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Comparative NanoUPLC-MS^E analysis between magainin I-susceptible and -resistant *Escherichia coli* strains

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In recent years, the antimicrobial peptides (AMPs) have been prospected and designed as a promise of new alternatives to conventional antibiotics. Indeed, this class of pharmacological molecules has presented great potential action toward susceptible and resistant bacterial strains, in both their free-floating and biofilm lifestyles. However, increasing reports have reported the mechanisms by which bacteria resist AMP administration. Thus, here we performed a comparative proteomic study by using the total bacterial lysate of magainin I-susceptible and –resistant *E. coli* strains. After nanoUPLC-MS^E analyses, we identified 742 proteins distributed among the experimental groups, 427 proteins being identified in the *E. coli* (ATCC 8739) group, 664 in the *E. coli* susceptible (control) group and 651 in the *E. coli* resistant group. These proteins were also separated into 5 biological classes using KEGG orthology, being 73% related to metabolism. Also, 25 proteins were differentially expressed in the resistant strains, 10 proteins being upregulated, including outer membrane proteins (OMPs), periplasmic oligopeptide-binding protein (OppA) and zinc resistance-associated proteins (ZraP) and 15 downregulated, such as chaperone protein DnaK, glutaminase 1 (glsA1), glucosamine-6-phosphate deaminase (NagB) and NAD(P)H dehydrogenase (WrbA). Moreover, 60 exclusive proteins were identified in the magainin I-resistant strains, among which biofilm formation (YoaB), cell wall (DblB) formation and multidrug efflux pump (AcrA) proteins could be observed. Thus, data here reported show that several metabolic pathways have been related with *E. coli* resistance to cationic AMPs, revealing the crucial role of multiple "omics" studies in order to elucidate the global molecular mechanisms involved in this resistance.

Biography

Marlon Henrique e Silva Cardoso is a PhD student of Molecular Pathology at the University of Brasília, Brazil. He obtained his BSc in Biology/Biotechnology at the Catholic University of Brasília, Brazil. In 2012, he became a Member of the Center for Proteomics and Biochemical Analyses, coordinated by Prof. Dr. Octávio Luiz Franco. In 2014, he was invited by Dr. Franco to join the S-Inova Biotech as the Responsible for the Department of Structural Bioinformatics and Computational Biophysics. Since 2013, he has published more than 10 articles (7 during an year as a PhD student) in renowned journals and a book chapter.

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