

ABSTRACT (English)

Many of the metazoan phyla sense light by an opsin-based photopigment present in a photosensitive receptor cell (photoreceptor), with Cnidaria being arguably the earliest branching phylum containing a well-developed and complex visual system (advanced eyes morphologically similar to those of vertebrate). The evolutionary history of phototransduction and visual components (ranging from light-sensing opsins to structural genes of the lenses) is a long standing question. In this work, we decided to address this issue by applying a comprehensive multidisciplinary approach combining modern molecular biology methods with bioinformatics. Comprehensive genome-wide inspection of a cubozoan jellyfish *Tripedalia cystophora*, was complemented with gene expression analyses, together with functional (cell culture based assays) and behavioural (pharmacogenetics) testing.

First, genome analysis uncovered the presence of a surprisingly large number of opsin genes with distinct tissue- and stage-specific expression. Our extensive phylogenetic analysis classified cubozoan opsins as a sister group to c-type opsins and documented a lineage-specific expansion of opsin gene repertoire. Functional tests in cell cultures provided evidence for the use of Gs-cAMP signalling pathway only in a small subset of opsins, indicating that the majority of cubozoan opsins likely signal by a distinct, yet unidentified pathway. In addition, these functional tests uncovered subtle differences among individual cubozoan opsins, suggesting a possible fine-tuning for specific photoreceptor tasks. The opsin expression data led to identification of two distinct photoreceptors in the retinas of *T. cystophora*, revealing yet another level of complexity of cubozoan advanced eyes. Furthermore, novel opsin expression domains were documented for the first time. Finally, genome analysis revealed the presence of vertebrate-like phototransduction cascade components, together with additional structural proteins of the lenses.