The second messenger cGMP regulates a broad range of cell processes in eukaryotes. In contrast to the lack of evidence of a cGMP pathway in the published genomes of ascomycete and basidiomycete fungi, the blastocladiomycete Blastocladiella emersonii was shown to present cGMP, and a high degree of variation in its levels during the fungus' life cycle. Evolutionists attribute the absence of cGMP to the sedentary life style of the higher fungi. Differently from filamentous fungi, B. emersonii presents motile cells in at least one stage of its life cycle, which could explain the existence of this pathway in this fungus. Therefore, the purpose of this study is to characterize the cGMP signaling pathway in B. emersonii. Sequences obtained by 454 genome sequencing and 5’RACE experiments revealed the complete nucleotide sequence of three putative guanylate cyclases (BeGC1-3), a cGMP phosphodiesterase (BePDE) and a putative cGMP-activated channel (BeCNG). Through comparative sequence analysis and western blot analysis, we hypothesized the probable localization and the activators of BeGC1 and BeGC3. BeGC1 is apparently activated by light and is localized in organelles and / or flagellum. BeGC3 appears to be a NO-regulated cyclase and is localized in the cytoplasm. qRT-PCR showed that changes in BeCNG transcript levels follow the same pattern of BeGC1 mRNA. In addition, Western blots confirmed the presence of BeCNG in the plasma membrane of zoospores. Recombinant BePDE presents activity toward hydrolysis of cGMP, suggesting that this enzyme is active in this fungus. We will further characterize the enzymes involved in this pathway.

Word Keys: cGMP, fungi, cGMP-phosphodiesterase

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