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

Michel Leclerc*
Immunology of Invertebrates, Orléans University, France

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 amplificator [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/

5’GGA TCC GGA GATG CGTGGCAGTAG CCGTCTCTATGGATGTTCTTCTT
TGTCGTGGGGGATAACTTTACAACGGAGTTTGGCGATTTACACGTTTCGCG
AGCAACCCTGGGACACTAGGCGGTGTCAGGGAGCAAGTGTGCTTTCCAC
TGCTCAGTCTAGACACCAAGAAGACTGAAATTGTCCAGTCTTAAACA
CCGACCAGCTCACAAGACAGTCCGGGCTCAGGGGGCACTCTCGG
CTGTCAGATG TAA GAA TTC3’
with the translation https://web.expasy.org/translate/

**Figure 1.** Sea star (Starfish) IGKappa gene sequencing.

```
G S G G M R H D N M A S L W M F F F F F V V G
ata act tta cca cgg agt tgt cag att tac agc ttt cgc gag caa cag tcg gag acct agc
IT L Q R S L A I Y T F R E Q P S D T S
ggc agg acc aga caa ggt ggt ctt cag ttc ggg ggc ctt atc aac acc agc
A L Q G S T V V L H C S V E Q Y I N T T
gcc agg ggt cgg acc gca tgt cgg cta aac cac ccg cag aac cag ccc cct
A I V W W S R D S V I S H N K D L K L S
agt cta aac gcc cag ctc cca agg tac cgg tta aat cgg gcc gcc gca tac cgc ttt cag atg
S L N T D Q L Q R Y S I S G D A S R G E
ftc aac ctt aaa atg aac ttt acc gcc aca 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
```

OR in ANOTHER WAY

```
MRGNMASLWMMFFVVGITLQRSLAIYTFRQPS- DTSALQGSTTVLHCSEVQYINNTAIVWWRSVDVISIHKDLK- LSSLNTDQLQRYISISGDASRGEFNLKIVNFTATDAASYRCFA
```

II) Table II Alignments

```plaintext
<table>
<thead>
<tr>
<th>Species</th>
<th>Gene and allele</th>
<th>Domain label</th>
<th>Smith-Waterman score</th>
<th>% identity</th>
<th>Overlap</th>
<th>Show alignment</th>
</tr>
</thead>
<tbody>
<tr>
<td>Pongo abelii</td>
<td>IGKV1-5*01</td>
<td>1-VKAPPA</td>
<td>121</td>
<td>33.3</td>
<td>90</td>
<td></td>
</tr>
<tr>
<td>Pongo pygmaeus</td>
<td>IGKV1-4*01</td>
<td>1-VKAPPA</td>
<td>119</td>
<td>33.3</td>
<td>90</td>
<td></td>
</tr>
<tr>
<td>Homo sapiens</td>
<td>IGKV1-5*01</td>
<td>1-VKAPPA</td>
<td>119</td>
<td>33.3</td>
<td>90</td>
<td></td>
</tr>
<tr>
<td>Homo sapiens</td>
<td>IGKV1-5*01</td>
<td>1-VKAPPA</td>
<td>119</td>
<td>33.3</td>
<td>90</td>
<td></td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Species</th>
<th>Gene and allele</th>
<th>Domain label</th>
<th>Smith-Waterman score</th>
<th>% identity</th>
<th>Overlap</th>
<th>Show alignment</th>
</tr>
</thead>
<tbody>
<tr>
<td>Pongo abelii</td>
<td>IGKV1-5*01</td>
<td>1</td>
<td>7</td>
<td>100.0</td>
<td>1</td>
<td></td>
</tr>
</tbody>
</table>
```

**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)

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

.....EQPSDTSALQGSTTVLHCSEVQYINNTAIVWWRSVDVISIHKDLK.........SSLNTDQLQRYISISGDASRGEFNLKIVN- FTATDAASYRC.............

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).

Undoubtedly

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.

**REFERENCES**


