

The intra-vector viral dynamics challenge a common assumption in vector-borne diseases modeling

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Arboviruses = threat to public and veterinary health.
-> **Intra-vector viral dynamics (IVD) is key element of arboviruses transmission.**
BUT
-> Most of vector-borne disease models use the mean of extrinsic period of incubation (EIP) and **IVD has not been considered** so far.
Current models assume then an **exponential distribution of durations in EIP within mosquitoes population.**

EXPERIMENTAL DATA

-> Data from blood meal mosquito infection experiments.

Viruses	Mosquito species and origin
CHIKUNGUNYA [3] -> CHIKV, alphavirus, strain 06.21 from Indian Ocean lineage	<i>Aedes albopictus</i> (from Villeurbanne et Pierre-Bénite)
ZIKA [2] -> ZIKV, flavivirus, isolate SL1602 belong to the Asian lineage	<i>Aedes albopictus</i> (from Marseille and La Réunion)
DENGUE [1] -> DENV, flavivirus, isolate of genotype I from Thailand/Laos/New Caledonia and genotype V from Gabon/Haiti	<i>Aedes aegypti</i> (wild type from Kamphaeng Phet Province/Thailand)

MODELING

-> An experimental IVD model was built and implemted with R

INFERENCE

-> Inference was performed with ABC rejection algorithm^[4]

Parameters	Significance
qI	Proportion of mosquitoes for which the infection barrier will be passed (VEE → VEI)
qD	Proportion of mosquitoes for which the dissemination barrier will be passed (VEI → VED)
alpha	Beta law parameters of mosquitoes distribution in
beta	VEI_1 to VEI_n compartments

RESULTS

- Differences between IVD of different virus species.
- **Non exponential distribution of durations in the infected state for ZIKV and DENV.**

Is this exponential distribution assumption of durations always applicable?

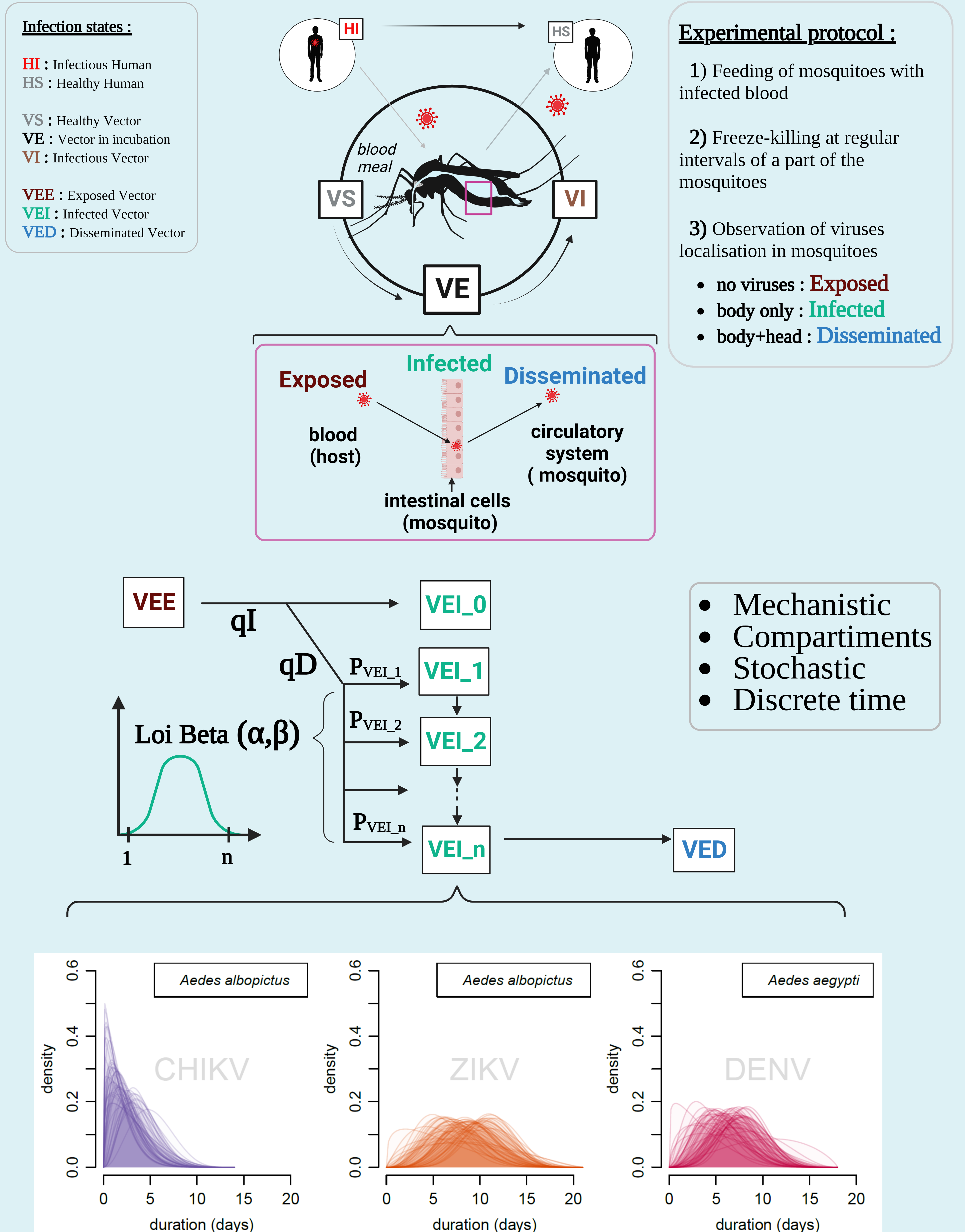


Figure 1 : Estimated distribution of durations in the infected state of the IVD within study mosquitoes for Chikungunya (left), Zika (middle) and Dengue (right) viruses. Figures were obtained from a part (100) of selected particules (1000) from the model inference (100 000 simulations). Use of infectious doses : $10^{6.07}$ FFU/mL (CHIKV), $10^{6.5}$ FFU/mL (ZIKV), $10^{5.81}$ FFU/mL (DENV).

CONCLUSION AND PERSPECTIVES

- Assuming exponential distribution of durations to approximate IVD does not always seem relevant.
- Further research of IVD will refine its modeling so that it can be incorporated into vector-borne disease models that contribute to the development of vector-borne diseases management measures.

[1] Fontaine et al. 2018. « Epidemiological Significance of Dengue Virus Genetic Variation in Mosquito Infection Dynamics ». PLOS Pathogens 14 (7): e1007187. <https://doi.org/10.1371/journal.ppat.1007187>
[2] Lequime et al. 2020. « Modeling Intra-Mosquito Dynamics of Zika Virus and Its Dose-Dependence Confirms the Low Epidemic Potential of Aedes Albopictus ». PLOS Pathogens 16 (12): e1009068. <https://doi.org/10.1371/journal.ppat.1009068>
[3] Viginier, et al. 2022. « Statistical Modeling of Chikungunya Virus Intra-Vector Infection Dynamics in a French Aedes Albopictus Population Reveals an Explosive Epidemic Potential ». medRxiv. <https://doi.org/10.1101/2022.11.06.22281997>
[4] Sisson S. A., Fan Y., & Beaumont M. 2018. « Handbook of Approximate Bayesian Computation ». Chapman and Hall/CRC

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