American Journal of Immunology 10 (1): 33-34, 2014
ISSN: 1553-619X

doi:10.3844/ajisp.2014.33.34 Published Online 10 (1) 2014 (http://www.thescipub.com/aji.toc)

A NEW PRESUMED IGKAPPA GENE IMPLIED IN THE SEA STAR IMMUNE RESPONSE

[1]Michel Leclerc, [1]Magne Osteras and [2]Patricia Otten

[1]Independent Researcher: 556 Rue Isabelle Romee, 45640 Sandillon, France
[2]Fasteris S.A, CH-1228, Plan-les-Ouates, Switzerland

Received 2014-03-07; Revised 2014-03-15; Accepted 2014-03-19

ABSTRACT

The existence of another candidate IgKappa gene of 697 nucleotides, was recently, demonstrated, in the sea star Asterias rubens genome. This last gene was cloned and shown, with its sequence, in the present study. Its potential role in the sea star immune response was accentuated.

Keywords: Sea Star, Igkappa Gene, Axial Organ

1. INTRODUCTION

We had discovered another candidate IgKappa gene of 697 nucleotides (Leclerc *et al*., 2011) in 2014.

2. MATERIALS AND METHODS

Like in 2011, we used sea stars, after immunizations to Horse-Radish Peroxydase (HRP), to study their genomes. Experimental methods were the same than those chosen, at that time (Leclerc *et al*., 2013; Leclerc and Otten, 2013).

As for the cloning of the gene, we used the experimental protocol concerning the SMART kit PCR cDNA Synthesis (Clontech).

This SMART was specifically designed for the recovery of the target gene.

Poly A fraction was purified, first stalk of DNA was synthesized with an oligodT.

A non-specific amplification was performed in: 5'-CAGATTCAGAAACACATGTATTTCC-3' and followed by a specific one in: 5'-TTTAGCATGGCATGTAAAGACACC-3.

The PCR products showed in agarose gel 4 bands for the negative control and one band for the specific PCR. This last was purified and sequenced on Illumina 's GSII platform sequencing.

3. RESULTS

In **Fig. 1**, we recall the obtained transcriptome of assimilated Ig kappa chain V-V region K2, which is composed of 697 nucleotides.

After cloning we obtained an assimilated Ig Kappa chain V-V region K2 as shown in **Fig. 2.**

Locus_7375_Transcript_1_1_Confidence_1.000_Length_697
5'TTCAGATTCAGAAACACATGTATTTCCATACTTCTATGAAGAAGTAC
GACAAGTACATCTTTGCTAAGTT
CATTTAATCTGACTATTAACTTAAAACTTTTTGTCGTTCGATGACGTCA
CATCGTTGGATGAAGCAAGTG
GTCCACGAGTTCAACACTCTTTTGAAGTCAACAAAACTTCAACAAAG
ACTTTAAAACCCTTTTACGAGTT
TAACACAGCATCAAGTGAAGATGTTCCTAATAGCTTTTGCGGTGTTTT
CTCTGTTGTGTTACGGAGGGAG
AGCGTGTGATCTCACGGGCCAGCCAATGGATGTCGTGGCTGAGGTAG
GAGCGGAGGCAATACTTACCTGT
CCAACTGACTTAGAGGAGTGCACGGCCAATTGTAAGGTTTCATGGTA
TCTTCTGAAGAATAAGACATATA
CACCGATTAGTTCATGTAAACAAGTTTATGAGAATTTCGAAAACAGGT
TTTCAATATCTGGTGGTCCCAA
CTGGACTCTTACTCTCAGCGGAGTTGAGCCGAATGATGCTCGCAAAT
ACAGGTGCAAGGTAAAGAGTAAT
GAAACAAAACCAGCAACTTCAGAAAGCATGACACTCATTATACCATC
AACCATCAACATTACGTTGAGTG
CAGCATCTTCTCAAATAACTGGTAGGGGAAGTGGTGTCTTTACATGCC
ATGCTAAAAACACGAAAG
>sp|P01635.1|KV5A3_MOUSE RecName: Full=Ig kappa chain V-V region K2;
Flags: Precursor
Length=115
Score = 35.4 bits (80), Expect = 0.005
Identities = 27/101 (27%), Positives = 45/101 (45%), Gaps = 8/101 (8%)
Frame = +3

Fig. 1. DNA sequence of "second" candidate IgKappa gene

Corresponding Auther: Michel Leclerc, Independent Researcher: 556 Rue Isabelle Romee, 45640 Sandillon, France

5'CAGATTCAGAAACACATGTATTTCCATACTTCTATGAAGAAGTACGA
CAAGTACATCTTT
GCTAAGTTCATTTAATCTGACTATTAACTTAAAACTTTTTGTCGTTCGA
TGACGTCACAT
CGTTGGATGAAGCAAGTGGTCCACGAGTTCAACACTCTTTTGAAGTC
AACAAAACTTCAA
CAAAGACTTTAAAACCCTTTTACGAGTTTAACACAGCATCAAGTGAA
GATGTTCCTAATA
GCTTTTGCGGTGTTTTCTCTGTTGTGTTACGGAGGGAGAGCGTGTGAT
CTCACGGGCCAG
CCAATGGATGTCGTGGCTGAGGTAGGAACGGAGGCAATACTTACCTG
TCCAACTAACTTA
GAGGAGTGCACGGCCAATTGTAAGGTTTCATGGTATCTTCTGAAGAAT
AAGACATATACA
CCGATTAGTTCATGTATACAAGTTTATGAGAATTTCGAAAACAGGTTT
TCAATATCTGGT
GGTCCCAACTGGACTCTTACTCTCAGCGGAGTTGAGCCGAATGATGC
TCGCAAATACAGG
TGCAAGGTAAAGAGTAATGAAACAAAACCAGCAACTTCAGAAAGCA
TGACACTCATTATA
CCATCAACCATCAACATTACGTTGAGTGCAGCATCTTCTCAAATAACT
GGTAGGGGAAGT
GGTGTCTTTACATGCCATGCTAA

Fig. 2. DNA Sequence of the"assimilated" IgKappa chain V-V region K2

4. CONCLUSION

At the beginning of the year 2013, we had found a first candidate IgK gene (Leclerc and Otten, 2013) which possessed an IgSF domain.

We supposed that this second cloned gene (**Fig. 2**), was implicated in the response to the antigen HRP as the first one (Leclerc and Otten, 2013).

In fact we don't know, at the moment, if there are, 2 candidate genes or more in response to HRP.

But, if we draw up a conclusion.

Currently, two IgKappa genes, in sea star genome have been cloned and our data contributes greatly to knowledge the molecular and genetic bases of non-self recognition by Invertebrates.

5. REFERENCES

Leclerc, M., S. Dupont, O. Ortega-Martinez, B. Hernroth and N. Krezdorn *et al*., 2011. Evidence of Kappa genes in the sea-star Asterias rubens (Echinoderma). Immunol. Lett., 138: 197-198. DOI: 10.1016/j.imlet.2011.01.016

Leclerc, M., N. Kresdorn and B. Rotterb, 2013. Evidence of complement genes in the sea-star Asterias rubens. Comparisons with the sea urchin. Immunol. Lett., 151: 68-70. DOI: 10.1016/j.imlet.2013.02.003

Leclerc, M and P. Otten, 2013. Revealed «oncologic markers» in the sea star antibody response to horse-radish peroxydaseam. Am. J. Immunol., 9: 130-131. DOI: 10.3844/ajisp.2013.130.131