaria Transmission Patterns in the Amazon



Since 2011, the Amazon has experienced the largest increase in malaria compared to any other region the world.



Our Bass team aims to understand the drivers of malaria in the Amazon related to three areas: (1) social network transmission (2) genetic strains of malaria (3) socio-demographic risk factors

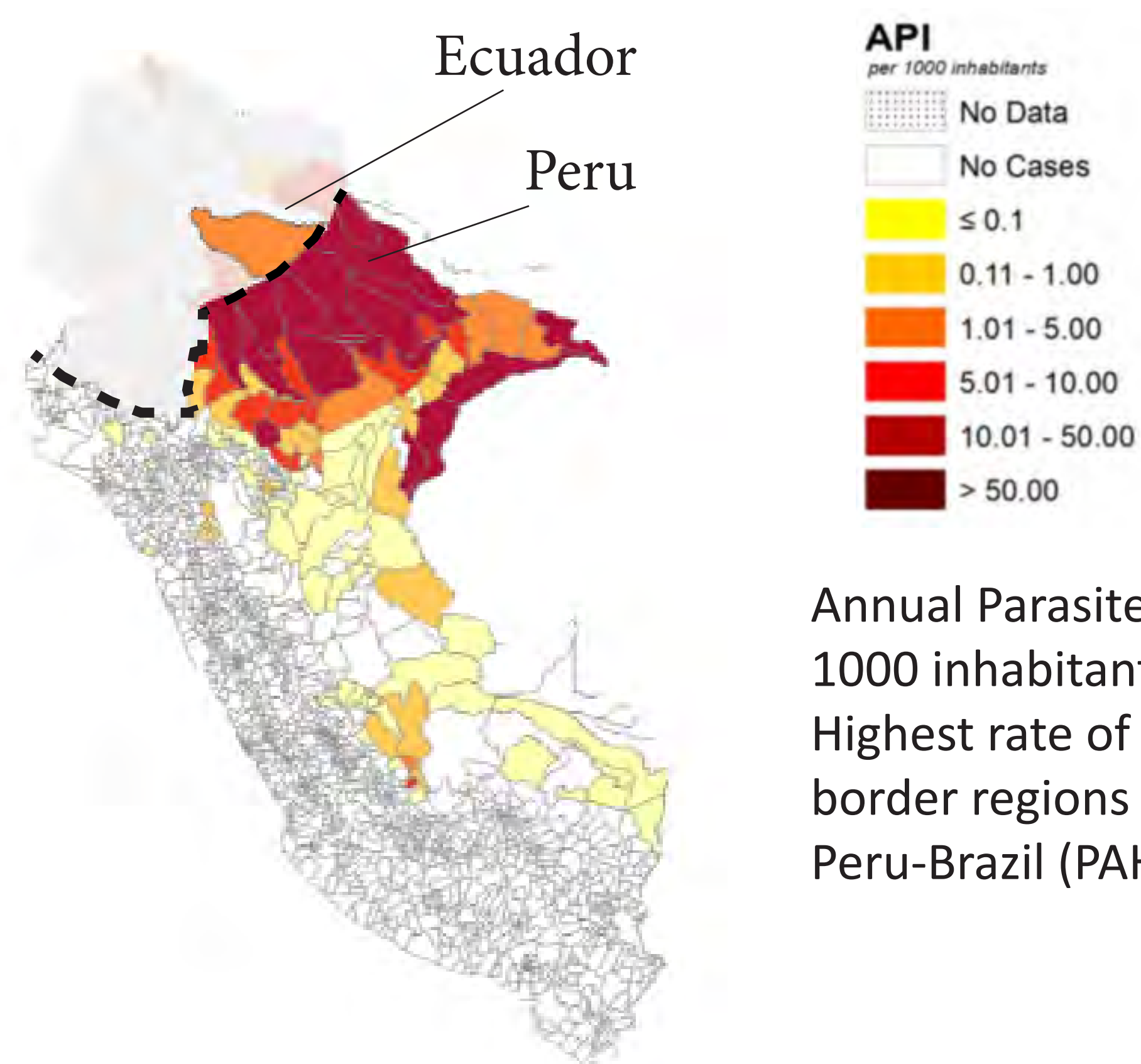


Malaria in the Amazon

- Malaria disproportionately affects rural and indigenous populations causing long-term morbidity, with high incidence near international borders due to disease spillover and shared risks.
- We focus on malaria cases in Peru and Ecuador. Malaria cases in Peru increased from under 10,000 in 2011 to over 60,000 cases by 2016. Concurrently, malaria cases re-emerged in Ecuador in 2015 now with 2000 cases in 2019.

Social Network Transmission

In collaboration with the University of San Francisco-Quito Ecuador, this team focuses on social connectivity and trans-border migration as a social determinant for malaria transmission along the Ecuador-Peru border.



Annual Parasite Index of Malaria per 1000 inhabitants in Ecuador and Peru. Highest rate of case detection along border regions of Peru-Ecuador and Peru-Brazil (PAHO, 2017).

>> Next Steps

- > Run a case-control study looking at relationship of migration and contraction of malaria and access to treatment.
- > Conduct geospatial analysis of mosquito habitat related to human risk exposure



Genomic Analysis

We obtained malaria positive blood slides from multiple health posts in Peru and Ecuador during the summer of 2019 and, through a partnership with the NCSU Vector Borne Disease Diagnostics Laboratory (Dr. Barbara Quorollo), we began sequencing malaria parasite DNA. The goal was to determine the origin of different circulating *Plasmodium vivax* strains near border regions of the two countries.

