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RNA-seq analyses of blood-induced changes in gene expression in the mosquito vector species, *Aedes aegypti*

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Abstract

Background

Hematophagy is a common trait of insect vectors of disease. Extensive genome-wide transcriptional changes occur in mosquitoes after blood meals, and these are related to digestive and reproductive processes, among others. Studies of these changes are expected to reveal molecular targets for novel vector control and pathogen transmission-blocking strategies. The mosquito *Aedes aegypti* (Diptera, Culicidae), a vector of Dengue viruses, Yellow Fever Virus (YFV) and Chikungunya virus (CV), is the subject of this study to look at genome-wide changes in gene expression following a blood meal.

Results

Transcriptional changes that follow a blood meal in *Ae. aegypti* females were explored using RNA-seq technology. Over 30% of more than 18,000 investigated transcripts accumulate differentially in mosquitoes at five hours after a blood meal when compared to those fed only on sugar. Forty transcripts accumulate only in blood-fed mosquitoes. The list of regulated transcripts correlates with an enhancement of digestive activity and a suppression of environmental stimuli perception and innate immunity. The alignment of more than 65 million high-quality short reads to the *Ae. aegypti* reference genome permitted the refinement of the current annotation of transcript boundaries, as well as the discovery of novel transcripts, exons and splicing variants. *Cis*-regulatory elements (CRE) and *cis*-regulatory modules (CRM) enriched significantly at the 5' end flanking sequences of blood meal-regulated genes were identified.

Conclusions

This study provides the first global view of the changes in transcript accumulation elicited by a blood meal in *Ae. aegypti* females. This information permitted the identification of classes of potentially co-regulated genes and a description of biochemical and physiological events that occur immediately after blood feeding. The data presented here serve as a basis for novel vector control and pathogen transmission-blocking strategies including those in which the vectors are modified genetically to express anti-pathogen effector molecules.

Background

Insect vector-borne pathogens cause some of the most widespread infectious diseases worldwide, including dengue fever, yellow fever, malaria, encephalitis, filariasis, leishmaniasis and trypanosomiasis [1,2]. The corresponding vectors are hematophagous insects that become infected by ingesting pathogens during blood feeding. Transmission of the pathogen to a subsequent vertebrate host occurs during the acquisition of another blood meal.

Hematophagy is a behavior exhibited by more than 14,000 species of insects [3-5], but genome-wide information regarding blood meal-regulated gene expression