



Phylogenetic Analysis of Fibroin Proteins from Some Spiders Species: Exploration of Species Relationships

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Authors' contributions

This work was carried out in collaboration between both authors. Both authors read and approved the final manuscript.

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ABSTRACT

Silk are structural proteins produced by arthropods. Silk contains two proteins, fibroin and sericin, which promote wound healing. A study analyzed the relationship of fibroin proteins between some insect species, providing crucial knowledge in nanotechnology, material science, and biotechnology. The findings can guide scientists and engineers in exploring potential applications of fibroin proteins in various fields, such as biomedical engineering and biodegradable plastics. This research opens doors for innovative advancements in biotechnology, benefiting society as a whole.

Keywords: *Fibroin protein; silk production; commercial applications; biocompatibility; recombinant insect silks; silk inspired materials; silk processing.*

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1. INTRODUCTION

Silk is unique and essential due to its fibroin protein component, which plays a critical role in its strength and beauty. Fibroin is the dominating structure in silk and gives it its distinctive features. It is derived from silk glands in certain organisms, such as *Bombyx mori* and Arachnida plays a vital role in creating the silk [1,2]. Fibroin is particularly instrumental in the formation of the intricate webs produced by spiders. Silk produced through silkworms is known for its specificity, and the activities involved in its production result in the creation of delicate and robust cocoons [3]. The fibroin protein encapsulated in these cocoons is a natural example of creation, highlighting its historical role as an adornment in various societies and civilizations [4]. In recent years, scientists have explored the unique properties of fibroin protein and initiated studies on the applications beyond traditional silk production. The distinctive structure and characteristics of this protein have opened for new research and development in fields ranging from biotechnology to material science [5].

The primary structure of fibroin typically displays repetitions of (Gly-Ser-Gly-Ala-Gly-Ala), indicating the presence of the amino acids glycine (Gly), serine (Ser), and alanine (Ala) in a specific sequence [6]. This repetition can occur multiple times, resulting in a long silk filament that aids in the creation of various patterns [7,8]. Fibroin protein is used in various commercial applications due to its unique properties. The textile industry utilizes it for producing silk fabric known for its softness, sheen, and strength. Due to its biocompatibility and strength, it is used in medical sutures, retaining their integrity over time [9]. It exhibits minimal tissue reaction and very low antigenicity, making it ideal for surgeries. The fibroin can be employed in drug delivery systems like Reduce Diabetes, opening new possibilities for potential applications of fibroin protein in various fields [10]. Fibroin protein, obtained primarily from organisms involved in silk production, is finding diverse commercial applications due to its unique properties. The study uncovers the commonality in fibroin protein across species such as *Bombyx mori*, Arachnida, and butterflies. Additionally, it identifies alternative sources for fibroin protein.

2. METHODS AND MATERIALS

This study describes a methodology for analyzing the phylogenetic relationships of fibroin

proteins from five different species using genomic sequence data from NCBI. The following steps were taken: Valuable phylogenetic information on fibroin proteins from five different silk-producing insect species was obtained through sequence retrieval from NCBI. Sequences from *Bombyx mori*, *Trichonephila clavipes*, *Latrodectus hesperus*, *Argiope bruennichi*, and *Danaus plexippus* were used. Sample sequences of fibroin proteins were identified from each of the species. These included fibroin heavy chain precursor and fibroin light chain precursor from *Bombyx mori*, dragline silk fibroin from *Trichonephila clavipes*, egg case fibroin from *Latrodectus hesperus*, and fibroin-like proteins from *Argiope bruennichi* and *Danaus plexippus*. [11,12,13,14,15].

The sample sequences, initially stored in FASTA format using Notepad, were processed through a series of steps using the MEGAX tool. First, the tool was downloaded and installed from online sources [16]. Next, the sample file in FASTA format was imported into MEGAX, where parameters like alignment algorithms were set and other adjustments made. Subsequently, after processing, the results were retrieved in ClustalW file format. Finally, the contracted phylogenetic tree of fibroin proteins was evaluated alongside the contracted trees of other organisms to explore the phylogenetic relationships [17].

