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Predicting *Culex pipiens/restuans* population dynamics using a weather driven dynamic compartmental population model

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Background

In northern U.S.A., *Cx. pipiens/restuans* is the predominant genus. As vectors, they are key to the spread of arboviruses, and thus further knowledge of vector population dynamics is crucial.

Table 1. Definition of the transition parameters used

Parameter	Description
bE(T,P)	birth rate eggs - reciprocal value of the length of the gonotrophic cycle multiplied with the number of female eggs laid per egg raft
mE(T)	mortality rate eggs
bL(T)	birth rate larvae - reciprocal value of the length of the egg stag
mL(T, KL)	mortality rate larvae and pupae combined
KL(P)	carrying capacity of the larvae
bA(T)	birth rate adults - reciprocal value of the length of the larval and pupal stage combined
mA(T)	mortality rate of active adult mosquitoes
h(T,D)	diapausing rate - rate of adult mosquito leaving active stage and entering diapause stage
mH	mortality rate adult mosquitoes during winter diapause

Method

We developed a compartmental population model to investigate the dynamics of *Cx. pipiens/restuans*. The three basic model inputs are temperature, precipitation, and day length, in a model that incorporates a genetic algorithm (Figure 1).

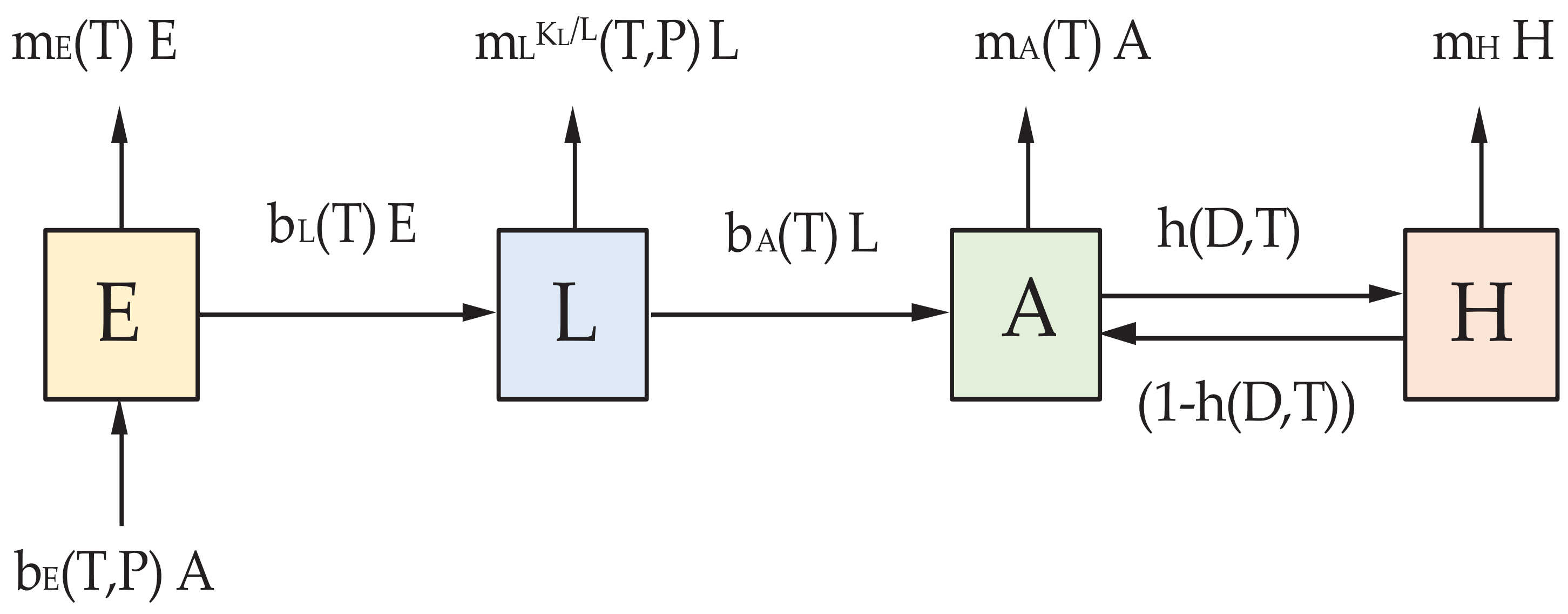

Figure 1: Block diagram of the Culex-population model incorporating 4 stages: E - eggs, L - larvae (inclusive pupal sage), A - active adults; H - hibernating adults.

