Climate-Dengue nexus: Europe’s increasing transmission suitability under anthropogenic Climate Change

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BACKGROUND

Climate change is one of the major drivers of the transmission and geographic expansion of mosquito-borne infectious diseases. In Europe, **Dengue virus (DENV)** is a public health concern due to continuous northward spread mosquito vector *Aedes Albopictus* and its increasing intensity of transmission.

Transmission cycle and temperature

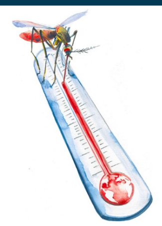
- DENV is maintained in a transmission cycle between mosquitoes (genus *Aedes*) and human populations
- DENV transmission is climate sensitive largely due to direct impacts of ambient temperature traits that characterize the mosquito life cycle and their transmission competence
- Models that quantify these relationships allow mechanistic climate-driven DENV risk assessment

Objectives

- Updated database of experimental studies measuring mosquito-virus traits at different temperatures (Da Re et al.)
- Statistical framework for analysing temperature responses across mosquito species and experiments with limited data
- Incorporate the derived relationships into mathematical models of DENV transmission
- Monitor temperature-driven changes in transmission suitability of DENV transmission across Europe
- Quantify the impact of climate change on DENV transmission suitability by comparing current and counterfactual (pre-industrial) climate scenarios

METHODS

We fit parametric functions to the trait data



Credit: Chris Sharp

For example: Briére function

$$f^B(T;\theta_{ij}) = q_{ij}T\left(T - T_{\min_{ij}}\right)\sqrt{T_{\max_{ij}} - T}$$

with

$$\theta_{ij} = (q_{ij}, T_{\min_{ij}}, T_{\max_{ij}})$$

Estimated with Bayesian hierarchical models

Measurement-level
$y_{ij,T}|\theta_{ij}, s \sim N\left(f^X(T;\theta_{ij}), s^2\right)$

Experiment-level
$\theta_{ij}|\theta_i, \sigma^{\exp} \sim N\left(\theta_i, \mathrm{diag}\left({\sigma^{\exp}}^2\right)\right)$

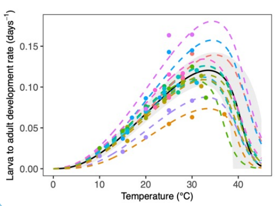
Species-level
$\theta_i|\mu, \sigma \sim N\left(\mu, \mathrm{diag}(\sigma^2)\right)$

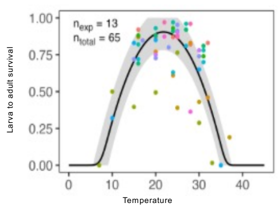
Population-level
$\boldsymbol{\mu}$: mean of parameters across species
$\boldsymbol{\sigma}$: between-species variability
$\boldsymbol{\sigma}^{\mathbf{exp}}$: between-experiment variability

This approach offers:

- Partial pooling of data (species with sparse data can borrow information)
- Accounting for between-experiment variability avoids biased and overconfident estimates
- Sampling from hierarchical prior to quantify uncertainty in temperature response of a species in absence of data

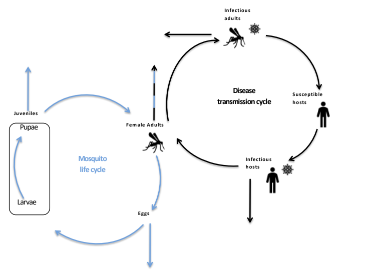
Posterior trait fits





RESULTS

Transmission suitability model



Mosquitoes:

