International Journal of Bioprocess & Biotechnological Advancements
IJBBA, 8(5): 462-465
www.scitcentral.com

ISSN: 2380-0259

Short Commentary

Sea Star *Asterias Rubens* Fab Gene and Bioinformatic Data

Michel Leclerc[*]

[*]556 rue Isabelle Romée, 45640 SANDILLON, Immunology of Invertebrates, France.

Received January 22, 2022; Revised January 26, 2022, 2021; Accepted January 28, 2022

ABSTRACT

The *Asterias rubens* Fab gene was isolated in 2016. Its transcriptome was analyzed in bioinformatics according the method of Marchler-Bauer. Identities mainly with other sea star genomes were repertoried in the precedent report.

INTRODUCTION

The objective of this work is to analyze Fab DNA sequence from the sea star *Asterias rubens* (Asterids, Echinodermata) which belong to Invertebrates [1].

Our Starting material is the following DNA sequence which is translated in 5'-3'

```
CAGAGTCACCAGGTGCTGTGTTGACATCAGCACTTT
CTGAATCCACCTCCATTGGTTGATCCACTTCCTCTTT
CACTATAGTTGACGATTTGATATCAACACTGTCACC
TGTAAGCGCATCAACACCGCTTGTTATATCAACAG
ACGATCTCCTTTGTGGATCCACTTTTTGATCGGTGG
ATAGAGGCGGAGTGGATGACTCCATCTTTGCTAAT
GTTTTGTCATCGGCTAATGTTGATGAACTTTCTTCA
GCTTTTACCTCGGTCTTCACATCCACTGTTTGGTTTT
CTGATTTCACGGAAACAGTTGATGTCGTTTTGACTG
GATCCACTGACTTATCAGCCAATGTTCCCTGCGGAG
TTGTTGATGTACTTTGTTGAGAGATGGCTGTGAAGG
GATTTGTGGCGGGATCGAAGGAAGCTCCTAAGCCT
TCCTCCCCTGGGGTTGGCGTTTCTAGAAGCGAGGA
ATCTTTGGCATCTTCGAAACACAAGGGATGGTATGT
CCTGGAGTTGAACCTGACAGCATCTCTCAGTTTCCA
AACCTCTTCATCTTCATCAAAGAATTGCTCAAACGG
CTCATGACACAGAGAACACATCTCATCGCCAGTGA
CGTTTCCATCAATAGCCACACAGAGGATGCCATCTT
TATCAGGTTTAGACTCTGCAGTCATCTCCTCAAAGA
AACTGCTCCTCTCTTCATCCACTTCGTTGATTTCTTC
AAAGTCCAACCACTGATCGACTTCATAGAACCACT
TCCTGGACTGAACAGCCTTCACTCCATCCTTCTCAC
GACGATTCTGACGGAAGTGCCAGTCCAGATGTTTC
CGATATCTGTCCATTTCATCAATGACAAAGCGCATA
CCA
```

RESULTS

1. Blastn original sequence Data base:

Standard data bases (nr.) have been used [2,3] and optimized for highly similar sequences (megablast)

The DNA molecule included a query length of 863

Among sequences producing significant alignments, 5 sequences were selected as shown in **Table 1.**

The graphic summary follows below **Figure 1**.

2. BlastX original sequence:

As precedingly the Molecule type is DNA. The characteristics were the following:

a) Query length: 863

b) Genetic code: Standard

c) Database: Non-redundant protein sequences (nr)

d) Sequences producing significant alignments: more than 100 sequences were found as shown below in **Table 2.**

The graphic summary was resumed as shown below **Figure 2**.

Conclusion

No putative conserved domains as homologies with Ig domains have been found. Such homologies were detected with the Fc receptor gene from *Asterias rubens* [4].

In the present study alignment sequences present mainly analogies between Fc receptor genes and sophisticated proteins which belong especially to *Asterias rubens* (Protein Pcf11-like: 99, 19 %identities) or other starfishes at a less degree. **Table 2** corroborates these same results.

We retain Fab gene and Fc receptor gene exist in Echinodermata as it was already demonstrated in 2016.

Corresponding author: Michel Leclerc, 556 rue Isabelle Romée, 45640 Sandillon, France, Tel: +92219926130; E-mail: mleclerc45@gmail.com

Citation: Leclerc M. (2022) Sea Star *Asterias Rubens* Fab Gene and Bioinformatic Data. Int J Biopro Biotechnol Advance, 8(5): 462-465.