Results

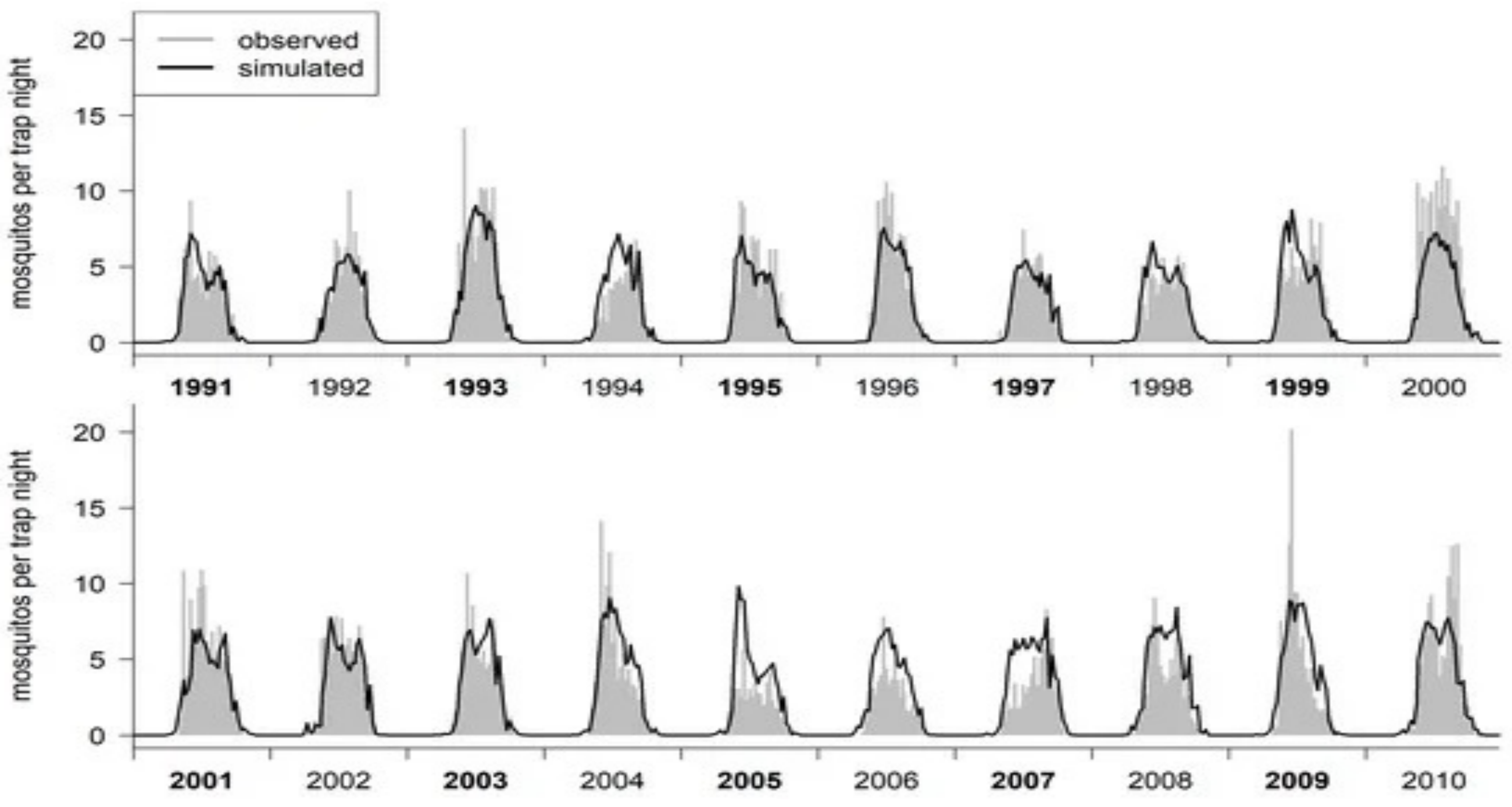

Figure 2: The final model fitted the observations from the training data at a high rate (*RMSE = 1.3457, rS = 0.905*).

