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MOLECULAR CHARACTERIZATION OF RHODOPSIN GENE FROM INDIAN SQUID, *Uroteuthis duvaucelii*

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Squids are a group of invertebrates (class: Cephalopoda) that occupy a wide range of oceanic photic environments. They are an ideal group of animals, in which to study the evolution of the rhodopsin gene. The sequence of the Indian squid *Uroteuthis duvaucelii* rhodopsin gene was determined by cDNA sequencing. We obtained a cDNA encoding a rhodopsin gene with an open reading frame of 1359 bp. The deduced protein comprises 452 amino acids, with an estimated molecular mass of 50.49 kDa and an isoelectric point of 6.59. *U. duvaucelii* rhodopsin, has a repetitive proline-rich C-terminus (residues 340-452), characteristic of cephalopod rhodopsins. The rhodopsin gene of *U. duvaucelii* is intron less as reported in other myopsid squids but contrary to all other vertebrates where either four or five introns are invariably found. SignalP program analysis revealed that the cDNA contained no putative signal sequence within the coding region. Domain architecture analysis by SMART and Scan-Prosite server predicted six transmembrane regions (37-59,72-94,109-131,152-174,202-224,262-284) and three low complexity regions (340-358,361-380,381-444). The protein has a close similarity to veined squid species *Loligo forbesi* (96.23%) inferred by Bayesian inference Phylogram constructed by MrBayes. A 3D model constructed by the SWISS-MODEL Protein Modelling Server using the rhodopsin gene predicted a similar structure to that of *Loligo forbrsi*. The present data opens new opportunities for the generation of recombinant variants with improved properties for various optobioelectronic applications through computer modelling, site-directed mutagenesis, expression, and purification.

Keywords: Squid, Rhodopsin gene, Phylogeny