were identified. DENV 1 strains were grouped within genotype V creating a new clade. All DENV 2 sequences clustered within a clade in the American/Asian genotype which was recently also identified in other Caribbean and Brazilian strains. DENV 3 strains were grouped within genotype III. All DENV 4 strains were phylogenetically grouped within a modern Caribbean basin clade in genotype II.

CONCLUSIONS Travelers provides unique insights into the global picture of circulating DENV strains. This study from the Caribbean region led to the identification of novel clades. Moreover, we were be able to detect dengue strains circulating in Cuba from 2011 to 2013, although officially no dengue was reported during that time period. Travelers serve as sentinels to provide timely information about current distribution of dengue serotypes and genotypes associated or not with outbreaks and track the spread of DENV strains in areas with scarce epidemiological information.

DISCLOSURE Nothing to disclose.

O.4.4.1.003

Identification of potential novel *P. vivax* vaccine candidates: naturally-acquired immune responses to a panel of *P. vivax* blood-stage antigens are associated with reduced risk of clinical malaria episodes in Papua New Guinean children

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Dramatic reductions in the burden of malaria have occurred in the last few decades, with several countries now attempting to permanently eliminate this disease. Eliminating *Plasmodium vivax*, now the most prevalent species in almost all endemic sites outside Africa, is particularly challenging, but would be greatly facilitated by an effective *P. vivax* vaccine. While individuals living in endemic areas rapidly acquire protective immunity to *P. vivax* malaria, the targets and mechanisms underlying this process are complex and poorly understood. We therefore assessed antibody responses to an extended panel of *P. vivax* blood-stage protein antigens, investigating their relationship with prospective risk of malaria in a cohort of 264 children aged 1–3 years in a region of very high malaria endemicity in Papua New Guinea. The levels of total IgG specific for each protein were measured using a Luminex bead array. Our results show that antibody levels tended to be higher in children with concurrent infections and in those with a higher overall exposure to *P. vivax* blood-stage infections (as measured by molecular force of infection). For multiple antigens tested (e.g., GAMA, P41, P12, AMA1, MSP3a, MSP9, RBP, DBP and hypothetical proteins), high levels of antibodies were associated with protection against clinical malaria, independently of exposure, age, and transmission season. These data identify antigens that appear to be key targets of naturally-acquired immunity and thus promising *P. vivax* vaccine candidates.

DISCLOSURE Nothing to disclose.

O.4.4.1.004

Mathematical models for *P. vivax* elimination

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The importance of spatial transmission heterogeneity and human movement is often entirely neglected in vector borne transmission models, including those for malaria. Most models assume homogenous transmission (i.e., spatial features such as human households and mosquito habitats are not considered).

It is now widely acknowledged that malaria transmission is maintained in *hotspots* i.e., very focal areas with high transmission. *Plasmodium vivax* hypnozoites pose an additional challenge for the elimination of hotspots, as they facilitate persistence of transmission.

Methods to attack residual transmission hotspots are being tested, including focalized drug administration e.g., after reactive case detection. It is not possible to use conventional models to forecast the impact these control strategies as their impact is directly linked to local, micro-scale (few metres) variation in transmission. The only class of mathematical models that can be used to simulate such heterogeneous transmission environments are spatially explicit, individual based simulation models.

Here, we built such a spatial mathematical transmission model for *Plasmodium vivax*. The model allows for the transmission of multiple parasite clones as well as heterogeneous human and mosquito populations embedded in a realistic village structure based on that on the North Coast of Papua New Guinea.

Using the model we simulate mass drug administration, mass screening and treatment, as well as focal screening and treatment interventions and compare the results with predictions from a standard transmission model.

DISCLOSURE Nothing to disclose.

O.4.4.1.005

Prevalence of strongyloidiasis in immigrants and in the autochthonous, elderly population in a formerly endemic area of Northern Italy

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INTRODUCTION Strongyloides stercoralis (Ss) causes a neglected parasitic infection that may affect more than 300 million people. This soil transmitted helminth (STH) infection is underestimated, primarily because most cases, including severe