

Complementary-Determining Region Invertebrate Primitive Antibody From;Sea Star »Modelization 3d With Human Igk

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Abstract:

Our findings consist of the importance of an individualized approach based on infectious risk and prudent antibiotic management to prevent antibiotic resistance, and highlight the need for further research to better assess the clinical impact of antibiotic prophylaxis in this specific context of transurethral resection of bladder tumor.

Keywords: artificial intelligence; urology; medical training; learning; technological advances

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 amplifier [1]. It allowed, in a second time, to verify that the Young Protein, or anti-HRP Protein recognizes the HRP antigen [1,2]

In the present work we research Complementary Determining Regions called more briefly CDR1, CDR2, CDR3. Or Complementary-Determining Regions[3,4]

First, anti-HRP sequence in nucleotids is given :

5'GGA TCC GGA GGA ATG
CGTGGCAACATGGCGTCTCTATGGATGTTCTTCTT

TGTCGTGGGGATAACTTTACAACGGAGTTTGCGGATTACACGT
TTCGCG

AGCAACCGTCGGACACTAGCGCGTTGCAGGGGAGCACAGTGGT
GCTTCAC

TGCTCCGTTGAGCAGTACATAAACACCACGGCCATCGTTTGGTG
GAGCCG

TGACTCGGTTCATCAGCCACAACAAAGACCTGAAACTGTCCAGTC
TAAACA

CCGACCAGCTCCAAAGGTAAGTACTCGATTTCAGGCGACGCATCTCGG
GGGGAA

TTCAACCTTAAAATAGTGAACCTTACC GCCACAGACGCCGCCAG
TTACCG

CTGTCAGATG TAA GAA TTC3'

with the translation <https://web.expasy.org/translate/>

gga tcc gga gga atg cgt ggc aac atg gcg tct cta tgg atg ttc ttt gtc gtc 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 ccg tcg gac act agc
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 gtc gtc 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 gtc 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 .

OR in ANOTHER WAY :

MRGNMASLWMFFVVGITLQQRSLAIYTFREQPSDTSALQGSTVVLH
CSVEQYINTTAIVWWSRDSVISHNKLKLSLNTDQLQRYISISGDAS
RGEFNLKIVNFTATDAASYRCQMFA

Results :

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

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

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

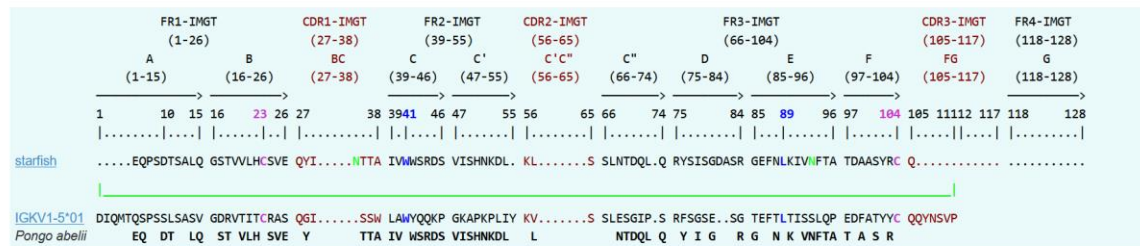
Closest reference gene and allele(s) from the IMGT V domain directory: (All species)

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

...EQPSDTSALQGSTVVLHCSVEQYI.....NTTAIVWWSRDSVISHNKD L.KL.....SSLNTDQL.QRYSISGDASRGFEFLKIVNFTATDAASYRCQ.....

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.

It appears clearly that CDR1 and CDR2 exist in the sea star primitive antibody and less clearly for CDR3 [1] amino acid which is conserved)

Undoubtly :

These new parameters 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] with specially Invertebrate MHC genes

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 sequences . More recently, in a work concerning Modelizations in 3D of the sea star anti-HRP protein, we found a CDR3 region (see below this modelization when compared to AlphaFold prediction of IGKV1-5 03 from Homo sapiens (Figure.1)

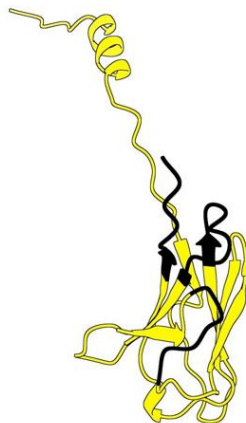


Figure 1 : Alfold prediction of IGKV1-5*03 Homo sapiens

In black sea star CDR1, CDR2, CDR3(at the left) determining regions

References :

1. Leclerc, M. et al (2014) SAJ Biotechnol 1 :104	3. Ehrenmann,F et al (2010) Nucleic Acid Res 38 : 301-307
2. Leclerc,M (2024) J. Stem Cell Res Ther 9(1):1	4. Ehrenmann, F et al (2011) Cold Spring Harbor Protoc 6 :737-749
	5. Leclerc, M et al (1993) Thymus 21(3) : 133
	6. Brillouet C et al (1984) Cell. Immunol '84(1) :138



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