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MGDRIVE: A MOSQUITO POPULATION FRAMEWORK TO EVALUATE AND OPTIMIZE RELEASES OF GENE-DRIVE INTERVENTIONS FOR VECTOR-BORNE DISEASES CONTROL

HÉCTOR M. SÁNCHEZ C., SEAN L. WU, JARED BENNETT, JOHN M. MARSHALL
AND HÉCTOR M. SÁNCHEZ C., SEAN L. WU, JARED B. BENNETT, JOHN M. MARSHALL

iiiiiii HEAD Recent developments of CRISPR-Cas9 based homing endonuclease gene drive systems for the suppression or replacement of mosquito populations have generated much interest in their use for control of mosquito-borne diseases (such as dengue, malaria, chikungunya and Zika). This is because genetic control of pathogen transmission may complement or even substitute traditional vector-control interventions, which have had limited success in bringing the spread of these diseases to a halt. Despite excitement for the use of gene drives for mosquito control, current modeling efforts have analyzed only a handful of these new approaches (usually studying just one per framework). Moreover, these models usually consider well-mixed populations with no explicit spatial dynamics. To this end, we are developing MGDrivE (Mosquito Gene DRIVe Explorer), in cooperation with the "UCI Malaria Elimination Initiative", as a flexible modeling framework to evaluate a variety of drive systems in spatial networks of mosquito populations. This framework provides a reliable testbed to evaluate and optimize the efficacy of gene drive mosquito releases. What separates MGDrivE from other models is the incorporation of mathematical and computational mechanisms to simulate a wide array of inheritance-based technologies within the same, coherent set of equations. We do this by treating the population dynamics, genetic inheritance operations, and migration between habitats as separate processes coupled together through the use of mathematical tensor operations. This way we can conveniently swap inheritance patterns whilst still making use of the same set of population dynamics equations. This is a crucial advantage of our system, as it allows other research groups to test their ideas without developing new models and without the need to spend time adapting other frameworks to suit their needs.

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Potential new first few lines?

Traditional vector-control interventions, such as insecticide-treated nets and indoor residual spraying, have had limited success in halting the spread of malaria, dengue fever, or Zika virus. Recent developments in CRISPR-Cas9 gene drive systems provide an advanced method for the suppression or replacement of mosquito populations, thereby controlling the spread of vector-borne diseases.

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