

The Complement System in Echinodermata. A Third Pathway: A Lectin Pathway?

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ABSTRACT

Complement Classical and Alternate pathways co-exist in Echinodermata (Asterids, Ophuirids and Crinoïds). A third pathway: the Lectin Pathway appear in Ophuirids and Crinoïds.

Keywords: Echinodermata; Invertebrates; Complement; Lectin Pathway

INTRODUCTION

Complement component genes of the classical and alternate pathway have been described in Asterids (Ref.1) then in Ophuirids (Ref.2) at last in Crinoïds (Ref.3). All these components found in these Echinodermata can be completed, to day, by MBL2 gene and MASP1 gene which characterize the well-known: Lectin Pathway. They are present in 2 classes of Echinodermata which are just studied: The Ophuirids and the Crinoïds

MATERIAL AND METHODS

Animals

Ophiocoma nigrum (Ophuirid) Antedon bifida (Crinoïd) were obtained at the station « Of Biologie Marine of Roscoff » France.

RESULTS

A table 1: summarizes the obtained results with first Ophuirids. A table 2 shows those obtained with Crinoïds:

QueryID	Query Name	SubjectID	Identity (%)	Length	Mismatch	Gapopen	Query cover	E-value	Bitscore
NM_000242.2	MBL2	TRINITY_DN15627_c0_g1_i1	100	22	0	0	1	2,30E-02	41,7
NM_001031849.2	MASP1	TRINITY_DN55866_c0_g1_i1	95,65	23	1	0	1	2,00E-01	38,1

Table 1

The transcriptomes of MBL2 and MASP1 genes are the following

TRINITY_DN15627_c0_g1_i1

5'GTTGAAATTAATATAAAATATAAACC
AGAACTACTAGCAAAGCTCTGAGCAAGT
TGCA
TCTACCTGGATGCAATTGTGTTGTTAGCTT
TCAACAGGCTGATATTATACCCAATCTATT
CCCATATTTAAAGCAGTGACCTGGCTAT

Obtention of Ophuirid and Crinoïd Mrna

Digestive coeca were excised from their bodies and mRNA were obtained from Uptizol (Interchim) then quality controls 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 make blast db 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.

ATCATACGCAGCACATTGTAGGGTATTCT
CT
TCAAAATGCAGAGAAAGAAAATATGAAT
AAATAAAATATGATTTCAATTTTCAGCAG
CAT
ACCACAAGTTATTTTTTCTACTGTAGAGAT
ACAATATCAATCATCATCTTGTCTTCTACA3'
>TRINITY_DN55866_c0_g1_i1
5'TATCAAACCTGAAAACCTAGTAAAATATT

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CACTAGTTTTTAAACGCCATTCAATCAATA
GCC
AGTCTGGTGTCCATCGGACGTTTATTGTT
TGACATTTAAAAACAGTCGAGATAAGTGT
TA
AAATTCGAAAGAAAATCATGAAAAA
ATGTATGTGACACTGAAAAAACACCAC
TTTC

TAAAGTATTGATTATAAATAATGCGTAATA
ATTTTTTAACAAAAATCTAAATAATAAAAT
CTAAACAACCTAGATCATTGAAGAATTAAT
CAAAATGGAATAAATAAAATAAAAA
GA
TTACCGTATTAAAAGTACAAAATAGTAA
TATGAG3'

table 2: appropriate sequences concerning the transcriptomes of Crinoids genes are following:

QueryID	Query Name	SubjectID	Identity (%)	Length	Mismatch	Gapopen	Query cover	E-value	Bitscore
NM_000242.2	MBL2	TRINITY_DN19440_c3_g1_i1	100	23	0	0	1	7,00E-03	43,6
NM_001031849.2	MASPI	TRINITY_DN20737_c10_g1_i2	92	25	2	0	1	7,80E-01	36,2