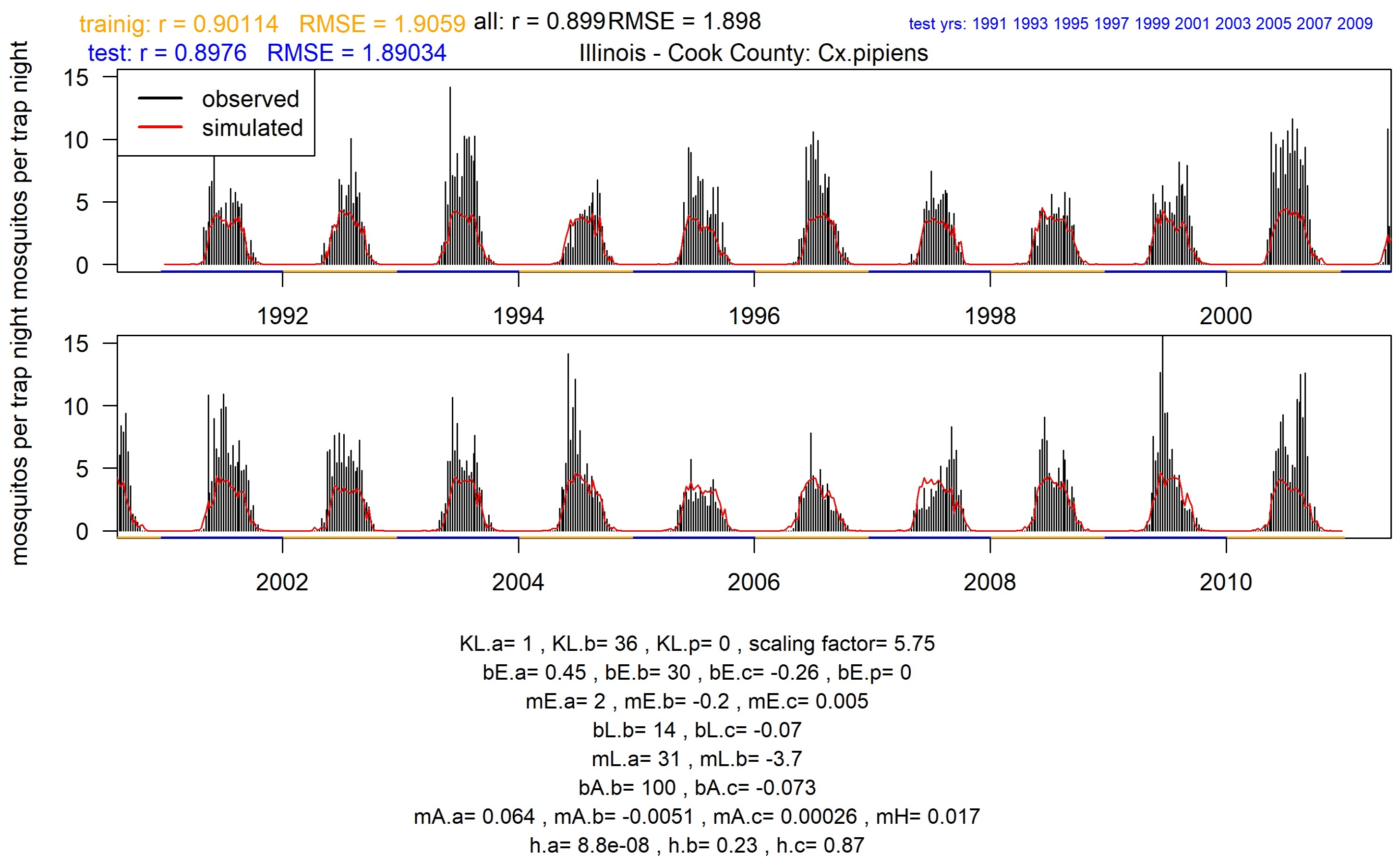

Figure 3: The results from the test data set showed an equally good fit (*RMSE* = 1.898, *rS* = 0.899).