- We utilized strain-specific microsatellites to assess whether strains originated from Ecuador or Peru.
- A main challenge was sequencing the *P. vivax* DNA without sequencing the human DNA with which it was combined.
- Eventually, we were able to successfully separate and analyze *P. Vivax* DNA.

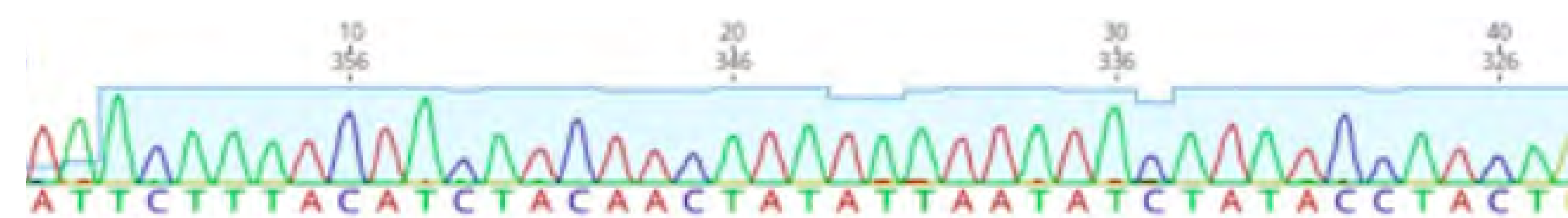


Figure illustrating a portion of the PCR results of the first *P. vivax* sample we sequenced.

>> Next Steps

- > Determine microsatellite differences between the Ecuadorian and Peruvian malaria positive slides to identify whether similar strains of malaria circulate in both countries.



Socio-Demographic Risk Factors

In the Amazon, women often marry and begin having children before the age of 18. Our data suggests that this early marriage and childbirth is a risk factor for child malaria contraction.

Objective

Using both previously collected prospective longitudinal data from Loreto, Peru and sociodemographic data collected from Indigenous communities in Ecuador in 2019, we will evaluate whether risk factors for maternal reproductive health and family migratory behavior are associated with elevated malaria risk.

Primary Hypotheses

- Young maternal age at marriage and childbirth is associated with increased risk of malaria among children.
- Labor mobility interacts with younger age of marriage to multiplicatively increase malaria risk for children and adolescent offspring.



Students collecting survey data in Ecuador related to socio-demographic risk factors.

>> Next Steps

- > In the process of drafting a paper to submit for journal publication.