2020_04: Do habitat and distributional traits predict which European mosquito species vector important viruses?

Supervisor: Bethan Purse (beth@ceh.ac.uk)

Department: UK Centre for Ecology and Hydrology / Biodiversity Science Area

(a) Motivation for the project

Mosquito-borne diseases cause substantial mortality and morbidity worldwide and are changing in distribution and impact due to globalisation and environmental change. Europe is dealing with more frequent importation and local transmission of exotic arboviruses as well as endemic transmission of West Nile Virus in the Mediterranean basin. Furthermore, invasive mosquitoes have become widely established across Europe this century and are implicated in subsequent outbreaks of dengue and chikungunya virus. The spread and persistence of arboviruses following arrival in a new region is driven by the abundance, seasonality and interactions of competent mosquito vector species. By looking across virus and vector species at virus-vector relationships, studies in the Americas[1] have shown that the mosquitoes with particular ecological traits transmit flaviviruses such as Zika, yellow fever and dengue, namely those are widespread, live near human habitation and prefer to bite humans.

This project aims to compile and analyse habitat and distributional traits for European mosquito species to determine whether these ecological traits govern the ability to transmit arboviruses Europe and Africa, to predict which species might be involved in transmission of priority pathogens across which ecosystems, to inform future research and surveillance.

(b) Context and background

The project is hosted by the UK Centre for Ecology and Hydrology in collaboration with the University of Reading as well as consultancies involved in delivering information on disease vectors to national and European Public Health agencies (ERGO consultancy, Oxford, UK and Francis Schaffner Consultancy, Switzerland). It aligns with NERC remit in that it addresses source, sinks and pathways of potentially harmful organisms present in the natural environment that may have an effect on human health and advances understanding of community ecology of mosquito-arbovirus interactions in Europe.

The model outputs will have potential to inform horizon scanning and surveillance efforts in Public Health Agencies, through the consultancy collaborators. The student will develop skills in desk-based literature review and in manipulating and integrating large ecological datasets using the R language and statistical software. They will gain

knowledge and experience of statistical community modelling techniques to analyse linkages between vector-virus associations, ecological traits and phylogeny and participate in the process of writing up such models. By working remotely across an inter-disciplinary collaborative group of researchers and consultants, the student will gain an understanding of the policy landscape and real-world application of quantitative ecology of mosquito-borne diseases in Public Health.

(c) Objectives and methodology

The project objectives are to determine (i) whether ecological traits, namely host and habitat use and distribution, govern the ability of mosquito species to transmit arboviruses Europe and Africa; (ii) whether these trait-based relationships can predict which species might be involved in transmission of priority pathogens across which ecosystems; (ii) whether these models are informative for targeting Public Health Surveillance or ecological research on mosquito vectors in the region.

The student will work with an inter-disciplinary team of collaborators and stakeholders to interpret ecological data and co-develop hypotheses and statistical models to explain differences between mosquito species in their traits and associates with arboviruses. They will have the opportunity to review and select appropriate traits and modelling approaches and will gain an understanding of the policy landscape in which the research is embedded, through the consultancy collaborators who have strong links through to national and European Public Health Agencies (such as the European Centre for Disease Control and the European Food Standards Agency). The student will also have the opportunity to contribute to engagement with European vector experts around building centralised databases for mosquito traits through UKCEH and Reading. The student will also interact with the scientists in Biodiversity and the Population Ecology group at UKCEH, that are conducting ongoing modelling projects on vector-borne diseases, plant pathogens and invasive species.

The student will benefit from existing data collected by the team which cover around 100 species of mosquito and include molecular barcode data and phylogenetic trees, vector-virus association data for flaviviruses and alphaviruses (from EIDC2), distributional data at national scale (site scale for some species). The steps involved in the work will therefore be to:

- Collate and code available habitat traits from the literature and through mosquito expert elicitation (through an online questionnaire) for European mosquito species.
- Analyse distributional traits and invasion status from available national and site-level geographical data.
- Integrate distributional and habitat traits into phylogenetic models of vector-virus associations to determine whether traits can be used to predict vector roles

- Interpret the value of the model outputs for targeting Public Health Surveillance or ecological research on mosquito vectors in the region

Project timeline

- Project orientation, background reading, existing databases at CEH (week 1)
- Design of habitat database and collation of data, analysis of distributional traits (weeks 2 - 6)
- Review and selection of statistical modelling approaches (weeks 6-7)
- Application of statistical models and visualisation/reporting of model outputs (weeks 7 - 9)
- Interpretation of model results and presentation with support from inter-disciplinary team (week 10)

References

1. Evans et al. 2017 Data-driven identification of potential Zika virus vectors eLife 2017;6:e22053 DOI: 10.7554/eLife.22053

Project length: 10 Weeks