

8. *Insilico* Physico-Chemical Analysis of Probiotic Spirulina Protein

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Abstract

Now a days and in Future Food with Nutrition will be the major issue. One of the potent Biological Source is Probiotics. They are live microbes providing numerous health benefits upon intake into digestive track. Generally probiotics are in role by activating microenvironment intending to restore gut flora [1]. Probiotics are suggested to be considered safe but there extra cellular interaction with host cell may cause the side effects [2].

The most commonly used probiotic tool is spirulina. It is the biomass of blue-green algae consumed by different host. The two species are *A. platensis* and *A. Maxima* [3]. It is consider as anti-diabetic, HIV, feed supplement in the Aquatic life and Aquaculture [4, 5]. By comparing the biomolecule contain of Spirulina, significant protein percentage was found between 30-65%. Therefore proteomic analysis is needful in understand and providing rescue measures of side effects of Spirulina.

Keywords: Probiotics, Spirulina, proteomic, side effects.

Introduction

Now a days and in Future Food with Nutrition will be the major issue. One of the potent Biological Source is Probiotics. They are live microbes providing numerous health benefits upon intake into digestive track. Generally probiotics are in role by activating microenvironment intending to restore gut flora [1]. Probiotics are suggested to be considered safe but there extra cellular intraction with host cell may cause the side effects [2].

The most commonly used probiotic tool is spirulina. It is the biomass of blue-green algae belongs to photosynthetic microorganisms consumed by different host. The species *A. maxima* and *A. platensis* were once classified in the genus *Spirulina* [3]. *Spirulina* servive at pH around 8.5 and a temperature around 30 °C. As they are autotropic i.e. They are able to make their own food [4]. It is consider as anti-diabetic, HIV, feed supplement in the Aquatic life and Aquaculture[5].

On the other hand, Spirulina may have harmful effects when taken simultaneously with prescribed drugs. Generally, it was found that Spirulina has interaction with immune system and blood clotting factors [4]. Therefore, considering the biomolecules contain of Spirulina, significant protein percentage was found between 30-65%. Thus, proteomic analysis is needed in understand and providing rescue measures of side effects of Spirulina

Methods and Methodology

1. **NCBI-Protein** (<https://www.ncbi.nlm.nih.gov/protein>)
 - The protein database is collection of sequence submitted from different sources. Protein sequences are the fundamental determinants of biological structure to function [6].
2. **ProtParam** (<https://web.expasy.org/protparam>)
 - ProtParam tool allows the analysis of various physical and chemical parameters for a given protein stored in Swiss-prot and user protein sequence. The calculation of parameters includes the mol. weight, theoretical pI, amino acid composition, atomic composition and extinction coefficient etc.[7].
3. **Cn3D** (<https://www.ncbi.nlm.nih.gov/Structure/icn3d>)
 - A stand alone application that allows you to view 3-dimensional structures from NCBI Entrez entry. Simultaneously, displays structure, sequence, and alignment, annotation and alignment editing features [8].
4. **UniProt Knowledgebase (UniProtKB)** (<https://www.uniprot.org/uniprot/>):
 - The UniProt provide the scientific information with a comprehensive, high-quality and freely available resource of protein sequence and function. UniProt Knowledgebase (UniProtKB) is the tool for information and biological Function of protein [9].

Result

- The C-PHYCOCYANIN is fundamental protein of spirulina Containing 24 subunits were found in NCBI. The Sequence of Chain X, C-PHYCOCYANIN BETA Subunit is retrieved from Protein Resource of NCBI. The FASTA Sequence of BETA Subunit is given below:>pdb|1GH0|X Chain X, C-PHYCOCYANIN BETA SUBUNIT
MFDAFTTIVVSQADTRGEMLSTAQIDALSQMVAESNKRLDVVNRITSNASTIVS
NAARSLFAEQPQLIAPG

GXAYTSRRMAACLRDMEIILRYVTVAVFAGDASVLEDRCLNGLRETYLALGTP
 GSSVAVGVGKMKEAALA IVNDPAGITPGDCSALASEIAGYFDRAAAAVS

- The biophysical and physicochemical parameters of C-PHYCOCYANIN BETA Subunit with 172 Amino Acids having Theoretical pI 4.96. The number of negatively charged residues and positively charged residues are 18aa and 15aa respectively. Extinction coefficients (assuming all pairs of Cys residues form cystines) are 7575. Estimated half and Instability index is 30hrs and 40.16 (Table1).

amino acids	Molecular weight	Theoretical pI	number of -ve residues	number of +ve residues	Extinction coefficients	Estimated half-life	Instability index
172	18056	4.96	18	15	7575	30 hours	40.16

Table1: Estimation of physicochemical properties of C-PHYCOCYANIN BETA subunit using ProtParam Tool.