3. RESULTS AND DISCUSSION

Collecting data from NCBI, storing it in FASTA format, conducting Neighbor-Joining method using the MEGAX tool and evolutionary distances were computed using the poisson correction method. This analysis involves 9 amino acid sequence and retrieving results in ClustalW format is a promising effort genomic relationship. This analysis focuses on three key fibroin proteins: the heavy chain precursor of *Bombyx mori*, the partial dragline silk fibroin of *Trichonephila clavipes*, and the heavy chain-like protein of *Danaus plexippus*. According to this phylogenetic tree show that fibroin proteins of five different organism have common node, indicating close relationships between them and suggesting proximity and shared ancestry. Even similarity between these proteins confirms that they may be shared some evolutionary lineage [18]. There is a significant similarity between the sequences of the heavy chain precursor of *Bombyx mori* and the partial dragline silk fibroin of *Trichonephila clavipes*, revealing that they might be some ancestral history. The similarity is

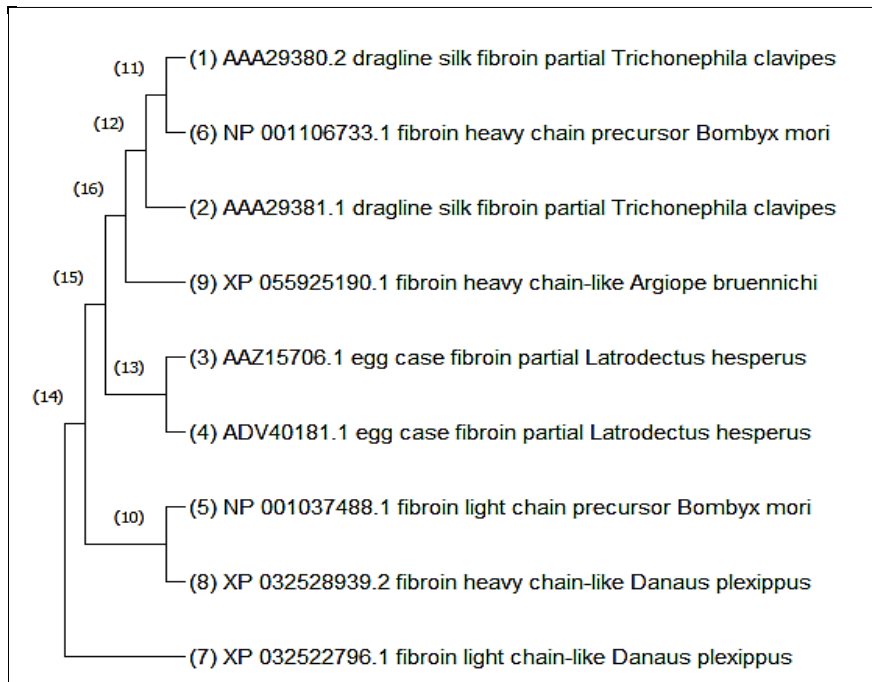


Image 1. Result of the phylogenetic analysis in clustal W format obtained using MEGA software

also evident between the light chain precursor of *Bombyx mori* and the fibroin heavy chain-like protein of *Danaus plexippus* (XP_032528939.2, GI 2635188275).

4. CONCLUSION

In summary, this phylogenetic analysis focus on the relationship of fibroin proteins between five diverse insect species. The findings suggest the existence of shared functional elements among these proteins, offering valuable insights into silk production and mechanical properties. Particularly noteworthy is the close relationship observed between fibroin proteins from *Bombyx mori* and *Trichonephila clavipes*, indicating conservation of functional elements crucial for silk production among phylogenetically distant groups. In the last few decades, great efforts have been made to study silk-producing animals and the properties of their silks and to identify the underlying gene and protein sequences. This research in bridging gaps between distantly related organisms and provides a framework for understanding the evolutionary trajectory of fibroin proteins. Such insights not only enrich our comprehension of biomaterials but also offer guidance for future studies in functional genomics, Recombinant production of insect silk proteins in appropriate hosts and related fields.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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