



P3.117



Estimating the potential risk of transmission of arboviruses in the Americas and Europe: A modeling study

Agnese Zardini¹, Andrea Gobbi¹, Fabrizio Montarsi², Beniamino Caputo³, Angelo Solimini³, Cecilia Marques-Toledo⁴, André Wilke⁵, Roberto Rosà⁶, Giovanni Marini⁷, Daniele Arnoldi⁷, Andrea Pugliese⁸, Gioia Capelli², Alessandra della Torre³, Mauro Teixeira⁴, John Beier⁹, Annapaola Rizzoli⁷, Alessandro Vespignani¹⁰, Marco Ajelli⁵, Stefano Merler¹, [Piero Poletti](#)¹

¹ Bruno Kessler Foundation, Italy. ² Zooprophyllactic Experimental Institute of Veneto, Italy. ³ University of Rome La Sapienza Department of Public Health and Infectious Diseases, Italy. ⁴ Federal University of Minas Gerais Department of Biochemistry and Immunology, Brazil. ⁵ Indiana University Bloomington School of Public Health, USA. ⁶ University of Trento Center Agriculture Food Environment, Italy. ⁷ Edmund Mach Foundation Research and Innovation Centre, Italy. ⁸ University of Trento Department of Mathematics, Italy. ⁹ University of Miami - Miller School of Medicine, USA. ¹⁰ Northeastern University, USA

Abstract

Background & aims of study. Estimates of the spatiotemporal distribution of different mosquito vector species and the associated risk of transmission of arboviruses are key to design adequate policies for preventing local outbreaks and reducing the number of human infections in endemic areas.

Methods & results. We develop a computational model to quantify the daily abundance of *Ae. albopictus* and *Ae. aegypti* and the reproduction number of dengue, Zika, and chikungunya in Europe and the Americas, at a resolution of 250 m x 250 m. The model leverages temperature and precipitation records and is calibrated on mosquito surveillance data collected during 2,437 trapping sessions in 115 locations in Europe and the Americas between July, 2007 and December, 2018.

In areas colonized by both *Aedes* species, *Ae. aegypti* is estimated to be the main vector for transmission of dengue, Zika, and chikungunya. Our estimates highlight that these arboviruses are endemic in tropical and sub-tropical countries, with the highest risks of transmission found in Central America, Venezuela, Colombia, and Central-East Brazil. A non-negligible potential risk of transmission is also estimated for the Southern US (especially for Florida, Texas, and Arizona). The broader



that these arboviruses are endemic in tropical and sub-tropical countries, with the highest risks of transmission found in Central America, Venezuela, Colombia, and Central-East Brazil. A non-negligible potential risk of transmission is also estimated for the Southern US (especially, for Florida, Texas, and Arizona). The broader ecological niche of *Ae. albopictus* could contribute to the emergence of chikungunya outbreaks in temperate areas of the Americas, as well as in the Mediterranean Europe (in particular, in Italy, Southern France, and Spain).

Implications. Our results provide a comprehensive overview of the transmission potential of arboviral diseases in Europe and the Americas, highlighting areas where surveillance and mosquito control capacities should be prioritized.

SESSION DETAILS

Poster Session 3, with Refreshment Break & Meet the Editor Session

📍 Europa Foyer & Italia Foyer
15:40-17:10
Thursday, 30 November, 2023

IN THIS SESSION

Can carrier animals support FMD persistence in endemic regions? A model exploration of explanations of FMD persistence

How effective are control methods for endemic FMD? A simulation study in the Republic of Turkey

Collateral impacts of pandemic COVID-19 drive the nosocomial spread of antibiotic resistance: a modelling study

Active learning sampling design (A-LSD): A new adaptive survey design paradigm to improve representativeness of subpopulations

Number of COVID-19 importations averted by travel restrictions in Japan

Impact of risk heterogeneity on the feasibility of Hepatitis C elimination among people who inject drugs

Social contact patterns following the COVID-19 pandemic: A snapshot of post-pandemic behaviour from the CoMix study

Data assimilation for estimating change points of time-varying reproduction numbers

Monitoring contacts to efficiently control pathogen spread in hospital settings