DAV International Journal of Science

BIOINFORMATIC ANALYSIS OF CARBON PROFILE IN SILK PROTEIN OF SILKWORM, *SAMIA SYNTHIA RICINI*

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ABSTRACT
Silk protein is a hydrophilic protein produced by Eri silk worm *Samia synthia ricini* (Indian silk moth). In this work, Carbon content in this protein has investigated. The carbon distribution in the silk proteins contain below the average of 35% of carbon. The carbon distribution plot gives the pattern of repeats in these proteins. As per this carbon distribution pattern a further reduction at appropriate place of sequence is possible to improve the cleaning effect of this glue protein. CARBANA tool can be used for mutational studies on any functional proteins for improvement in productivity.

KEY WORDS: carbon profile, carbana, hydrophilic, *Samia synthia ricini*, silkworm.

INTRODUCTION

The eri silk worm is the only completely domesticated silkworm other than *Bombyx mori*. There are two kinds of silk proteins, such as, fibroin and sericin. This protein contains essential amino acids. Introduction of new gene might produce this glue protein with other useful applications. Eri silk is a staple fiber unlike other silks which are continuous filament. Due to its thermal property it is warm in winters and cool in summer (Jayaramiah, 2009). It is important to study of changes in sequence of carbon distribution in protein. Many works leading to understand the protein stabilization at atomic level is explained by our group (Rajasekaran *et al.*, 2011; Senthil *et al.*, 2009, Vinobha *et al.*, 2010). Now, to study and report the carbon distribution in this commercially important protein for future applications.

MATERIALS AND METHODS

The silk protein sequences of silk moth, *Samia synthia ricini* were collected from UniProtKB (www.uniprot.org/uniprot) are shown in Table 1.

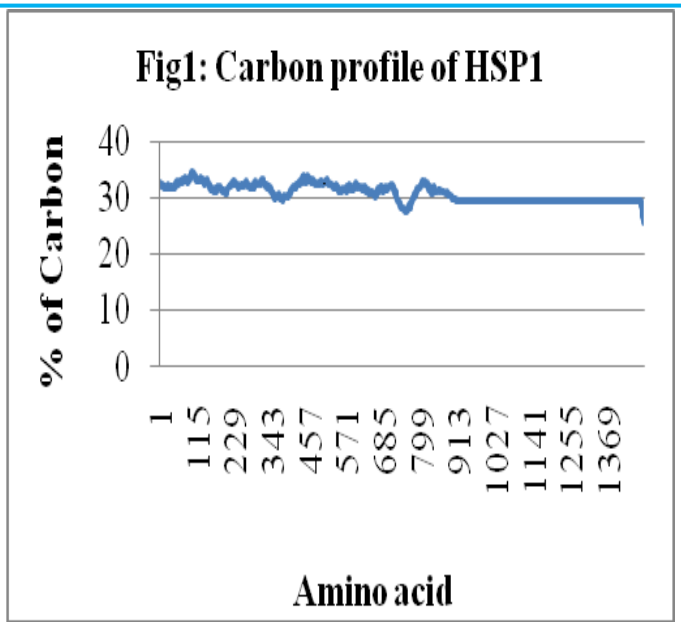
Table 1. Silk protein and its UniProtKB details.

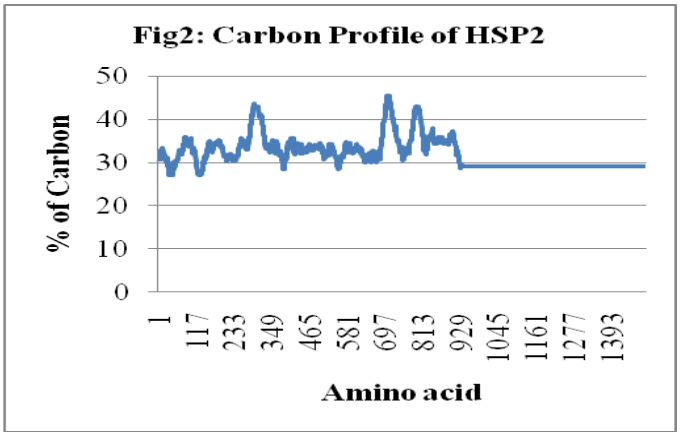
Protein name	Accession No.	Gene Name	Protein Sequence length
Haemolyph storage protein 1	A1ILJ9	SP1	88306
Haemolyph storage protein 2	A1ILK0	SP2	83814
Carotenoid binding protein	E5RSD1	Cbp	10754

