Proteome analysis and Identification of heme-regulated proteins in two Gram-negative bacteria

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Introduction: *Pseudomonas putida* and *Chryseobacterium sp.* were isolated from midgut of blood-fed *Aedes aegypti*. In these insect, midgut bacteria have to deal with heme-induced oxidative stress during blood digestion. Thus, this work aimed to investigate the molecular response of these bacteria cultured in medium contained excess of heme. **Material and methods:** These bacteria were cultured in CASO medium supplemented with hemin 0.1 mM. Proteomic analyses combined the shotgun method and the nanoESIHDMSE technology. Proteins were filtered on the basis of 0.5 log2, presenting proteins that were up and down regulated. **Results and discussion:** Proteomic analysis identified a total of 973 *Chryseobacterium sp* proteins, which were 117 up-regulated and 78 down-regulated in the presence of hemin. Only two and three unique proteins were found in the presence and absence of hemin, respectively. Among up-regulated proteins, five were related to oxidative stress and 40 proteins possessed ion-binding capacity. Also, several synthesis and energy-related proteins were highly expressed. Among down-regulated proteins, six were related to oxidative stress, 28 possessed ion-binding capacity and two were related to heme metabolism. *P. putida* presented 545 differentially expressed proteins, which 40 and 34 were up and down-regulated in the presence of hemin. In this bacteria, 15 and 10 ion-binding proteins were up and down-regulated, respectively. Also, several stress-induced proteins were identified. These results suggest that both bacteria are able to respond and adapt to heme-induced oxidative stress and can assist in the metabolism of heme generated during mosquito digestion process.

Keywords*:* Bacteria, heme and proteome.

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