Structure: structure of C-PHYCOCYANIN

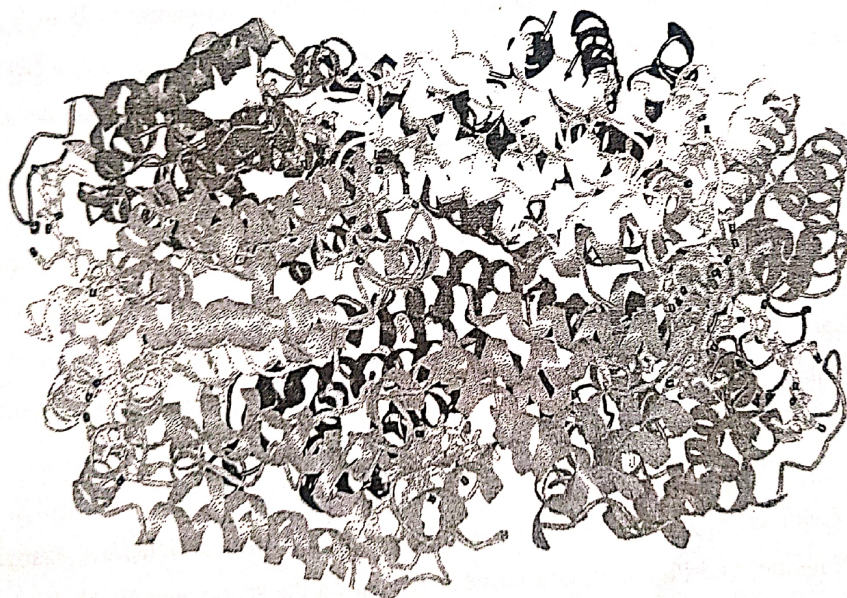


Fig 1: Crystal structure of C-PHYCOCYANIN Spirulina Platensis at resolution 2.2 Å [10].

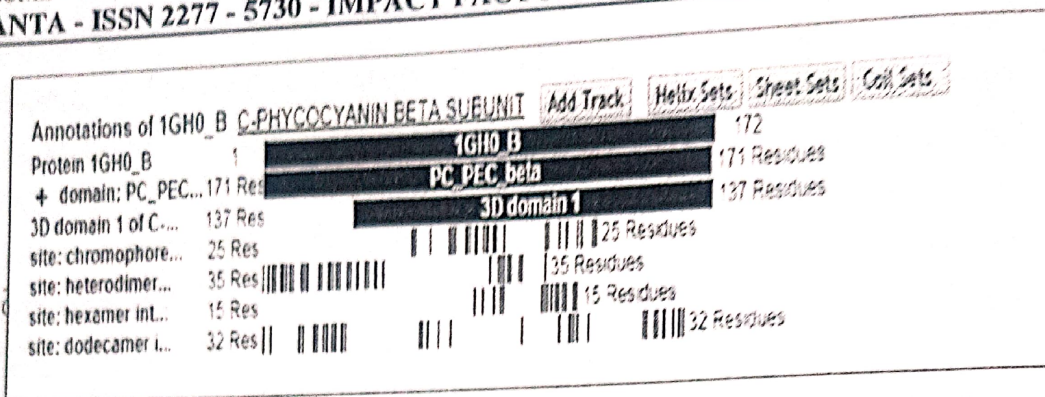


Fig 2: Sequence and annotation of C-PHYCOCYANIN BETA Subunit including Conserved Domains, 3D Domains and Functional Sites.

- The structural arrangement of functional polypeptides is depicted in structure (Fig 1). Were alpha-helix, Beta-sheets, Turn and coils are depicted with different colours (Fig 1). The protein having PC_PEC_beta domain of 171 residues and single 3D domain 1 (Fig. 2). The four functional sites at different residues position are observed (Fig. 2).

Function

- The UniProt result shows the ID number P72508 with gene name cpcB in *Spirulina Platensis*. C-phycoerythrin beta chain has biological function as Light-harvesting photosynthetic bile pigment-protein of phycobiliprotein complex. It is also involved in oxidation-reduction, photosynthesis and protein chromophore linkage [11, 12].

Conclusion

The Nutritional food requirement in future will be the major issue in upcoming days. The probiotics and their biological products are the potent source to meet the need. The Resulted physicochemical analysis and structure prediction of C-PHYCOCYANIN of *Spirulina* give understanding of structure to function relationship. The results also supporting physiological condition and stability in living systems.

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