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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 Ophuirids. At last, the Crinoïds, which are ancestral Echinodermata, we study now, have 5 component complement genes.

Keywords: *Invertebrates;Echinodermata; Crinoïds; complement component genes.*

INTRODUCTION

In recent papers (Ref.1 ,2) Complement components have been found in the Asterid: Asterias rubens, and in the Ophuirid: 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.

RESULTS

Table 1. *summarizes the obtained results with the five component complement*

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_c0_g9_i1	93,94	33	2	0	1	3,00E-05
NM_001735.2	C5	TRINITY_DN19647_c0_g1_i3	88,89	36	2	2	1	0,01
NM_000587.3	C7	TRINITY_DN20662_c3_g1_i4	90,32	31	3	0	1	0,04

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 .

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’TGTAATCCCAGCACTTTGGGAGGCCGAGGCGGGC-GGATCACGAGGTCAGGAGATCGAGACCATCCTGGCT AACACAGTGAAACCCCGTCTCTACTAAAAATACAAA AAATTAGCCGGGCGTGGTGGCGGGCGCCTGTAGTC CCAGCTACTCGGGAGGCTGAGGCAGGAGAATG-GCGTGAACCCGGGAGGCGGAGCTTGCAGTGAGCCGA-GATCGCGCCACTGCACTCCAGCCTGGGCGACAGAGCGA-GACTCTGTCTCAAAAAAAAAAAAAAAAAAAAAAAA3’ Second the A.bifida C1s transcriptome in 5’-3’ is given

>TRINITY_DN17397_c0_g9_i1 (C1S)

5’TAAAAAAAAAAAAAAAAAAAAAATTTTATAAA AAAAAAAAAAAAAAAAAAAAAAAATATTTAAA ATGTTAAAAAAAAAAAATAATAAAAAATAAATAA AAATACAAAAAAAAGTAGTGTTAGGTAAAGATCT TCTGTATCTATAGCAACACTCCATTTGCTTAGCCA-ATGCAATTAAAAGTTAAACAATCGCATTAAATTAT-TAAATAAATGCTGTTTTTTAAAGGTGTATATAGTGCT ATAGATTTTATTTACTCTTGGTAC 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 functionnal in ALTERNATE PATHWAY and CLASSICAL PATHWAY. (Ref.3)

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

In Antedon bifida which presents also an Igkappa 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 IGKappa gene which matches with Homo sapiens IGKappa gene and alternate, classical, complement components genes which stimulate the primitive antibody.

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