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# SEQUENCE AND STRUCTURAL ANALYSIS OF CYTOCHROME OXIDASE IN *GRACILARIA EDULIS*

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## ABSTRACT

Seaweed or marine algae are the group of plant that live either in marine or brackish water environment. Like the lands seaweed contain photosynthetic pigments and with the help of sunlight and nutrient present in the seawater they photosynthesize and produce food. Green algae they are found in the fresh and marine habitats. Brown algae are exclusively marine forms. The seaweed gracilaria edulis contain the protein cytochrome oxidase. In eukaryotes, the phosphorylating electron transfer chain is located in the inner membrane of their mitochondria and uses oxygen as the terminal sink for electro An excellent summary of the liganding of the metal centers in cytochrome oxidase is provided by the promise site page. The sequences of cytochrome oxidase retrieved from National Cenre for Biotechnology Information in fasta format. The structural homology of cytochrome oxidase were carried out by using bioinformatics tools like prop search, scan prosite and primary structural analysis of target protein done by using protscale tool, secondary structure analysis of cytochrome oxidase were carried out by porter tool and tertiary structure analysis is done through CPH models. Further studies are required to investigate the cytochrome oxidase of for potential pharmacological properties.

**KEYWORDS:** Seaweed or marine algae, gracilaria edulis, protscale.

## INTRODUCTION

Seaweed or benthic marine algae are the group of plants that live either in marine or brackish water environment. Like the land plants seaweed contains photosynthetic pigments and with the help of sunlight and nutrient present in the seawater, they photosynthesize and produce food. Seaweeds are found in the coastal region between high tide to low tide and in the sub-tidal region up to a depth where 0.01 % photosynthetic light is available. Plant pigments, light, exposure, depth, temperature, tides and the shore charestrstics combine to create different environment that determine the distribution and variety among seaweeds. They are basically classified according to colour into three main groups i.e. green (Chlorophyta), brown (Phaeophyta) and red (Rhodophyta).

They are found in the fresh and marine habitats. They range from unicellular to multi-cellular, microscopic to macroscopic forms. Their thalli vary from free filaments to definetely shaped forms. The photosynthetic portion of the thalli may be moderately to highly calcified appearing in variety of forms as fan shaped segments, feather like or star-shaped. They possess photosynthetic pigments such as Chlorophyll a & b, contained in the special cell structure known as chromatophores. The cell wall of this group composed of an outer layer of pectin and an inner layer of cellulose. The photosynthetic product of this group is starch.

The seaweed industry provides a wide variety of products that have an estimated total annual value of US$ 5.5-6 billion. Food products for human consumption contribute about US$ 5 billion of this. Substances that are extracted from seaweeds - hydrocolloids - account for a large part of the remaining billion dollars, while smaller, miscellaneous uses, such as fertilizers and animal feed additives, make up the rest. The industry uses 7.5-8 million tonnes of wet seaweed annually. This is harvested either from naturally growing (wild) seaweed or from cultivated (farmed) crops. The farming of seaweed has expanded rapidly as demand has outstripped the supply available from natural resources. Commercial harvesting occurs in about 35 countries, spread between the Northern and Southern Hemispheres, in waters ranging from cold, through temperate, to tropical.

## MATERIALS AND METHODS

### Protein Receptor Identification

The potential target protein was retrieved from ncbi database in order to perform protein sequence analysis and protein modeling studies.

**The protein sequence**

The cytochrome oxidase, protein sequence was applied in to PROTSCALE TOOL for primary structure analysis and the secondary structure analysis was done using **Porter** server.

**Three Dimensional Structure Predictions**

Tertiary structure prediction was performed using an automated knowledge based homology modeling server CPH model http://www.cbs.dtu.dk/services/CPHmodels/ to model the 3D structure of the (CYTOCHROME OXIDASE) protein.

**Molecular visualization tools**

The Predicted modeled protein structure was viewed with the help of molecular visualization tools like, Rasmol, JMOL.

## RESULTS AND DISCUSSION

In Literature collection, we focus on the sequence of (cytochrome oxidase,) gene. The gene coded protein sequence was retrieved from NCBI (Fig:1) database. This sequence retrieval is one of the primary steps for future protein modeling and sequence analysis studies Fig 2. Primary sequence analysis studies were done using protscale tool the result obtained using PROTscale tool describes the various physico-chemical parameters obtained such as Total number of amino acids is 600aa, Molecular weight (m/w) is (67030.0) iso-electrical point is (9.35), Total number of atoms is (9490), Aliphatic index (63.27), Hydropathicity index is (-1.145).The index stability index shows that the protein is unstable. These values of the (cytochrome oxidase) gene translated protein sequence. In Fig:3, the result of the secondary structure analysis Porter shows the molecular structural regions such as helix , sheets and truns. In this paper we report improvements brought about by predicting all the sequences of a set of aligned proteins belonging to the same family. 126 chains of non-homologous (less than 25% identity) proteins. Finally, from these results we obtained the total percentage of the Antigen binding sites (50.67%) present in the cytochrome oxidase protein sequence. The protein sequence of cytochrome oxidase was converted in to 3 Dimensional structures using an automated protein modeling server CPH 3.0 Model server. The 3D structure of the modeled protein was viewed using Jmol,Rasmol software.

