

The spread of *Aedes albopictus* in Spain: linking human mobility and habitat suitability

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The tiger mosquito, *Aedes albopictus*, is an invasive urban vector responsible for transmitting diseases like Dengue and Chikungunya. Its introduction to Spain was first documented in 2004 in Sant Cugat del Vallés [1], and since then, it has progressively spread along the Spanish Mediterranean coast and is moving inland. Experimental research indicates that these mosquitoes are capable of hitchhiking in vehicles [2], facilitating their ability to cover vast distances.

In this study, we delve into the colonization patterns of *Aedes albopictus* over the past decade, utilizing data collected from the citizen science platform, Mosquito Alert. Our analysis focuses on two primary factors: human mobility and habitat suitability. To comprehensively understand the effect of different dispersal modes on the colonization process, we integrate human mobility, habitat suitability, and distance to previously invaded regions in a metapopulation model. This model represents a variation of the well-known Hanski metapopulation model [3].

Within this metapopulation model, a pivotal variable determines the habitat suitability of individual patches. To accurately gauge this suitability, we calculate the Mosquito basic reproduction number, R_M , employing a mechanistic ODE model. This model intricately incorporates a range of parameters associated with the mosquito life cycle, such as temperature, rainfall, and human population density. By leveraging thermal biology and experimental data from the literature, we ascertain the functional form for each mosquito trait.

Moreover, we enrich our analysis by leveraging fine-scale mobility data sourced from the MITMA dataset for Spain at hourly scale. Our ultimate goal is to gain insights into the invasion process and identify key factors that promote colonization. To achieve this, we aim to infer key parameters, including colonization rates, extinction rates and a key parameter measuring the impact of each dispersal mode. After that, we intend to project our findings into the future using CMIP6 climate change predictions to anticipate potential future colonization hotspots.

References

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