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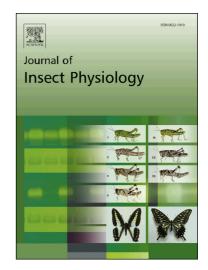
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## **ACCEPTED MANUSCRIPT**

Wide-scale analysis of protein expression in head and thorax of Aedes albopictus females

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**ABSTRACT** 

The recently available genome of Aedes albopictus - the most worldwide-spread human arbovirus

vector – has revealed a large genome repertory and a great plasticity which are believed to have

contributed to the species success as an invasive species and opened the way to genomic,

transcriptomic and proteomic studies. We carried out the first wide-scale quantitative proteomic

analysis of Ae. albopictus female head and thorax by means of a 'shotgun' approach based on nano

liquid chromatography-high resolution mass spectrometry associated to protein Label Free

Quantification (LFQ) which allows to assess differences in protein expression between tissues and

different physiological stages. We identified 886 and 721 proteins in heads and thoraxes

respectively, 5 of which were exclusively expressed in thoraxes and 170 in heads, consistently with

the more complex head physiology. Head-protein expression was found to be highly divergent

between virgin and mated females and limited before and after blood-feeding and oviposition. The

large repertoire of proteins identified represents an instrumental source of data for genome

annotation and gene-expression studies, and may contribute to studies aimed at investigating the

molecular bases of physiological processes of this successful invasive species.

**Keywords:** mosquito; proteome; mating; blood feeding; oviposition; head; thorax.

1

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