

A Survey of Mosquito Populations for Evidence of Lateral Gene Transfer.

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Lateral gene transfer is an important evolutionary mechanism between organisms through a variety of processes. In prokaryotes it can be mediated by conjugation, transformation and transduction, and in eukaryotes, transposable elements and viruses play a key role. Additionally, complex evolutionary relationships driven by lateral gene transfer can exist in eukaryotic organisms infected with prokaryotes. One such evolutionary system is seen in mosquitoes carrying *Dirofilaria immitis* (the causative agent of heartworm) and WO phage-infected *Wolbachia pipientis*. The studies herein explored evidence of lateral gene transfer in this system of coevolution.

Mosquitoes were trapped using resting boxes or light traps and identified taxonomically. Mosquito genomic DNA was used to perform polymerase chain reaction (PCR) to detect the *W. pipientis* surface protein (wsp) gene. PCR products from *Culiseta melanura* (856 bp) and *A. quadrimaculatus* (806 bp) were cloned, sequenced and subjected to genomic analysis. DNA sequencing data showed a 29 bp region corresponding to the upstream primer region at the beginning of the PCR product with 100% homology to the wsp gene. A downstream region of 31 bp at the end of the DNA sequence had 92% homology to the wsp gene. In addition, the 856 bp and 806 bp PCR product was comprised of unidentified DNA with 73-74% homology to *Aedes aegypti*. A detailed analysis is difficult since the genomic DNA sequence for these mosquitoes has not yet been reported. However this data supports that these PCR products have mosquito origin. The data also evidence lateral gene transfer of wsp into these mosquito genomes. Additionally, Anopheles species may also contain *W. pipientis* DNA. These observations are noteworthy since, evidence of Wolbachia infection and lateral gene transfer of *W. pipientis* DNA in Anopheles mosquitoes has not been previously reported.