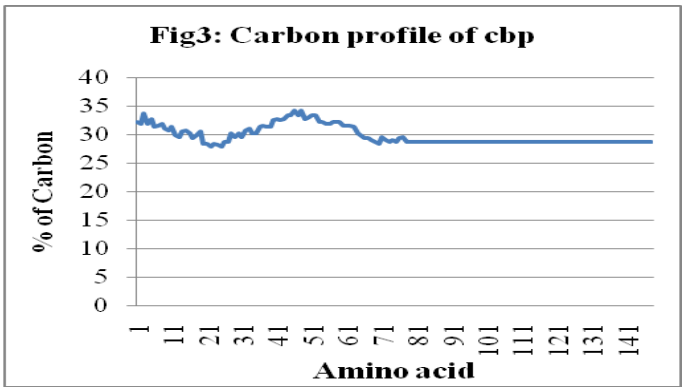
CARBANA program available online (www.rajasekaran.net.in/tools/carbana.html.) were used to study the carbon distribution profiles for all mention in the table of silk proteins. The details on this program on the principle, input, output, interpretations are discussed in reference paper (Rajasekaran *et al.*, 2011). It does a window analysis of carbon distribution with a principle that proteins prefer to have 35% of carbon for its stability. The results on carbon percentage versus amino acid numbers are plotted as shown in figures.

RESULTS AND DISCUSSION

The carbon distribution plots on various silk proteins are given in figures 1-3. All silk proteins are hydrophilic in nature. The scale of 35% of carbon is used to measure the hydrophobicity along the sequence. A line in each graph is drawn at 35% of carbon for comparison. Most of the times the sequences are below the line 35%, indicating that these proteins contain less carbon content. This is the reason why this protein soluble in water. A further reduction in hydrophobicity can be achieved for better and efficient removal this waste protein on removal of fibroin. There are many repeats found in all silk proteins based on carbon content. Sometime difference in sequences can have same carbon distribution and repeats. Two different portion of sequence can have similar carbon distribution pattern and are caller repeats.







The 93 amino acid length silk protein sequence was submitted to CARBANA. Due to small number of amino acid and window effect, itis not possible to get distribution plot (Figure 3). However multiple silk protein sequence ordered in sequence is tested for carbon distribution. It reveals that the carbon distribution is far below the value of 34.10%of carbon and highly hydrophilic. Unlike other functional proteins, there is no active site in silk proteins. However there is higher carbon content region between 84 and499 in Haemolyph storage protein1(Figure 1). Ordering more hydrophilic

amino acids in these regions might free the packing and easily washable in water. In Haemolyph storage protein 2(Figure 2) this can be done at 277and 760.Carotenoid binding protein has highly hydrophilic sequence which is far below the value of 35 % of carbon. Only at the terminals a marginal carbon contents are found. This protein may not be stable in biological condition as amino acids from 1 to277 and 346 to 691 contain less carbon content. These regions nowhere near the value of 35% carbon. Due tothis these portion has strain and cannot fold properly. May be washable easily but stability isn't there. On the other hand the Haemolymph storage protein2hasboth hydrophilicity and stability. It has a better carbon distribution for both glue and washable characters. In essence, Haemolymph storage protein2hasproper distribution of carbon all along the sequence than other proteins presented here. This can better exploited for commercial purpose.

CONCLUSION

In this study investigation of Carbon distribution in silk proteins were analyzed. The finding concluded that the proteins are highly hydrophilic in nature. As per the carbon distribution a further reduction at appropriate place of sequence is possible to improve the cleaning of this waste protein during silk production. From washing and stability point of view, Haemolymph storage protein2 has better carbon distribution over the other proteins presented here. This protein can be better exploited for commercial purpose. CARBANA tool can be used for exploitation for mutational studies on any functional proteins for betterment in production of commercial protein.

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