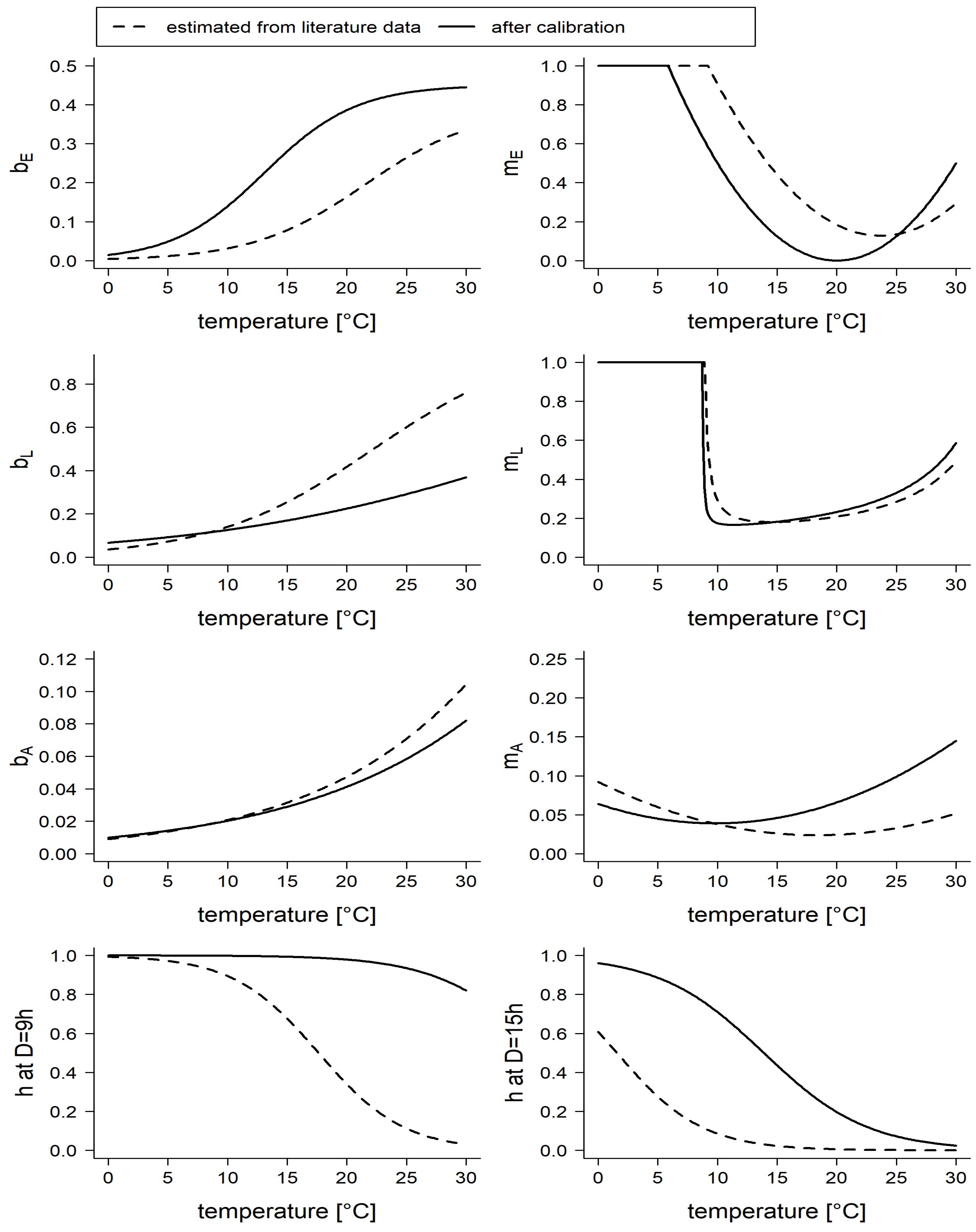

Figure 4: Dashed lines represent the estimated values and the solid line is the after-calibration with the training data set.

Conclusion

The presented dynamic compartmental model was able to reproduce the weekly mean *Cx. pipiens/restuans* abundance for Cook County at a high precision. The model requires a few input parameters, namely temperature, precipitation, and latitude, and this can be adapted to other regions and easily implemented in *SIR* models for pathogens transmitted by *Cx. pipiens/restuans* mosquitoes.

Source: Bakran-Lebl et al. (2023):
https://www.mdpi.com/2075-4450/14/3/293