Defeating dengue: new mosquito genome, old promise?

In a news item in the Bulletin, Orozco outlines some of the history and extent of dengue transmission in tropical countries since the 1970s. According to experts, a major reason for the disease’s re-emergence in Latin America during the past two decades is the widespread presence of the mosquito vector, the female *Aedes aegypti* mosquito, which transmits dengue among humans. The balanced call for a combination of measures, including vector control, dengue prevention and, preferably, developing a vaccine, is to be commended. Overemphasis of, and too much reliance on, any single approach should be avoided.

To illustrate, Chadee et al. see much promise in the recent release of the *Aedes aegypti* genome, which comes four years after the genome sequence of *Anopheles gambiae*, the key mosquito vector of malaria in Africa. Even while acknowledging that there are challenges ahead in using the genetic code to better control dengue and yellow fever, the authors title their report in *Science* “A breakthrough for global public health”, suggesting that tangible results could be just around the corner.

But from the experience with *Anopheles gambiae* which transmits malaria to some 400 million people globally per year, of whom up to 3 million die of the disease, we know that mosquito-associated diseases are enormously complex. Malaria is caused by parasites of the genus *Plasmodium* and, according to the United States Centers for Disease Control and Prevention, some 30–40 different *Anopheles* species may serve as vectors. This did not prevent the claim being made in the course of the Malaria Genome Project that a solution to malaria might be only five years away. But despite the deciphering of the genome of *Plasmodium falciparum* in 2002 and the release of the *Anopheles gambiae* genome in the same year, the director of WHO’s Global Malaria Programme, Arata Kochi, recently urged not high-tech genome-based measures but the old-fashioned and “politically unpopular” indoor spraying with DDT to effectively prevent malaria.

Mapping the genome of the second mosquito species in full is an important achievement, but there is no reason to expect that issues surrounding *Ae. Aegypti* will be less complex than those concerning *Anopheles gambiae*. In fact, the vector–virus–disease relationships may be even more complex to unravel (the *Ae. aegypti* genome is about five times the size of the genome of the malaria mosquito), and it is likely to be a long time before genome sequence information can be translated into “new approaches for vector-targeted control of disease”. A real breakthrough in global public health is likely to take even longer.

Comprehensive prevention plans, as suggested by Orozco’s article, seem a must to fulfil the difficult tasks of defeating dengue.

Thomas C Erren* & Michael Erren

References


* Institute and Polyclinic for Occupational and Social Medicine, School of Medicine and Dentistry, University of Cologne, Kerpener Straße 62, D-50937 Köln, Lindenthal, Germany.

† Institute of Clinical Chemistry and Laboratory Medicine, Westphalian Wilhelms-University of Münster, Münster, Germany. Correspondence to Thomas C Erren (e-mail: tm.erren@uni-koeln.de).