



Evidence of Complement Genes in the Crinoïd:antedon Bifida. Comparisons with other Echinodermata

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Abstract

Fourth classes of Echinodermata out of five shown Complement component genes: The Echinids revealed 2 ones, the Asterids 10 ones as the Ophiurids. At last, the Crinoïds, which are ancestral Echinodermata, we study now, have 5 component complement genes.

Keywords: Invertebrates, Echinodermata, Crinoïds, complement component genes

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Results

Introduction

In recent papers (Ref.1,2) Complement components have been found in the Asterid: Asterias rubens, and in the Ophiurid: Ophiocomina nigra. It seemed interesting to study the ones of the Crinoïd: Antedon bifida since these third Echinodermata shared common genes as the IGKappa gene. (Ref.3)

Materials and Methods

Animals: Antedon bifida was obtained at the station Of Biologie Marine of Roscoff France.

Obtention of crinoïd mRNA: Digestive coeca were excised from the A. bifida body.

A. bifida mRNA was obtained from Uptizol (Interchim). Quality control were operated.

Sequencing : Sequencing was made on Illumina Next Seq 500 with paired-end : 2. 75 bp

Transcriptome was assembled from RNA-Seq fastq files using Trinity v2.1.1 (Ref.4) with default parameters. A BLAST database was created with the assembled transcripts using makeblastdb application from ncbi-blast+ (v2.2.31+). The sequences of transcripts of interest were then blasted against this database using blastn application from ncbi-blast+ (Ref.5) with parameter word_size 7.

QueryID	Query Symbol	SubjectID	Identity (%)	Length	Mismatch	Gapopen	Query cover (%)	E-value
NM_001282459.1	C2	TRINITY_DN19334_c8_g2_i1	83,97	287	37	7	16	2,00E-70
NM_001346850.1	C1S	TRINITY_DN17397_co_g9_i1	93,94	33	2	0	1	3,00E-05
NM_001735.29.1	C5	TRINITY_DN19647_c0_g1_i3	88,89	36	2	2	1	0,01
NM_000587.2	C7	TRINITY_DN20662_c3_g1_i4	90,32	31	3	0	1	0,04

Table 1: summarizes the obtained results with the five component complement

Table 1: alternate and classical complement components of the *Antedon bifida* (Crinoïd)

C3 was also found but the e-value was greater than 0,05 .

b)The *Antedon bifida* transcriptomes of C2 and C1s reveal their sequences en 5'-3':

First, the *Antedon bifida* C2 transcriptome is evaluated:

```
>TRINITY_DN19334_c8_g2_i1 (C2)
5'TGTAATCCCAGCACTTTGGGAGGCCGAGGCGGGCGGATCACGAGGTCAG
GAGATCGAGACCATCCTGGCTAACACAGTGAACCCCGTCTCTACTAAAA
ATACAAAAAATTAGCCGGCGTGGTGGCGGGCGCCTGTAGTCCAGCTAC
TCGGGAGGCTGAGGCAGGAGAATGGCGTGAACCCGGGAGGCGGAGCTTG
CAGTGAGCCGAGATCGCGCCACTGCACTCCAGCCTGGGCGACAGAGCGAG
ACTCTGTCTCAAAAAAAAAAAAAAAAAAAAAA3'
```

Second the *A.bifida* C1s transcriptome in 5'-3' is given

```
>TRINITY_DN17397_co_g9_i1 (C1S)
5'TAAAAAAAAAAAAAAAAAAAAATTTATAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAATATTTAAATGTTAAAAAAAAAAAAATAAAAAAAAAATAA
TAAAAATACAAAAAAGTAGTGTAGGTAAGATCTTCTGTATCTATAGC
AACACTCCATTTGCTTAGCCAATGCAATTAAGTTAAACAATCGCATTAA
ATTATTAATAAATGCTGTTTTTAAAGGTATATAGTCTATAGATTTTA
TTACTCTTGGTAC 3'
```

Discussion and Conclusion

First we recall that the genome of the famous sea urchin studied in USA has just revealed 2 complement components: among them , the C3.

With the sea star *Asterias rubens* 10 components appear from C1 to C9(Ref.1) .We envisage with these data, something fonctionnal in ALTERNATE PATHWAY and CLASSICAL PATHWAY.(Ref.3)

Similar results occur with the Ophuirids and *Ophiocoma nigra*: 10 complement components (Ref.2) and an IGH gene which is initiated by these last ones.

In *Antedon bifida* which presents also an IGH gene, we just find 5 complement components genes BUT the e-values , greater than 0,05 prevent to notice the 5 other missing ones.

In summary, 3 classes of Echinodermata : the Asterids, the Ophuirids, the Crinoïds out of 5, including also the Echinids and the Holothurids, present an IGH gene which matches with *Homo sapiens* IGH gene and alternate, classical, complement components genes which stimulate the primitive antibody.

It is time to consider the Invertebrate primitive Antibody as a great novelty in Invertebrates.

References

- 1)Leclerc, M. (2013) *Amer.J.Immunol*, 9(1) :26-29
- 2)Leclerc, M. Et al (2018) *Int.J. Biotech & Bioeng*, 4:1 07-10
- 3)Leclerc, M. Et al *Meta Gene* (2018) submitted
- 4)Grabherr, M.G et al(2011) *Nature Biotechnology*, 29:644-652
- 5)Altschul, S.F et al (1990) *J.Mol. Biol* , 215(3) : 403-410