

### This week in techniques

Approach	Summary	Licensing status	Publication and contact information
<b>Assays &amp; screens</b>			
<i>In vivo</i> infection system to predict epidemic variants of mosquito-borne RNA viruses	Mosquito and mouse studies suggest deep sequencing of saliva can help predict arbovirus strains that could become epidemic. In <i>Aedes albopictus</i> mosquitoes that carried a pre-epidemic strain of chikungunya virus, deep sequencing of saliva samples was used to detect the emergence of a mutation that results in an epidemic strain. In a prospective analysis of the virus, the epidemic strain acquired two additional mutations. In <i>A. albopictus</i> , the new viral strain had greater infection and dissemination titers than the parental strain. Next steps include applying the method to the chikungunya virus currently spreading in the Caribbean region and adapting the method for use against influenza virus.	Unpatented; licensing status not applicable	Stapleford, K.A. <i>et al. Cell Host Microbe</i> ; published online June 11, 2014; doi:10.1016/j.chom.2014.05.008 <b>Contact:</b> Marco Vignuzzi, Centre National de la Recherche Scientifique (CNRS) UMR 3569, Paris, France e-mail: <a href="mailto:marco.vignuzzi@pasteur.fr">marco.vignuzzi@pasteur.fr</a>
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