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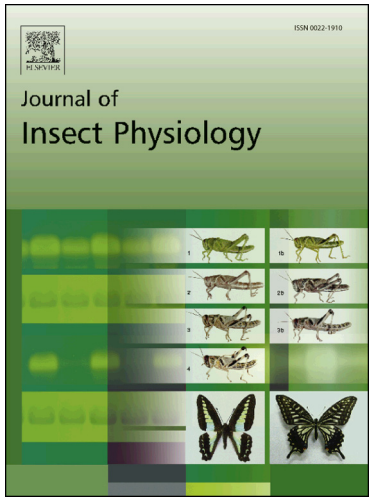

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Wide-scale analysis of protein expression in head and thorax of *Aedes albopictus* females

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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.