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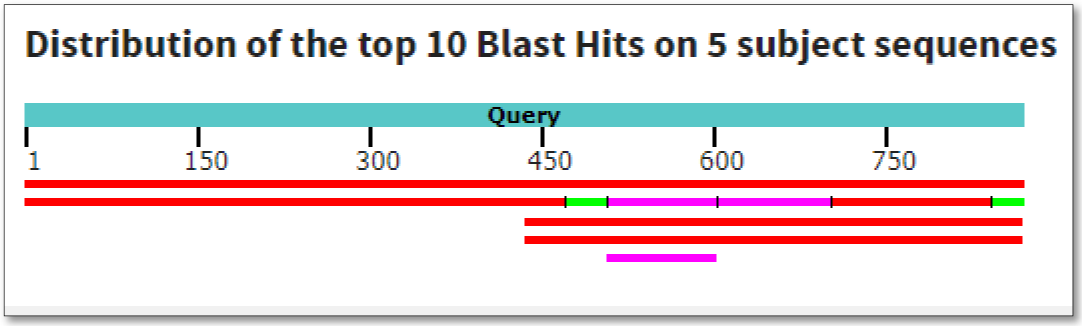
Table 1. Selection of Asterid sequences.

Description	**Scientific name**	**Max score**	**Total score**	**Query cover**	**E. Value**	**Per. Ident**	**Acc Len**	**Accession**
Predicted: *Asterias rubens* pre-mRNA cleavage complex 2 protein Pcf11-like (LOC117293273) mRNA	*Asterias rubens*	1555	1555	100%	0.0	99.19%	7600	XM_03377550/8.1
Asterias rubens genome assembly, chromosome 8	*Asterias rubens*	833	1576	100%	0.0	98.93%	21693562	LR699099.1
Predicted: *Acanthaster planci* uncharacterized LOC110976864 (LOC110976864), transcript variant X	*Acanthaster planci*	309	309	49%	4e-79	79.72%	9401	XM_022230513.1
Predicted: *Acanthaster planci* uncharacterized LOC110976864 (LOC110976864), transcript variant X	*Acanthaster planci*	309	309	49%	4e-79	99.29%	9455	XM_022230512.1
Marthasterias glacialis, genome assembly, chromosome: 10	*Marthasterias glacialis*	152	152	10%	6e-32	95.74%	25093327	OU452228.1

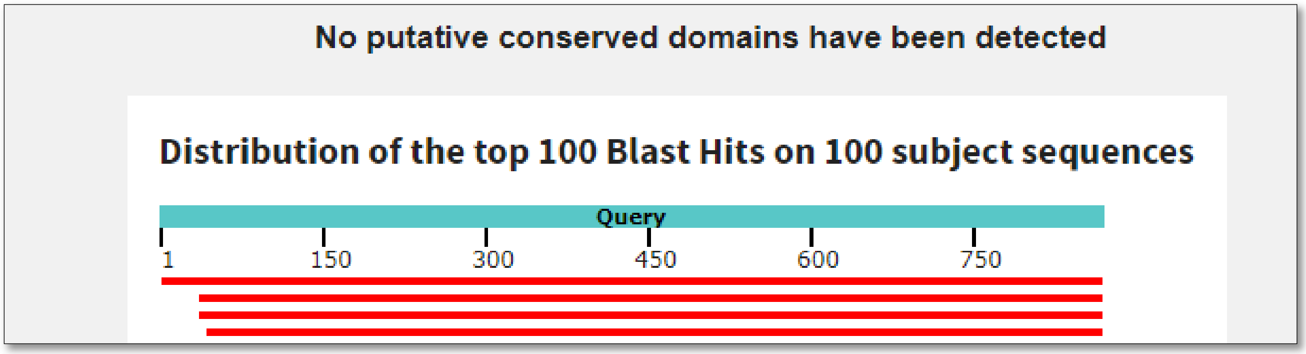


Distribution of the top 10 Blast Hits on 5 subject sequences

Figure 1. Selection of Asterid sequences.

Table 2. Alignment sequences.

Description	**Scientific name**	**Max score**	**Total score**	**Query cover**	**E. Value**	**Per. Ident**	**Acc Len**	**Accession**
Pre-mRNA cleavage complex 2 protein Pcf11-like [*Asterias rubens*]	*Asterias rubens*	536	536	99%	1e-171	98.61%	2426	XP_033631399.1
Uncharacterized protein LOC110976864 isoform X2 [*Acanthaster planci*]	*Acanthaster planci*	262	262	95%	2e-75	52.35%	2775	XP_022086205.1
Uncharacterized protein LOC110976864 isoform X1 [*Acanthaster planci*]	*Acanthaster planci*	262	262	95%	2e-75	52.35%	2793	XP_022086204.1
Low Quality Protein: pre-mRNA cleavage complex 2 protein Pcf11-like [*Patiria miniata*]	*Patiria miniata*	261	261	94%	5e-75	52.44%	2640	XP_038055691.1



No putative conserved domains have been detected

Distribution of the top 100 Blast Hits on 100 subject sequences

Figure 2. Alignment sequences.

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