>AIZ09157.1 cytochrome c oxidase subunit I, partial (mitochondrion) [Gracilaria edulis]
PDMAFPRLNNISFWLLPPSLCLLIASAIVEVGVGTGWTVYPPLSSIQSHSGGAVDLAIFSLHISGASSIL
GAINFISTILNMRNPGQSMYRMPLFVWSIFITAFLLLLAVPVLAGAITMLLTDRNFNTAFFDPAGGGDPV
LYQHLFWFFGHPEVYILILPGFGMVSHIVATFSRKPVFGYIGMVYAMVSIGVLGFIVWAHHMYTVGLDVD
TRAYFTAATMIIAVPTGIKIFSWIATMWEGSIHFKTPMLFATGFIFLFTIGGLTGIVLANSGLDISLHDT
YYVVAHFHYVLSMGAVFAIFAGFYYWFGKITGVQYPELLGKIHFWSTFIGVNLTFMPMHFLGLAGMPRRI
PDYPDAY

**Fig 1: NCBI – Sequence of Cytochrome oxidase subunits in fasta format.**

**PROTSCALE**

**User-provided sequence**

10 20 30 40 50 60
PDMAFPRLNN ISFWLLPPSL CLLIASAIVE VGVGTGWTVY PPLSSIQSHS GGAVDLAIFS

70 80 90 100 110 120
LHISGASSIL GAINFISTIL NMRNPGQSMY RMPLFVWSIF ITAFLLLLAV PVLAGAITML

130 140 150 160 170 180
LTDRNFNTAF FDPAGGGDPV LYQHLFWFFG HPEVYILILP GFGMVSHIVA TFSRKPVFGY

190 200 210 220 230 240
IGMVYAMVSI GVLGFIVWAH HMYTVGLDVD TRAYFTAATM IIAVPTGIKI FSWIATMWEG

250 260 270 280 290 300
SIHFKTPMLF ATGFIFLFTI GGLTGIVLAN SGLDISLHDT YYVVAHFHYV LSMGAVFAIF
310 320 330 340 350
AGFYYWFGKI TGVQYPELLG KIHFWSTFIG VNLTFMPMHF LGLAGMPRRI PDYPDAY

SEQUENCE LENGTH: 357

Using the scale **Hphob. / Kyte & Doolittle**, the individual values for the 20 amino acids are:

Ala: 1.800 Arg: -4.500 Asn: -3.500 Asp: -3.500 Cys: 2.500 Gln: -3.500
Glu: -3.500 Gly: -0.400 His: -3.200 Ile: 4.500 Leu: 3.800 Lys: -3.900
Met: 1.900 Phe: 2.800 Pro: -1.600 Ser: -0.800 Thr: -0.700 Trp: -0.900
Tyr: -1.300 Val: 4.200 : -3.500 : -3.500 : -0.490

Weights for window positions 1,..,9, using **linear weight variation model**:

| 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 |
|---|---|---|---|---|---|---|---|---|
| 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 |
| edge | | | center | | | | edge | |

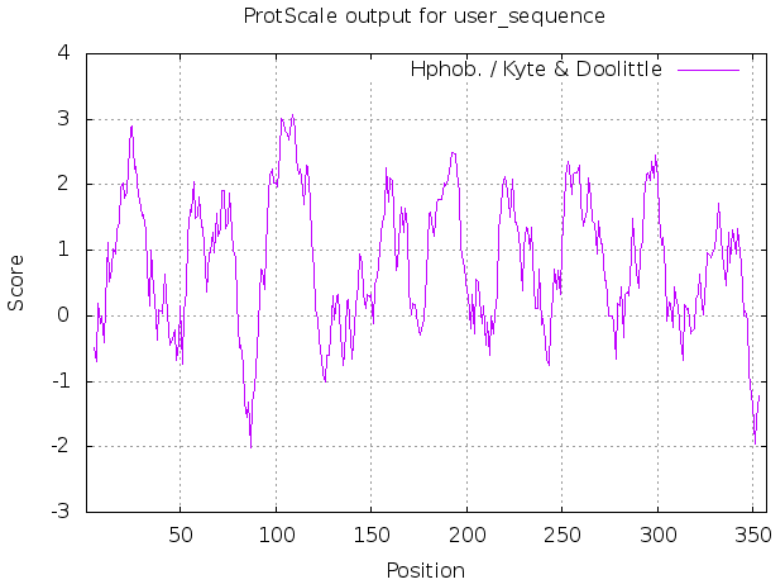


**Fig 2: Primary analysis of cytochrome oxidase.**

The above result shows the primary analysis of cytochrome oxidase.

