MIDIIVEC

EXPLORATORY PROJECT

2022-2024

New modelling approaches to anticipate vector-borne disease transmission

Coordination

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INRAE units involved

BIOEPAR
IVPC
MaIAGE

Partnerships

Inria

Context and challenges

Emerging arboviruses (e.g. Zika, West Nile virus) represent a global threat to human and veterinary public health. Mostly of zoonotic origin, these viruses are transmitted to vertebrate hosts by arthropod vectors, such as mosquitoes or ticks.

Transmitted by mosquitoes of the genus Aedes and Culex, the Rift Valley fever virus (RVFV) is endemic in Africa. However, its area of incidence is gradually expanding (Arabian Peninsula, Mayotte) with imported human cases reported in mainland France and China, making RVFV research a priority for the WHO and WOAH .

Arbovirus transmission is a dynamic, multi-scale process where small-scale individual infection dynamics can impact large-scale inter-population circulation, under the influence of several (a)biotic factors. At the vector scale, the abil-ity of a mosquito to get infected then subsequently transmit an arbovirus is referred as vector competence, which depends notably on vector and virus genotype as well as temperature. Vector competence is characterized by three major steps :

1. Viral infection of the vector's gut following a blood meal on a viremic host
2. Dissemination of the virus from the gut into the circulatory system of the vector
3. Infection of the saliva, which conditions virus transmission to a new host during the next bite

At each barrier, infection can be stopped. However, each state of the vector (infected (I), disseminated (D) or infectious (T)) is irreversible, as the virus is not eliminated by vector’s defences.

In epidemiological modelling on a population scale, vector competence is mostly studied as a qualitative phenotype (a vector is classified as competent or not), thereby ignoring the dynamic aspect of intra-vector viral infection (IVD) and its high potential epidemiological impact.

At epidemic scale, the distribution (in the mosquito population) of the time to reach the infectious state can have a major role on the epidemiological dynamics and the impact of biotic (genotype & viral dose) and abiotic (temperature) factors on IVD remains poorly characterized. Finally, the impact of IVD variability on large-scale vector transmis-sion remains unknown. Characterising IVD and its (a)biotic determinants is therefore a major biological challenge.

The MIDIIVEC project aims to fill this knowledge gap in order to better anticipate and control the circulation of vector-borne diseases.

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Goals

By mobilising an integrative and interdisciplinary approach linking experimental and numerical biology, the MIDIIVEC project intends to develop new models of IVD in order to better characterise its inter-individual heterogeneity. This will require the removal of several methodological barriers, both in mathematical modelling (in order to integrate IVD into multi-scale epidemiological models), in inference (to take into account an observational model in addition to the mechanistic model) and on issues of identifiability (i.e. to determine whether the available data allow the parameters to be estimated and with what bias and precision).

More precisely, the methodology is broken down into four steps:

1. Co-construction of mechanistic models of IVD with virologists to incorporate biological hypotheses of interest
2. Estimation of key parameters of these models to characterise the inter-individual heterogeneity of IVD
3. Co-construction of reasoned experimental designs to guide future experiments
4. Comparison of several modelling approaches at the vector scale to guide the integration of IVD in future epide-miological models on a larger scale

The ultimate goal is to propose new approaches for modelling IVD, in order to better understand its impact on arbo-virus transmission.

Research units involved and partnerships

INRAE scientific division	INRAE research units	Expertises
Animal health	BIOEPAR	Mathematical modelling in epidemiology, stochastic simulations and inference
	IVPC	Entomology, Virology
Mathematics, computer and data sciences, digital technologies	MaIAGE	Stochastic modelling, inference (particle filtering)
External partners		**Expertises**
Inria	Équipe projet RAPSODI	Deterministic models (PDE), numerical analysis, optimisation

Métaprogramme
DIGIT-BIO

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