Reflections on the *Anopheles gambiae* Genome Sequence, Transgenic Mosquitoes and the Prospect for Controlling Malaria and Other Vector Borne Diseases

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Abstract

The completion of the *Anopheles gambiae* Giles genome sequencing project is a milestone toward developing more effective strategies in reducing the impact of malaria and other vector borne diseases. The successes in developing transgenic approaches using mosquitoes have provided another essential new tool for further progress in basic vector genetics and the goal of disease control. The use of transgenic approaches to develop refractory mosquitoes is also possible. The ability to use genome sequence to identify genes, and transgenic approaches to construct refractory mosquitoes, has provided the opportunity that with the future development of an appropriate genetic drive system, refractory transgenes can be released into vector populations leading to nontransmitting mosquitoes. *An. gambiae* populations incapable of transmitting malaria. This compelling strategy will be very difficult to achieve and will require a broad substantial research program for success. The fundamental information that is required on genome structure, gene function and environmental effects on genetic expression are largely unknown. The ability to predict gene effects on phenotype is rudimentary, particularly in natural populations. As a result, the release of a refractory transgene into natural mosquito populations is imprecise and there is little ability to predict unintended consequences. The new genetic tools at hand provide opportunities to address an array of important issues, many of which can have immediate impact on the effectiveness of a host of strategies to control vector borne disease. Transgenic release approaches represent only one strategy that should be pursued. A balanced research program is required.

Keywords: genome sequence, transgenics, vector borne disease control

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