

Gene flow by urbanization: predictions on population structure of *Aedes aegypti*

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ABSTRACT

The mosquito *Aedes aegypti* is a main vector of dengue virus, which causes dengue fever in the tropic region. To suppress the spread of the virus, insecticides and mosquito nets have widely been used because we still lack effective vaccine. However, recent studies have reported an emergence of the mosquitoes developing genetic resistance to our measures. Thus it is important to reveal risks of those mosquitoes spreading among populations and to seek another solution from population genetics aspects. We developed an individual-based simulation for regenerating the microsatellite data of mosquitoes collected in the Philippines from 15 sea ports. *A. aegypti* populations are more genetically similar when those ports are strongly connected by cargo shipments. This implies that human-mediated marine dispersal is common in this system and isolation by geographic distance is not held. By combining the simulation and Approximate Bayesian Computation method, we estimated each population size and the number of migrants among populations per generation based on cargo shipments data. These results enable us to predict a spread of a functional mutation on the estimated population-network and a possibility of more effective vector control strategies.

REFERENCES

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