# Strain Variation in the Transcriptome of the Dengue Fever Vector, *Aedes aegypti*

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**ABSTRACT** Studies of transcriptome dynamics provide a basis for understanding functional elements of the genome and the complexity of gene regulation. The dengue vector mosquito, *Aedes aegypti*, exhibits great adaptability to diverse ecological conditions, is phenotypically polymorphic, and shows variation in vectorial capacity to arboviruses. Previous genome sequencing showed richness in repetitive DNA and transposable elements that can contribute to genome plasticity. Population genetic studies revealed a varying degree of worldwide genetic polymorphism. However, the extent of functional genetic polymorphism across strains is unknown. The transcriptomes of three *Ae. aegypti* strains, Chetumal (CTM), Rexville D-Puerto Rico (Rex-D) and Liverpool (LVP), were compared. CTM is more susceptible than Rex- D to infection by dengue virus serotype 2. A total of 4188 transcripts exhibit either no or small variation (<2-fold) among sugar-fed samples of the three strains and between sugar- and blood-fed samples within each strain, corresponding most likely to genes encoding products necessary for vital functions. Transcripts enriched in blood-fed mosquitoes encode proteins associated with catalytic activities, molecular transport, metabolism of lipids, carbohydrates and amino acids, and functions related to blood digestion and the progression of the gonotropic cycle. Significant qualitative and quantitative differences were found in individual transcripts among strains including differential representation of paralogous gene products. The majority of immunity-associated transcripts decreased in accumulation after a bloodmeal and the results are discussed in relation to the different susceptibility of CTM and Rex-D mosquitoes to DENV2 infection.

**KEYWORDS**
*Aedes aegypti*
strain variation
bloodmeal
RNA-seq

*Aedes aegypti* (Diptera, Culicidae) is the primary vector for dengue (DEN), yellow fever, and Chikungunya viruses throughout most tropical and subtropical areas of the world (Charrel *et al.* 2007; Gubler 2002). In addition to its significance as a public health concern, ease of laboratory breeding and maintenance makes it a good vector mosquito model system (Clemons *et al.* 2010; Kuno 2010). Importantly, a key component of a model organism is the ability to use information gathered from transcriptomics from one strain to make inferences about other strains within the species. This information then can be used in studies that test possible interactions among genotypic variation, transcriptional regulation, and environmental factors (Wagner 2011).

This mosquito species is phenotypically polymorphic, has great adaptability to diverse ecological conditions, and shows variation in vectorial capacity for arboviruses (Bennett *et al.* 2002; Black *et al.* 2002; Kuno 2010). Genetic polymorphism among geographically distinct *Ae. aegypti* populations is documented (Urdaneta-Marquez and Failloux 2011); however, the extent of genome sequence polymorphism and its effects on transcriptional activity are not known.

The transcriptional profiles of three *Ae. aegypti* strains, Liverpool (LVP), Chetumal (CTM), and Rexville D Puerto Rico (Rex-D), were


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RNA-seq data for the CTM and Rex-D strains have been submitted to the GEO database at NCBI as series GSE32074.
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