**SECONDARY STRUCTURE ANALYSIS**

**PORTER**

Subject: Porter response to protein
Query_name: protein
Query_length: 357
Prediction:
PDMAFPRLNNISFWLLPPSLCLLIASAIVEVGVGTGWTVYPPLSSIQSHSGGAVDLAIFS
CCCCCHHHHHHHHHHHHHHHHHHHHHHHHCCCCCCCCCCCCCCCCCCCCCCHHHHHHHH
LHISGASSILGAINFISTILNMRNPGQSMYRMPLFVWSIFITAFLLLLAVPVLAGAITML
HHHHHHHHHHHHHHHHHHHHHHCCCCCCCHHHCCHHHHHHHHHHHHHHHHHHHHHHHHHLTDRNFN
TAFFDPAGGGDPVLYQHLFWFFGHPEVYILILPGFGMVSHIVATFSRKPVFGY
HHHHHCCCCCCCHHHCCCHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHCCCCCCCH
IGMVYAMVSIGVLGFIVWAHHMYTVGLDVDTRAYFTAATMIIAVPTGIKIFSWIATMWEG
HHHHHHHHHHHHHCCCCHHHHCCCCCCCHHHHHHHHHHHHHCHHHHHHHHHHHHHHCCC
SIHFKTPMLFATGFIFLFTIGGLTGIVLANSGLDISLHDTYYVVAHFHYVLSMGAVFAIF
CCCCCHHHHHHHHHHHHHHHHHHHHHHHHHCHHHHHHHCCEHHHHHHHHHHHHCHHHHHHH
AGFYYWFGKITGVQYPELLGKIHFWSTFIGVNLTFMPMHFLGLAGMPRRIPDYPDAY
HHHHHHHHHHHCECCCHHHHHHHHHHHHHHHHHHHCHHHHHHHCCCECCCCCCCHHC
Predictions based on PDB templates (seq. similarity up to 72.3%)
Query served in 1006 seconds

**Fig 3: Secondary analysis of cytochrome oxidase.**

## TERTIARY STRUCTURE ANALYSIS

### CPHmodel

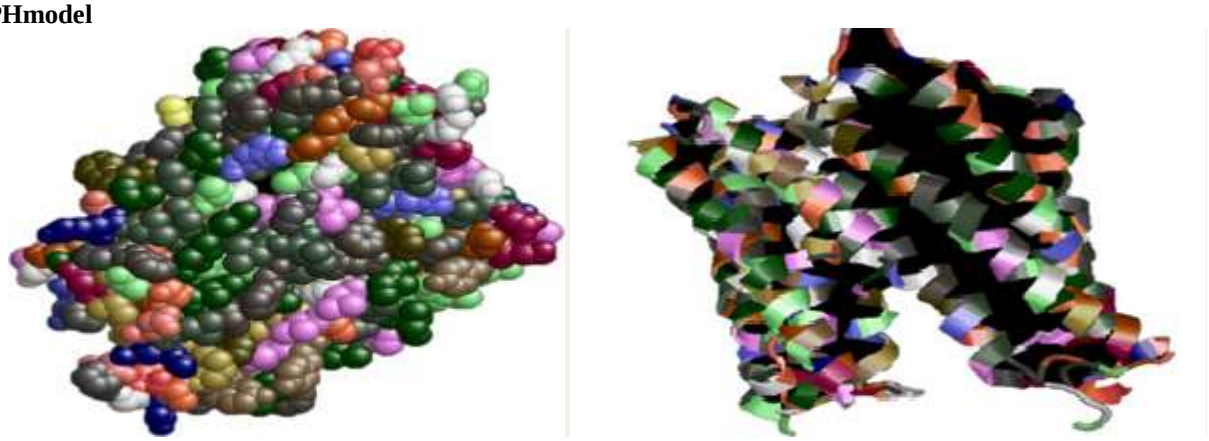

**Fig 4: Three Dimensional structure of cytochrome oxidase.**

The above results show different structural level of cytochrome oxidase. Here pink colour indicates helix, yellow indicates the sheets, blue indicates turns and white indicates coils region in cytochrome oxidase.

## CONCLUSION

The seaweeds used in human food cosmetics, fertilizers and extraction of industrial gums and chemicals marine algae may also be used as energy collectors and potentially useful substances may be extracted by fermentation. The cytochrome oxidase is the terminal complex of the electron transfer chain. The protein sequence of cytochrome oxidase was retrieved from NCBI database. Structural and Sequencial analysis of cytochrome oxidase was carried out insilco bioinformatics tools. A comprehensive study of the protein may be further used in research.

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