The Zika virus, like hundreds of other arboviruses, has been circulating among African primates for millennia transmitted by various species of Aedes mosquitoes. One African primate (*Homo sapiens*) and one Aedes mosquito (*Aedes aegypti*) have escaped Africa and spread around the world. So it is to be expected that when one of these viruses escapes, *Ae. aegypti* is the most efficient vector. *Ae. aegypti* is an invasive species that continues to have a dynamic distribution. Human populations at risk for Zika coincide with the distribution of *Ae. aegypti*. I will discuss recent population genetic studies on *Ae. aegypti* that contribute to our understanding of present day distributions, ongoing dynamics, and likely future changes in this mosquito. These findings have significance for not only understanding where Zika is likely to spread, but also how best to control the mosquito including genetic control. Controlling this one species of mosquito will also control other diseases presently affecting humans (e.g., dengue, chikungunya, and yellow fever) as well as prevent future Zika-like new escapees from Africa to become widespread public health threats.