Expression of Immune-Related Genes in Aedes Aegypti

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Using qPCR we have studied the expression of some key genes from *Aedes aegypti* main immune pathways: Toll (Rel1, MyD88, Cactus, Serpin), IMD (Rel2, Defensin) and JAK/STAT (STAT, TEP1), in different developmental stages (larva, pupa, male and female mosquitos) and tissues (fat-body, ovary, midgut, head and thorax) of the adult *Aedes aegypti* mosquito. Fat-body was the tissue that presented higher expression levels for most of the studied genes. Males presented higher expression levels than sugar fed females of most of the genes. We examined the expression profile of the same genes in blood fed females. Toll pathway genes were not up-regulated by blood feeding while genes from IMD and JAK\STAT pathways were, reaching expression levels similar to the ones exhibited by males. In relation to the midgut, we observed that three major mosquito immune-related transcription factors (Rel1, Rel2 and STAT) were up regulated 24 hours after a blood meal while only STAT seems to be induced by an albumin meal. When mosquitoes were fed with SBTI, inhibiting blood digestion, Rel1 decreased its expression, suggesting that Toll activation, but not IMD or JAK\STAT pathways, depends on blood digestion. Preliminary data suggests that plasma fed mosquitoes exhibit a very low expression profile of genes from Toll and Jak/STAT pathways, but not of IMD.

Furthermore antibiotics treated mosquitoes showed reduced expression of STAT and Rel2, but not of Rel1. These results suggest that blood meal can activate these major immune pathways by different means, such as protein uptake, digestion products or gut microbiota growth and much remains to be understood in how the immune response genes are regulated in non-infected insects.

Supported by CNPq, HHMI and FAPERJ.