MARIE SKŁODOWSKA-CURIE POSTDOCTORAL FELLOWSHIPS 2024

EXPRESSION OF INTEREST FOR HOSTING MARIE CURIE FELLOWS

HOST INSTITUTION

Institute of Hygiene and Tropical Medicine, NOVA University of Lisbon

RESEARCH GROUP AND URL

Individual Health Care, https://ghtm.ihmt.unl.pt/research/research-groups/individual-health-care-ihc/

SUPERVISOR (NAME AND E-MAIL)

Marcelo Urbano Ferreira, muferrei@ihmt.unl.pt

SHORT CV OF THE SUPERVISOR

Dr. Marcelo Ferreira is a medical parasitologist with 30 years of experience in field-oriented and laboratory malaria research, mostly in Amazonian Brazil. He graduated in Medicine from the University of São Paulo, Brazil (1988), where he was trained in Internal Medicine (1999-2004) and obtained his MSc (1993) and PhD (1997) degrees in Parasitology. Further research training was obtained in Parasitology in Japan (research student in Nagoya University, 1995-97) and in Evolutionary Biology in the United States (visiting scientist in Harvard University, 2005-06). His overall research goal is to provide scientific evidence that can be translated into effective public health interventions for malaria control, spanning from molecular epidemiology and parasite evolution to antimalarial drug resistance. Dr. Ferreira is currently a senior researcher at the Institute of Hygiene and Tropical Medicine of the NOVA University of Lisbon, Portugal.

5 SELECTED PUBLICATIONS

Fontoura PS, Macedo EG, Calil PR, Corder RM, Rodrigues PT, Tonini J, Esquivel FD, Ladeia WA, Fernandes ARJ, Johansen IC, Silva MF, Fernandes AOS, Ladeia-Andrade S, Castro MC, Ferreira MU. Changing Clinical Epidemiology of *Plasmodium vivax* Malaria as Transmission Decreases: Population-Based Prospective Panel Survey in the Brazilian Amazon. J Infect Dis. 2024 Apr 12;229(4):947-958. doi: 10.1093/infdis/jiad456.

Ferreira MU, Corder RM, Johansen IC, Kattenberg JH, Moreno M, Rosas-Aguirre A, Ladeia-Andrade S, Conn JE, Llanos-Cuentas A, Gamboa D, Rosanas-Urgell A, Vinetz JM. 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. Lancet Reg Health Am. 2022 May;9:100169. doi: 10.1016/j.lana.2021.100169.

de Oliveira TC, Rodrigues PT, Early AM, Duarte AMRC, Buery JC, Bueno MG, Catão-Dias JL, Cerutti C, Rona LDP, Neafsey DE, Ferreira MU. *Plasmodium simium*: Population Genomics Reveals the Origin of a Reverse Zoonosis. J Infect Dis. 2021 Dec 1;224(11):1950-1961. doi: 10.1093/infdis/jiab214.

Corder RM, Ferreira MU, Gomes MGM. Modelling the epidemiology of residual *Plasmodium vivax* malaria in a heterogeneous host population: A case study in the Amazon Basin. PLoS Comput Biol. 2020 Mar 13;16(3):e1007377. doi: 10.1371/journal.pcbi.1007377.

de Oliveira TC, Corder RM, Early A, Rodrigues PT, Ladeia-Andrade S, Alves JMP, Neafsey DE, Ferreira MU. Population genomics reveals the expansion of highly inbred *Plasmodium vivax* lineages in the main malaria hotspot of Brazil. PLoS Negl Trop Dis. 2020 Oct 28;14(10):e0008808. doi: 10.1371/journal.pntd.0008808.

PROJECT TITLE AND SHORT DESCRIPTION

Genomic architecture of malaria parasite adaptation to the New World

More than 500 years after its introduction by settlers from Portugal and Spain and enslaved people displaced from West and Central Africa, malaria still causes 500,000 clinical cases each year across Latin America, with 120 million people at risk of infection. When *Plasmodium falciparum* and *P. vivax* arrived in the New World, they encountered anopheline species that were evolutionarily divergent from the African and European vectors with which they had coevolved. Once in the Americas, *P. vivax* has also adapted to local platyrrhine monkeys along the Atlantic Coast, originating the sister species *P. simium*. We hypothesize that present-day *P. falciparum*, *P. vivax*, and *P. simium* populations from the Americas might still carry detectable genomic signatures of their geographic origin and their adaptation to Neotropical vectors and new vertebrate hosts, provided that putative source parasite populations from Africa and Europe are sampled for comparison. To test this hypotheses, we will: (1) generate high-quality whole-genome sequences for *P. falciparum, P. vivax*, and *P. simium* clinical isolates from Brazil (2018-20) and for archival blood-smear samples from Portugal (1944-52) and (2) apply population genomic analysis to determine the geographic origins of malaria parasites introduced in the Americas after the European conquest and to identify the genomic signatures of selection and adaptation to New World vectors and non-human vertebrate hosts.

SCIENTIFIC AREA WHERE THE PROJECT FITS BEST*

Life Sciences (LIF)

***Scientific Area where the project fits best** – Please select/indicate the scientific area according to the panel evaluation areas: Chemistry (CHE) • Social Sciences and Humanities (SOC) • Economic Sciences (ECO) • Information Science and Engineering (ENG) • Environment and Geosciences (ENV) • Life Sciences (LIF) • Mathematics (MAT) • Physics (PHY)