

A generic climate-driven model to evaluate control strategies of mosquito populations in temperate wetlands

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Mosquitoes are vectors of major pathogens worldwide, resulting in diseases such as malaria or West-Nile, dengue, chikungunya or yellow fevers. The control of their populations is needed to fight such diseases. In temperate climate, this issue becomes central in the actual context of global change given rise to the extension of the repartition areas of certain mosquito species and to the emergence of associated vector-borne diseases. Simulation tools would enable to support decision making to improve the surveillance and control of vector populations.

A modelling approach is complementary to experimental and observational approaches, allowing integrating sparse and heterogeneous knowledge on the functioning of a complex biological system. Such an approach enables one to evaluate the robustness of predictions according to the precision of biological knowledge available, and thus to identify the most prejudicial gaps of knowledge and the needs for future experiments or observations. Moreover, it enables one to evaluate, and even prioritize, a large panel of control strategies under various scenarios of the system functioning.

To identify the principal determinants of the mosquito population dynamics and to assess control strategies, we developed a predictive model of mosquito abundance over time. This model has a generic structure: stages are common to all mosquito species whatever the geographical area. On the other hand, parameters and between-stage transitions change among species and areas, being specific of a given biological system "species x area". Our model is mechanistic and climate-driven, transitions depending on temperature, day length, or rainfall occurrence and intensity. It represents the seasonal dynamics of a mosquito population over several years, accounting for diapauses.

Aquatic and adult stages are considered resulting in 10 compartments: eggs (E), larvae (L), and pupae (P) for juveniles; emergent (Aem), nulliparous (A1), and parous (A2) for adults, the two latter stages being decomposed into host-seeking (h), resting (g), and ovipositing (o) adults. Among adults, only females are considered. Host-seeking and ovipositing females are assumed to do risky movements. The model is based on two coupled systems of ordinary differential equations (ODE): one for the favorable season during which mosquito are active, the other for the unfavorable season during which the diapause occurs.

The model has been applied to species of the genus *Anopheles*, *Culex* and *Aedes* present in temperate wetlands (Camargue, France). For *Anopheles* and *Culex*, nulliparous females are overwintering, whereas for *Aedes* eggs are the resistance stage. Transitions (climate-driven) and parameter values specific to one species per genus present in this region have been defined from the literature. Qualitative predictions of the models adapted to each genus are in agreement with entomological data available in Camargue. For *Aedes*, taking into account arbitrary artificial flooding was necessary to explain observed dynamics.

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A global sensitivity analysis of each model has been carried on to identify and compare parameters the most influent on prediction variations. The FAST (Fourier Amplitude Sensitivity Test) method has been used, relying on simultaneous variations of all model parameters in a +/- 10% interval around the nominal value. Parameters explaining more than 10% of the model output variance were considered to be influent. Adult mortality and times (in degree-days) needed for a gorged female to become gravid influenced the date of the peak of abundance in adults whatever the species, whereas for example mortalities of aquatic stages were highlighted as variation factors of this date for *Anopheles* species but not for other species. The maximum abundance was influenced by the habitat carrying capacity in pupae and the mortality at emergence whatever the species, whereas for example the additional mortality of host-seeking and ovipositing females due to their risk movements as well as oviposition rate only influenced abundance in *Anopheles*. A more precise estimation of these parameters would increase the reliability of model predictions. Moreover, these parameters are potential control points of the biological system and thus could be targeted by control strategies.

Finally, the model has been used to compare two strategies targeting larvae to control *Anopheles* population dynamics. We have shown that using a bio-larvicide similar to *Bacillus thuringiensis israelensis* (*Bti*) at regular time interval was a preventive measure to reduce mosquito abundance during the favorable period. At an identical number of treatments and surface sprayed, this strategy was more efficient than a strategy relying on the adult population surveillance and occurrence of treatment when an abundance threshold was reached.

To conclude, our model can be applied to any mosquito species in temperate climate, as long as sufficient knowledge is available on its biology, or those of a close species, to determine parameter values or the climate-driven transition functions. This model is a flexible and efficient tool which could next be coupled to epidemiological models of mosquito-borne diseases to compare control strategies targeting either the vector or the pathogen in the host and to identify the most efficient occurrence of treatments.