

DETERMINATION OF THE IMMUNOSTIMULATORY ROLE OF *ASAIA* IN *Aedes Aegypti*: A POTENTIAL SYMBIONT-BASED CONTROL APPROACH?

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Recurring outbreaks of arboviruses such as dengue on a global scale, it is imperative to adopt multi-faceted strategies to limit the transmission of mosquito-borne diseases (MBDs). Insecticide and drug resistance, coupled with the absence of effective vaccines, presents a significant obstacle in combating MBDs. Recent years have seen a deeper understanding of mosquito microbiota, revealing its role in different traits of the mosquito biology such as sexual reproduction, development, nutrition, and resistance to pathogens. As a reflection of this new knowledge, exploitation of symbiotic bacteria of vector mosquitoes has emerged as a potential control-strategy of MBDs. For instance, the symbiotic bacterium *Asaia* has been shown to activate immune genes in different insect hosts including *Anopheles* where it elicits an anti-plasmodium response (Gonnella et al., 2019. *Front Physiol*, 10:795; Cappelli et al., 2019. *Front Genet*, 10:836). The present study investigates the effect of *Asaia* on the immune system of a main vector of arboviruses such as *Ae. aegypti*. A laboratory strain of *Ae. aegypti* (New Orleans 2011) was reared at standard conditions. The experimental set up included three groups of female mosquitoes (a, b and c). Groups a and b received different dietary boosts of *Asaia*, respectively 105 cell/ml and 108 cells/mL while the control group c received a normal diet. Half of the mosquitoes per each group were feed with blood meal and collected daily for 5 days post feeding. The *Asaia* amount was monitored in all the tested samples by qPCR. The expression of transcription factors (Rel 1, Rel 2) and effectors genes of IMD and Toll (Cecropin A, Defensin C, Gambicin and C-type Lectin) cascades together with two genes (Heme peroxidase 7, Superoxide dismutase) codifying enzymes involved in the degradation of Reactive oxygen Species (ROS) were evaluated by qPCR. Moreover, the effect of *Asaia* supplementation on the microbiota composition was assessed through 16S MiSeq analysis. Outcomes suggest that the analysed antimicrobial peptide genes and transcription factors are not affected by *Asaia* overloads, nonetheless the expression of two ROS genes increased concurrently with the proliferation of the bacterium on the second day post-blood meal. These observations need to be corroborated by further analysis for quantifying specific metabolites associated with oxidative stress. Microbiota analysis indicates a marked proliferation of *Asaia* following blood-feeding, emerging as the predominant bacterium. Other symbiont such as *Pantoea* exhibited a modest increase in abundance and *Pseudomonas* experienced a sharp decrease. Exploring the *Asaia-Ae. aegypti* system to investigate the influence of symbiotic bacteria on stimulating the mosquito immune response against arboviruses, holds potential. This could pave the way for the development of symbiotic-based interventions that can complement existing approaches in the field.