

Determination of the CDR (CDR1, CDR2) Complementary-Determining Region Invertebrate Primitive Antibody from Sea Star

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ABSTRACT

The IPA (Invertebrate Primitive Antibody) was recently discovered, in the same time of *Asterias rubens* lymphocytes, humoral specific immune responses and Genomic assays with the sea star IGKappa gene or anti Horse-radish peroxydase. CDR1 and CDR2 were described in this paper. That corroborates the name of Invertebrate Primitive Antibody and not IG Like protein as it is thought by some people.

Keywords: Invertebrates, Invertebrate Primitive Antibody, CDR1, CDR2.

INTRODUCTION

10 years ago, we tried to clone, for the first time, the *Asterias rubens* sea star IGKappa gene by the use and the help of *E.coli* as amplificador [1]. It allowed, in a second time, to verify that the Young Protein, or anti-HRP Protein recognizes the HRP antigen [1]. The work which follows was made possible to the great open-mindedness of Dr S.Kossida (IGH Montpellier).

It consists to research Complementary Determining Regions called more briefly CDR1, CDR2, CDR3. Or Complementary-Determining Regions.

MATERIAL AND METHODS

A recalling of the anti -HRP sea star sequence [1] IGKappa gene (Figure 1) and the method of F.Ehrenmann and Lefranc [2,3] from the IMGT V domain directory were used.

First, anti-HRP sequence in nucleotids/

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5'GGA TCC GGA GGA ATG CGTGGCAACATGGCGTCTCTATGGATGTTCTTCTT
TGTCGTGGGGATAACTTTACAACGGAGTTTGGCGATTTACACGTTTCGCG
AGCAACCGTCGGACACTAGCGCGTTGCAGGGGAGCACAGTGGTGCTTCAC
TGCTCCGTTGAGCAGTACATAAACACCACGGCCATCGTTTGGTGGAGCCG
TGACTCGGTCATCAGCCACAACAAAGACCTGAAACTGTCCAGTCTAAACA
CCGACCAGCTCCAAAGGTACTCGATTTACAGGCGACGCATCTCGGGGGGAA
TTCAACCTTAAAATAGTGAACCTTACCGCCACAGACGCCGCCAGTTACCG
CTGTTCAGATG TAA GAA TTC3'
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with the translation <https://web.expasy.org/translate/>

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gga tcc gga gga atg cgt ggc aac atg gcg tct cta tgg atg ttc ttc ttt gtc gtg ggg
G S G G M R G N M A S L W M F F F V V G
ata act tta caa cgg agt ttg gcg att tac acg ttt cgc gag caa cgg tcg gac act acg
I T L Q R S L A I Y T F R E Q P S D T S
gcg ttg cag ggg agc aca gtg gtg ctt cac tgc tcc gtt gag cag tac ata aac acc acg
A L Q G S T V V L H C S V E Q Y I N T T
gcc atc gtt tgg tgg agc cgt gac tcg gtc atc agc cac aac aaa gac ctg aaa ctg tcc
A I V W W S R D S V I S H N K D L K L S
agt cta aac acc gac cag ctc caa agg tac tcg att tca ggc gac gca tct cgg ggg gaa
S L N T D Q L Q R Y S I S G D A S R G E
ttc aac ctt aaa ata gtg aac ttt acc gcc aca gac gcc gcc agt tac cgc tgt cag atg
F N L K I V N F T A T D A A S Y R C Q M
taa gaa ttc
- E F
    
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Figure 1. Sea star (Starfish) IGKappa gene sequencing.

OR in ANOTHER WAY

MRGNMASLWMFFVVGITLQRSLAIYTFREQPS-
 DTSALQGSTVVLHCSVEQYINTTAIVWWSRDSVISHNKDLK-
 LSSLNTDQLQRYISGDASRGFNLKIVNFTATDAASYRCQMFA

RESULTS

2 tables issued from IMGT resume the following analysis below: I):

<https://www.imgt.org/3Dstructure-DB/cgi/DomainGapAlign.cgi> with default settings, 17/01/2024

IMGT/DomainGapAlign version: 4.10.3 (2021-12-06)

Closest reference gene and allele(s) from the IMGT V domain directory: (All species)

Species	Gene and allele	Domain	Domain label	Smith-Waterman score	% identity	Overlap	Show alignment
<i>Pongo abelii</i>	IGKV1-5*01	1	V-KAPPA	121	33.3	90	<input checked="" type="radio"/>
<i>Pongo pygmaeus</i>	IGKV1-8*01	1	V-KAPPA	121	33.3	90	<input type="radio"/>
<i>Homo sapiens</i>	IGKV1-5*03	1	V-KAPPA	119	33.3	90	<input type="radio"/>
<i>Homo sapiens</i>	IGKV1-5*04	1	V-KAPPA	119	33.3	90	<input type="radio"/>
<i>Homo sapiens</i>	IGKV1-5*05	1	V-KAPPA	119	33.3	90	<input type="radio"/>

Species	Gene and allele	Domain	Domain label	Smith-Waterman score	% identity	Overlap
<i>Pongo pygmaeus</i>	IGKJ4*01	1		7	100.0	1

II) Table II Alignments

Alignment with the closest gene and allele from the IMGT V domain directory: (All species)

>starfish|IGKV1-5*01|33.3||Pongo abelii

FTATDAASYRCQ.....

.....EQPSDTSALQGSTVVLHCSVEQYI.....NTTAIVWWSRDS-
 VISHNKDL.KL.....SSLNTDQL.QRYISGDASRGFNLKIVN-

The conserved amino acids (positions 23, 41, 89, 104) are found in the starfish sequence.

This molecule appears to have an IG AA sequence as seen from the above analysis.

1. If it aligns with the Pongo IGKV1-5, the percentage of alignment is 33%, so it is a sequence that seems to have similarities to an IGKV gene when it comes to conserved amino acids.

DISCUSSION

It appears clearly that CDR1 and CDR2 exist in the sea star primitive antibody and not clearly for CDR3 (1 amino acid which is conserved).

Undoubtly

These new parameters [4] corroborate the existence of an Invertebrate Primitive Antibody and NOT IG-LIKE as it is often said. We recall also the discovery by us of T and B sea star lymphocytes [5] Humoral specific response [6] Genomic data [7].

ALL these elements assess the existence of an IPA: Invertebrate Primitive Antibody which shares strong sequence alignments (at least for CDR1 and CDR2) with the Primate: Pongo pygmaeus.

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