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The spatial dynamics of selfish genetic elements in *Aedes aegypti* arbovirus vector populations

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Novel strategies for controlling mosquito vectors of human diseases involve introductions of selfish genetic elements (SGEs), or elements that spread through the mosquito population by means of non-Mendelian inheritance. The releases of the endosymbiotic bacteria *Wolbachia* into *Aedes aegypti* populations in order to reduce their capacity for arbovirus transmission are the first application of an SGE introduction strategy in a field setting. Gene drive technologies for creating SGEs that reduce vectorial capacity are also being developed. SGEs are vertically transmitted between mosquito hosts, and their spread dynamics have complex interactions with natural mosquito population dynamics, population structure and fitness components. We develop a model of an *Ae. aegypti* metapopulation that incorporates empirical relationships linking variation in mosquito abundance to density-dependent fitness components. We first show that our model can produce patterns of demographic variation similar to those found in natural populations, and predict rates of spatial spread of *Wolbachia* matching those observed following field releases. We then explore different SGE release strategies over an operationally relevant spatial scale, and compare the spread dynamics of *Wolbachia* and gene drive. We find that the spatial release distribution strongly affects the rate of spread of both SGEs, with widely dispersed release distributions out-performing spatially aggregated distributions, especially when the SGE incurs fitness costs. Our results demonstrate how spatial and demographic structure in the mosquito host population impacts SGE spread, with implications for the design of effective release strategies.

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