Analysis of Expressed Sequence Tags of Liver of the Snake *Bothropoides jararaca*.

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*Bothropoides jararaca* is the main snake responsible for accidents in São Paulo State. Its bites cause both local and systemic envenomation effects, which are mediated by venom components. Considering that in vertebrate animals, the liver is an important organ responsible for synthesis of plasma proteins, it would be valuable to perform a transcriptomic analysis of this organ. Thus, the aim of this work was to analyze genic expression profile in *B. jararaca* liver, mainly concerning blood hemostasis molecules. For this purpose, we sequenced 1700 Expressed Sequence Tags (ESTs) from a cDNA library of *B. jararaca* liver. Nucleotide sequences were assembled into 462 contigs, which were submitted to the GenBank NCBI database using BLASTX and BLASTN algorithms. Transcripts showed 58% hits with NR database while 42% of ESTs had no homology. According to Gene ontology (GO) analysis, transcripts were assigned for biological process, cellular component and molecular function. Majority of transcripts were classified in biological process category distributed in metabolic process, cellular processes and biological regulation, whereas binding and catalytic activities were the main categories in molecular function. Cellular component analysis identified transcripts related to cell part, extracellular region and membrane-bounded organelle. The major group of transcripts was related to phospholipase A\(_2\) inhibitors, followed by metalloproteinase and serine proteinase inhibitors. Our results will help in studies of phylogenetic relationships between different snake species, and investigate differences in gene expression pattern. In addition, our findings are also helpful in the identification of active compounds for development of improved therapeutics for snake bites.

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