Abstract

Background: *Anopheles gambiae* larvae traditionally thrive in non-polluted environments. We previously documented the presence of the larvae in heavy metal polluted urban aquatic environments and the associated biological cost. The goal of this study was to unravel the molecular dynamics involved in the adaptation of the mosquitoes to the heavy metals.
Methods: Total RNA was extracted from third instar larvae of both cadmium treated populations and untreated control populations. The RNA concentrations were normalized and complementary DNAs were prepared. Then annealing control primer (ACP) technology was applied to establish transcriptional responses in *An. gambiae* larvae following several generational (n=90) chronic exposures to cadmium. Differentially expressed genes were determined by their differential banding patterns on an agarose gel. Gel extraction and purification was then carried out on the DEGs and these were later cloned and sequenced to establish the specific transcripts.
Results: We identified 14 differentially expressed transcripts in response to the cadmium exposure in the larvae. Most (11) of the transcripts were up-regulated in response to the cadmium exposure and were putatively functionally associated with metabolism, transport and protein synthesis processes. The transcripts included ATP-binding cassette transporter, eupolytin, ribosomal RNA, translation initiation factor, THO complex, lysosomal alpha-mannosidase, sodium-independent sulfate anion transporter and myotubularin related protein 2. The down-regulated transcripts were functionally associated with signal transduction and proteolytic activity and included Protein G12, adenylate cyclase and endoplasmic reticulum metallopeptidase.
Conclusions: Our findings shed light on pathways functionally associated with the adaptation to heavy metals that can be targeted in integrated vector control programs, and potential *An. gambiae* larvae biomarkers for assessment of environmental stress or contamination.