



# A Sea Star Asterias Rubens IGKappa Gene when Compared to 3 Other Sea Star Genomes from Patiria Miniata, Acanthaster Planci and Marthasterias Glacialis (Echinodermata)

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Short Communication

Volume 3 Issue 2

Received Date: November 30, 2021

Published Date: December 13, 2021

DOI: 10.23880/aii-16000156

## Abstract

The sea star IGKappa gene was cloned in 2014 by the use of primers. It was compared, in the present work, to 3 other sea star genomes: Acanthaster planci, Patiria miniata and Marthasterias glacialis sea star genomes. A high identity, from a bioinformatic point of view, was found, with these last ones, with, a significant e-value. Sea star Igekappa genes may be present in these 4 asterids which belong to the Echinoderm Phylum (Invertebrates)

**Keywords:** Gene; IGKappa; Bioinformatic Analysis

## Introduction

The sequence of the sea star Asterias rubens IGKappa gene was described by our team, in 2014 [1]. Since we have tried to find homologies between this gene and genes from three other Asterids: Patiria minata Acanthaster planci and Marthasterias glacialis. These Asterids belong to Echinodermata phylum.

We report, in the precedent paper, results obtained with these last ones by the use of blasts [2,3].

## Results

a) The sequence of the sea star IGKappa gene is the following [1]:

5'GGA TCC GGA GGA ATG  
CGTGGCAACATGGCGTCTCTATGGATGTTCTTCTT

TGTCGTGGGGATAACTTTACAACGGAGTTTGGCGATTTA-  
CAGTTTTCGCG  
AGCAACCGTCCGGACACTAGCGCGTTGCAGGGGAGCACAGTG-  
GTGCTTCAC  
TGCTCCGTTGAGCAGTACATAAACACCACGGCCATCGTTTG-  
GTGGAGCCG  
TGACTCGGTCATCAGCCACAACAAAGACCTGAAACTGTC-  
CAGTCTAAACA  
CCGACCAGCTCCAAAGGTACTCGATTTTCAGGCGACGCATCTCG-  
GGGGGAA  
TTCAACCTTAAAATAGTGAACCTTTACCGCCACAGACGCCG-  
CAGTTACCG  
CTGTCAGATG TAA GAA TTC3'

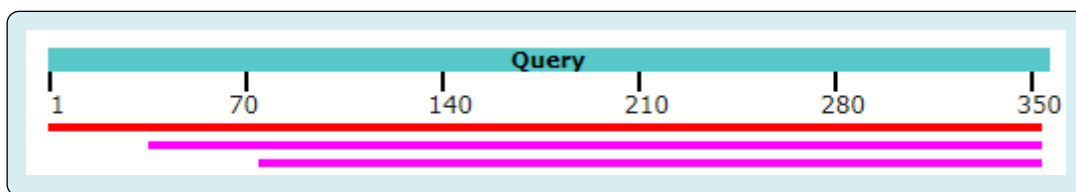
b) BlastX original sequence: BlastX results

Molecule type: DNA  
Query length: 357

Description	Scientific name	Max score	Total score	Query cover	E. Value	Per. Ident	Acc Len	Accession
uncharacterized protein LOC117296905 [Asterias rubens]	Asterias rubens	245	245	99%	2.00E-73	96,61%	932	XP_033635901.1
uncharacterized protein LOC119722929 [Patiria miniata]	Patiria miniata	104	104	89%	4.00E-23	44.25%	951	XP_038049262.1
uncharacterized protein LOC110978882 [Acanthaster planci]	Acanthaster planci	91.3	91.3	78%	2.00E-18	45.26%	933	XP_022089895.1

**Table 1:** BlastX original sequence.

The table above allows us to obtain the following Graphic Summary:



**c) As for Alignements we observe:**

97% Identities (114/118aa) with uncharacterized protein LOC117296905 [Asterias rubens] protein  
 Reference Protein Sequence: XP\_033635901.1  
 Reference dna Sequence: XM\_033780010.1  
 Length : 932 aa

Aligment : 14-131

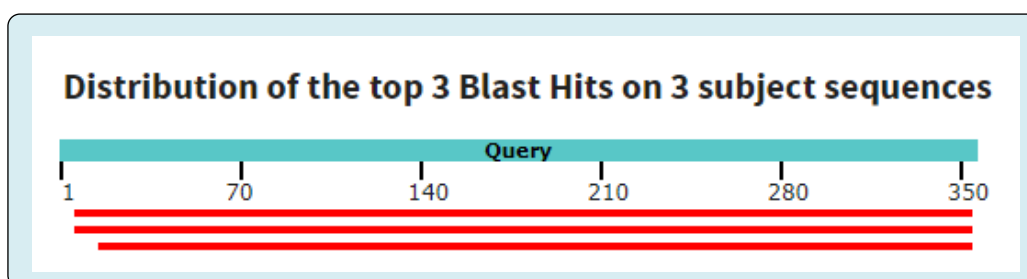
**d) Blastn original sequence: Blastn results**

Molecule type : dna  
 Query length : 357

Description	Scientific name	Max score	Total score	Query cover	E. Value	Per. Ident	Acc Len	Accession
Predicted: Asterias Rubens Uncharacterized Loc117296905 (Loc117296905), mRNA	Asterias rubens	634	634	97%	2.00E-177	99.43%	4538	XM_033780010.1
Asterias Rubens Genome Assembly, Chromosome: 11	Asterias rubens	634	634	97%	2.00E-177	99.43%	18069988	LR699102.1
Marthasterias Glacialis Genome Assembly, Chromosome: 6	Marthasterias glacialis	329	329	95%	9.00E-86	84.16%	28777708	OU452224.1

**Table 2:** The graphic summary gives the opportunity to see the top3 Blast Hits.

As for Alignements we find a high identity nearly 100% as shown below:



99% Identities (347/349bp) with Predicted: *Asterias Rubens*  
 Uncharacterized Loc117296905 (Loc117296905), mRNA  
 Reference Sequence: XM\_033780010.1  
 Length : 4539  
 Aligment : 1546-1894

## Conclusion

We retain from this bioinformatic analysis, the presence of high identities between the sea star IGKappa gene and the *Patiria miniata* genome, *Acanthaster planci* one, and the *Marthasterias glacialis* one. We discover that sea star *Asterias rubens* IGKappa gene presents a strong homology to *Marthasterias glacialis* genome (nearly 99% identities) when compared to two other sea star genomes (*Patiria miniata* and *Acanthaster planci* ones): 97% identities were found. IGKAPPA Gene may be present in at least 4 Asterids.

From another point of view, we have also described the Ophurid IGKappa gene we discovered 1 month ago [4]: it is more evolved in terms of Immune functions than sea star IgKappa gene and Crinoïd one [5].

These genes from Echinodermata (Invertebrates) bring us a new insight in comparative Immunogenetic World.

## References

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