YOGITA SHARMA, University of Victoria

Effect of stochasticity and spatial structure on homing-based gene drive spread

Since the discovery and application of CRISPR as a gene editing tool, interest has grown in gene drive systems and their ability to spread desirable genes into populations. A variety of modeling approaches have been applied to study the spatial spread of gene drive systems, including partial differential equations, metapopulation models, and deterministic, stochastic and individual-based formulations. Here, we focus on reaction-diffusion approaches in which gene drive spread is described as a "pushed" or "pulled" wave. We compare a deterministic reaction-diffusion model of gene drive to one incorporating stochasticity, and explore the impact that stochasticity has on model outcomes. We find that, first, incorporating stochasticity into the model expands the range of fitness costs and initial conditions that lead to spatial spread. Second, increasing the level of stochasticity causes traveling wave solutions in the model to display decreased wave speed. And third, while a barrier representing a selective disadvantage to gene drive organisms may halt a traveling wave in a deterministic model formulation, in the stochastic model formulation, a small number of gene drive organisms may permeate the barrier and reestablish a traveling wave on the other side. These results highlight the limitations of deterministic reaction-diffusion models and the importance of considering stochasticity and spatial structure in models of gene drive spread as projects move towards field implementation.