# Improving the Genome Editing Efficiency in Aedes aegypti

***by Maraiyah Baksh* | John Castillo | Matthew Degennaro, PhD.***

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*Aedes aegypti* is the central vector for three main arboviruses that affect humans, dengue, chikungunya and zika. Since these diseases are globally widespread and have a major effect on the population, being able to reduce the vector population essential. Improving genome-editing efficiency in *Aedes aegypti* is one crucial step in understanding the control and transmission of these diseases. It is possible to create a gene drive system that would introduce a gene to diminish the population of *Aedes aegypti*, using CRISPR/Cas9, a genome-editing tool that allows for site-specific mutagenesis. Although CRISPR/Cas9 has made it accessible to mutagenize virtually any genome using Watson-Crick base pairing, there are still concerns on the precision of the Cas9 endonuclease. Studies have shown that organisms expressing Cas9 in the germline have higher prevalence of CRISPR activity rather than embryonic injection. Using this approach, we want to compare the mutagenic rates of Cas9 expressing strains to wild type. Specifically, we want to assess the wellness and rate of off-target effects, if any, present in the offspring. Here we use two germline Cas9 expressing strains, p11 and p6 to determine the rates of mutagenesis of the yellow gene between endogenously expressed Cas9 compared to recombinant protein injected in a wild type strain. Our preliminary data shows that there is a difference in Cas9 activity between the Orlando (wild type) line, p11 strain, and p6 strain. Cas9 activity in the Orlando strain was found to be at ~ 34.6%, while the p11 strain showed ~33.3%. As of current trials, the p6 line has yet to show Cas9 activity. If these strains are shown to have increased mutagenic rates, an insight on how to create a precise gene drive system could potentially support population control.