

MATHEMATICAL MODELLING OF MOSQUITO DISPERSAL

Chiara Virgillito^{*1,2},
Giovanni Marini¹, Mattia Manica¹,
Beniamino Caputo¹, Alessandra della Torre² and
Roberto Rosà¹

¹Department of Biodiversity and Molecular Ecology,
Research and Innovation Centre, Fondazione Edmund Mach,
San Michele all'Adige, Trento, Italy

²Department of Public Health and Infectious diseases,
Sapienza University of Rome, Italy

chiara.virgillito@uniroma1.it (*corresponding author)

The presence of invasive mosquitoes in Italy, in particular *Aedes albopictus*, has a significant impact on public health. Indeed, this species can transmit several pathogens, including chikungunya virus, whose largest outbreak in Europe occurred in Lazio region (Central Italy) in 2017. Currently, health risk estimate for mosquito-borne pathogens is limited by the difficulty to predict the spatial and temporal spread of vectors at a small scale.

To address this problem, we treated *Ae. albopictus* dispersal as a diffusion process, which can be represented by a partial differential equation, and exploited data obtained in three Mark-Release Recapture (MRR) experiments carried out in Padua (northern Italy). In particular, we modelled this process using the heat equation, whose analytical solution is already known, taking also explicitly into account mosquitoes mortality, which was estimated based on data collected under semi-field conditions simultaneously to MRR experiments. Several theoretical functions (e.g. exponential, Gompertz and Weibull functions, as well as a regression model) were tested, obtaining an estimated average daily mortality, computed over a time window of two weeks, of 2% in the first experiment and 1% in the second and third experiment. We compared the different functions both by the mean square error and a likelihood test.

The only unknown parameter of the equation, i.e. the diffusion coefficient, was estimated through a Markov Chain Monte Carlo procedure by fitting the model to the observed mark-release recapture data.

The solution turns out to be a normal bivariate distribution that represents the probability of mosquito location at different time steps.

Our findings could help to better define the area to be treated by emergency insecticide treatments in the case of notification of any *Ae. albopictus*-borne pathogen infection.