

## 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.<sup>1</sup> 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.<sup>2</sup> see much promise in the recent release of the genome sequence of *Aedes aegypti*<sup>3</sup> which comes four years after the genome sequence of *Anopheles gambiae*, the key mosquito vector of malaria in Africa.<sup>4</sup> 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,<sup>5</sup> 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<sup>6</sup> and the release of the *Anopheles gambiae* genome in the same year,<sup>4</sup> 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.<sup>7</sup>

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),<sup>3</sup> 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".<sup>3</sup> 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. ■

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### References

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