$$E = \beta(T)\left(1 - \omega(T,S)\right)M - h(R,P)\delta_E(T)E - \mu_E(T)E$$
$$E_d = \delta_E(T)\omega(T,S)E_d - \sigma(T,S)h(R,P)\delta_E(T)E_d - \mu_{E_d}(T)E_d$$
$$J = h(R,P)\delta_E(T)E + \sigma(T,S)h(R,P)\delta_E(T)E_d - \delta_J(T)J - \left(\frac{J^2}{K_L(R,P)}\right) - \mu_J(T)J$$
$$A_e = \frac{1}{2}\delta_J(T)\, e^{-\left(\frac{J^2}{K_P(R,P)}\right)}J - \delta_{A_e}(T)A_e - \mu_{A_e}(T)A_e$$
$$S_M = \delta_{A_e}(T)A_e - a(T)\cdot b_M(T)\cdot S_M \cdot \frac{I_H}{N_H} - (\mu_M(T) + r)S_M$$
$$E_M = a(T)\cdot b_M(T)\cdot S_M \cdot \frac{I_H}{N_H} - (\alpha_M(T) + \mu_M(T))E_M$$
$$I_M = \alpha_M(T)E_M - \mu_M(T)I_M$$

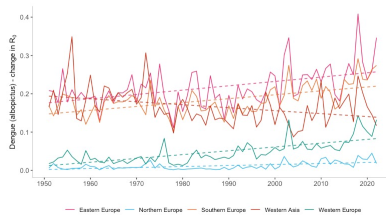
Hosts:

$$S_H = \Lambda - a(T)\cdot b_H \cdot I_M \cdot \frac{S_H}{N_H} - \mu_H S_H$$
$$E_H = a(T)\cdot b_H \cdot I_M \cdot \frac{S_H}{N_H} - \alpha_H E_H - \mu_H E_H$$
$$I_H = \alpha_H E_H - \gamma_H I_H - \mu_H I_H$$
$$R_H = \gamma_H I_H - \mu_H R_H$$

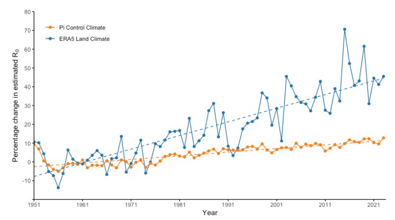
$$R_0(T) = \frac{m(T)a(T)^2 b_M(T) b_H \frac{\alpha_M(T)}{\alpha_M(T) + \mu_M(T)}\frac{\alpha_H}{\alpha_H + \mu_H}}{\mu_M(T)(\gamma_H + \mu_H)}$$

Basic reproduction number

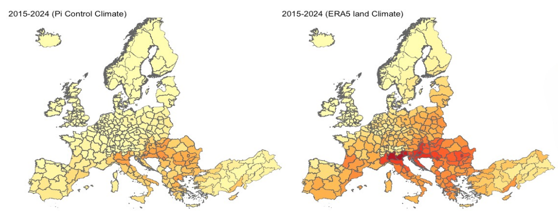
Application of the $\mathbf{R_0}$ model to temperature data



Our results from the recent Europe Lancet Countdown report suggest that DENV temperature suitability increased by 55.94% in Europe 2014-2023 compared to 1951-1960



Annual percentage change in transmission suitability of DENV estimates under ERA5 reanalysis climate conditions and Pi-control climate scenario.



Comparative spatial distribution of dengue transmission suitability across Europe, modelled under Pi Control and ERA5-Land climate datasets for the period spanning the last decade.

DISCUSSION & OUTLOOK

- Understanding how mosquito-borne disease transmission responds to changes in climatic conditions is critical for climate change adaptation and mitigation
- Experimental data allows to build mechanistic temperature-dependent transmission models
- We find that DENV transmission suitability peaks around 26.7°C for vector *Aedes Albopictus* which predominantly is driving the transmission in Europe

- Our uncertainty analyses identified data on adult mosquito lifespan, biting rate, and egg viability as key priorities for future experimental studies
- We will validate the predicted transmission suitability against DENV occurrence in Europe and incorporate the temperature response estimates in dynamic model simulations
- Multifactorial experiment designs needed to extend models to other environmental conditions (e.g., humidity)

Acknowledgements

HGS MathComp
IWR Interdisciplinary Center for Scientific Computing
UNIVERSITÄT HEIDELBERG ZUKUNFT SEIT 1386
IDAlert Infectious Disease decision-support tools and Alert systems

References

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