Dengue is a mosquito-borne viral pathogen that causes large amounts of disease in the tropics and subtropics. Dengue viruses are divided into four large clades, called serotypes: infection with a virus produces complete immunity to viruses within that same serotype, but increases the risk of severe disease upon infection with a virus from a different serotype. Multiple mechanisms have been hypothesized for this interaction between serotypes in the human immune system, which, combined with seasonal oscillations in mosquito abundances, lead to complex behavior in mathematical models. In addition, two new interventions for dengue are currently in intense development: a vaccine that protects against all four serotypes and transgenic mosquitoes that are less suitable vectors. In this talk, I will discuss a model for evolution of dengue viruses in response to these new interventions and work in progress on the best population groups to target with vaccine to minimize disease burden.