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Abstract

The first opsins prediction in *Achatina fulica* genome †

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Abstract: The variety of spectral properties of visual pigments is provided mainly by the amino acid sequences of their protein part, the so-called visual opsins. However, such data on these proteins of gastropod molluscs are very scarce, and for terrestrial species are absent at all. Meanwhile, the first sequenced genome of the terrestrial gastropod, *Achatina fulica*, was published (https://doi.org/10.1093/gigascience/giz124). So, the aim of this study is the prediction of the amino acid sequences of opsins in the *A. fulica* genome. To this purpose, all known mollusc opsin sequences from the NCBI Protein database were collected. To analyse them, we performed a multiple sequence alignment in Unipro UGENE by Clustal Omega and refined it by MUSCLE, and then constructed the HMM profile, which was used to predict opsins in the A. fulica genome. Prediction of opsin sequences was performed using HMMER. To confirm the obtained sequences belong to opsins, we searched for the conserved domain, 7tmA_Opsin_Gq_invertebrates. As a result, we determined five rhodopsin G-coupled protein sequences in A. fulica genome among them are Afu011750, Afu004575, Afu005002, Afu003765, Afu022267. This is the first attempt to annotate the Achatina fulica genome, which was started by searching for opsins. Our study opens up new opportunities for further more detailed evolutionary and genetic studies of molluscs, including the study of visual mechanisms. But it should be noted that opsins form a diverse multifunctional group of proteins, of which only some are part of visual pigments. Therefore, work towards the identification of visual opsins in Achatina fulica should be continued.

Keywords: molluscs; opsins; genome annotation; gastropods; Achatina

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