DIFFERENTIAL TRANSCRIPT AND PROTEIN EXPRESSION PROFILES IN *ANOPHELES GAMBIAE SENSU STRICTO* MOSQUITO LARVAE EXPOSED TO CADMIUM HEAVY METAL

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ABSTRACT

Anopheles gambiae sensu stricto mosquito larvae are known to thrive in non-polluted environments. However, the larvae have adapted to heavy metal polluted habitats at a significant biological cost. The molecular processes mediating the adaptation are poorly understood. This study assessed transcriptional and proteomic responses in *An. gambiae s. s* larvae following exposures to cadmium heavy metal as proxy assessment of adaptation of the mosquito to heavy metals. Three independent replicates of third instar larvae were exposed to cadmium or not (controls). Their RNAs were separately extracted and complementary DNA (cDNA) were synthesised from the RNA. Differentially expressed transcripts among cDNA transcripts were identified using the Annealing Control Primer (ACP) technology. Similarly, protein was concurrently extracted in triplicates from third instar larvae (n=50), separated using SDS gel and in-gel protein digestion using trypsin. The protein fragments were then analysed and profiled using Mass spectrometry (MS) and a suite of bioinformatics software. Transcriptomic analysis identified fourteen differentially expressed genes, of which eleven were up-regulated by the cadmium exposure while three were down-regulated. The up-regulated genes were clustered into biological functions that encompassed metabolism, transport and protein synthesis. The down-regulated transcripts included Protein G12, adenylate cyclase and endoplasmic reticulum metallopeptidase. Proteomics analysis revealed the down-regulation of immunity, protein synthesis and degradation and proton transport proteins by cadmium exposure in the mosquito larvae. There was an up-regulation of proteins with catalytic activity in the cadmium exposed larvae. There was also an up-regulation of signalling molecules of the small GTPase family. Other proteins induced included, transcription factor, ribosomal proteins and those in the protein degradation pathway involving ubiquitination. These findings provide information of cadmium responsive transcripts and proteins that are useful in designing more effective vector control methods that match changes in vector dynamics.

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