

FUNCTIONAL GENOMICS OF *Amblyomma cajennense*

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Ticks are blood-sucking arthropods of Order Acari, Class Arachnida, recognized as of medical importance and widely found in diverse ecosystems on all continents except Antarctica. Among these ectoparasites, the *Amblyomma cajennense* represents one of the more important vectors for human and animals diseases, potentially transmitting many pathogenic agents. To the process of infestation and during the development of microorganisms inside their body, various metabolic process occurs to permit their adequate development. The knowledge of the gene expression in the ticks *A. cajennense* under different situations and conditions represents an essential step to understand, at molecular level, the mechanisms involved in the development and interaction of this tick with their parasites and hosts. The advent of Next-generation high throughput sequencing platforms, makes it a key tool for functional genomic studies, especially for those organisms which whole genome information is not available, such as the tick *A. cajennense*. In this context, the study of global gene expression and the annotation of expressed sequence tags (*ESTs*) present in cDNA libraries is a suitable tool to obtain information about it. For example, the success of this arthropod during its parasitic phase, and the ability to pathogen transmission to vertebrate hosts, depends on the adaptation of their mouthparts and changes in gene expression pattern of the salivary glands during sucking blood. Using this approach will be possible to indicate and identify molecular events that will drive the development of this tick. Since the Next-generation sequencing platforms generate a large amount of information, it is necessary to perform *in silico* analysis through the aid of specialized computational gene annotation tools. Both tools, DNA machine sequencers and *in silico* analyses by specialized bioinformatics softwares, associated to the exponential reduction of costs and the interaction among different professionals, are at now very promising to the process of obtainment and study the patterns of gene expression and functional genomics.