Analysis of *Macrolampis* Firefly Lanterns cDNA Library: Identification of Candidates in Luciferin Biosynthesis and Bioluminescence Control

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The origin of beetle bioluminescence is enigmatic. Besides its purely scientific interest, understanding the origin of beetle luciferases and luciferin is of evident biotechnological interest. Whereas the origin of beetle luciferases is partially understood, the biosynthetic and functional origins of beetle luciferin are almost unknown. Therefore, using a cDNA library constructed from *Macrolampis sp2* firefly lanterns, with the aim to isolate luciferase cDNAs, we started to analyze the expressed genes in order to identify putative candidates involved with luciferin biosynthesis and bioluminescence control. We randomly selected 200 clones and isolated their plasmids. After partial sequencing of their cDNA inserts, the sequences were submitted to NCBI Blast analysis and 111 sequences were selected. Among them, 22% displayed high similarity with Coleoptera genomes products; 5% represented mitochondrial genes, which is also expected for a tissue rich in mitochondria such as the photogenic tissue. A luciferase gene was also isolated. Among gene products potentially involved with luciferin biosynthesis, genes involved with cysteine and sulfur metabolism were selected: cystathionine ß-lyase, an important enzyme in the detoxification pathway of homocysteine, and the *S*-Adenosylmethionine synthetase that catalyzes the synthesis of S-adenosylmethionine which is donor of metil group in biological systems. Among gene products potentially involved with bioluminescence control, several copies of cytochrome oxidase, which is an enzyme that was suggested to be involved with flash control through $NO^{\cdot}$ mediated availability of oxygen and ATP, were found. Full sequencing of luciferase and cytochrome oxidase genes, and sequencing of other genes in the library is underway. keywords: bioluminescence, luciferin, luciferase. (Acknowledgements: FAPESP and CNPq).