Spatial Dynamics of Insecticide Resistance in Mosquitoes

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Abstract

Mosquito- borne diseases are resurgent due to insecticide resistance. In this paper a model is presented combining insect dispersal and population genetics for the simulation of the emergence of pesticide resistance in dependence on management practices. Dispersal of populations and genetic information involves both physical and biological processes. In the case of high population densities such as mosquito populations the spatio-temporal dynamics can be described by systems of nonlinear reaction diffusion equations. The reaction terms model population- dynamics and genetics and the interaction between biotypes. The space operator captures typical biological dispersal modes such as random diffusion or the active migration along gradients of environmental signals. For the life cycle of species comprising mobile and immobile stages, systems of partial and ordinary differential equations for the winged and aquatic phase respectively are set up. Resistance is conferred by metabolic or target site changes in mosquitoes involving polygenic or monogenic inheritance respectively. According to the number of loci, which code resistance, a large number of biotypes with different resistance factors and their genetic interactions are implemented into the model, e.g. for 3 gene loci, n=27 biotypes have to be considered. For each biotype „i", the model integrates the dynamics of the aquatic phase Ai and of the winged phase Mi and their genetic interactions via the hereditary matrices Wi. Competition is mediated via the coefficents aij of the community matrix, Φi is he oviposition rate, the μ's are mortality rates and the γ's are hatching rates. The layout of the model is shown in Figure 1. Landscape structures and habitat suitability maps are implemented into the finite element tool COMSOL Multiphysics®. The system displays a richness of dynamic patterns such as travelling waves and hysteresis effects. If fitnness penalty is correlated with resistance, the establishment of refuges is a means to delay or even stop the spread of resistant biotypes. The model is used to find optimal management practices such as release of sterile males or the allocation of refuges.

Figures used in the abstract

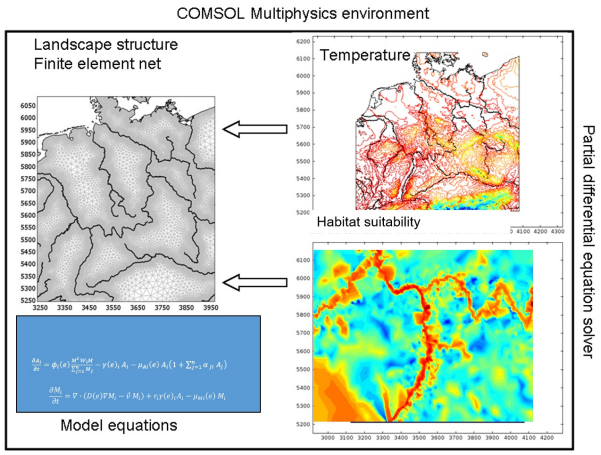

Figure 1: Concept for modelling large scale dispersal.