Table 2

>TRINITY_DN19440_c3_g1_i1

5'AAATAATATATTTGGAGGGTCACCCTTAT
CTATACTCTAAATATATAACTATAATTAATA
TAATTTTGTACAAAATAAATAATTTATCTAT
ATAGTATTAATTTACAATAGTTTTTATTT
ATATAATTATCAAACCTATAAAATATACA
ATAGTTGATCACCTATATATACATAAAATC
CATTATTATTGCACACATTCTGTTTAAACT
CTCAAACAAGTCCATATAAATACATTTTC
A
AATATTGATTGAACATCTACTCTATCAGAAT
TATACCAAATATAGTTCACCCAAAGAAAA
TGTTAGTGATATTAAAGCGTAGCTCCGGG
GTAAAGACATTGATGATAGCCCCACTTA
AT
TTTCGACAGAAGTTAAGCCGAAAGTATT
GTGAACAAAATGTGGTGGCAGAGGAATT
TATT
ATTCATGATTTTATATCAAATGAATTGAAA
ACAGTCATTCTGGCAAATATAAGTGGGG
T
TATTATCATTTGTAAATGTTTATATTTTTAT
AAAACAATAGAACTTTATGACTGGTACT
CTTTAAACAATTTTCTCTTCACTAATCTTT
CAGTTCAGTTCAAACTGTCTATTACAAA
C
TAGTACTAGCTCTAATTTAAATTAATCC
TTATTCACCAGAAACGTTTTTAGGCCTAC
T
ACTACTACTACTATTATTGCAATAACATCA
AATGTGTTTTAAGAAAAAATCAGAGG
TA
AAAGTAAATACATATAGCACTATTATTGGT
GGTGATACTTCAGAATAGTCTTAGAAATA
A
TAACAACCTTTATTATACCTGAGGTAAAAA
AGTGGTAGCTACCTATAGAATAATATTAA
C
AATTACCAGCATATCGTTATTAATAGTAAC
AAGATTTTATTAAAGAAAATGACATATTA
GACATTGTTTTACTACACATAACAAAAAG
TATGAAGTAACAGAACGCAACAAGCATT

TGG

ACATGCATTCATACACAGACCGTATCATT
CACATACTGTAGCTATGGAAGACAACATT
GG
AAGACAGAGAGACCAAAGAAGCAATATA
TAATATTATAAAGAATCACCAAATACAAT
AA
AGACAAATAAACACAAAGAATTATTGCA
GTATCACCATCATCATCATATAAATCAAT
CT
TTAAAATGATAAAAATAATGAAATAGAGAT
TCTAGATTCCTAAATGTAAATTTTGAGAAT
ATGCATCTGTAAAAATCAGTATTTCTCTGT
ATATATGGCTTATGAGCTATACAGTATTTA
TAGCACGTAACCTCTGTACACTCTCCCTGT
CCACTCTGGCTGCTATGATCTCAACATCT
TC
TGCACCACAGAATAGCAATAGAGAGCTT
TCGAAAGAGGTGAGTTGGTGTGCGACG
CGCA
ACTGAGCATGCGGATACAAGAAAACCTTC
TGCAGACCGAACGCGATTTGAAGGAAGA
TAAC
ACGAGGCTGTTTCTGACTTGCTTGCTCTCT
CCTAACCTGTATCACTATTTTCGTAAGCTCT
C
TATTGAACACCTATAAGGGGCAACAGCCT
TCATTATCAATTCTTTGTTCCACTAAATTC
A
CAGACTTTTCAATTTCTTTATCTTCTTTTT
CCAGCAAGAATCGTCCGATAATATACATA
G
CTCTTAGTACATTATCA3'

>TRINITY_DN20737_c10_g1_i2

5'ATTGATTGATAATTAATATCTTTTATAT
TAATACGTTTAATATGGTACCATGTGATT
TGT
TTTTTGTTGATTTTTTTTTTCAGGTGAAGA
CCTTTACCAAACCTCATGAAATAGTGTC
ATT
GTCAGGAACCTTTTCAAGATGCATTC

CATCTTCATGCTTCTATATCAGATGAGAA
TTC
TATGGTCTTTGGAGGTCACGTGATGGAG
GTAATGGAGACGTATACAACTATAGAGC
TCGT
GGTTGGTGAACCTCAAAAGCCTGAAATTTA
CAAGAGAATTTGACTCGAGTTCTGGATAC
AA
GGAGCTTGTCATACGAAACAGAGAACAA
TCATCTACTACAACAGATACATAATGATA
TTG
TCTGTGAGTTAACAACACTAATAATTGG
TATTATAAAGCATATCTTGTATAGACACT
ACA
GTGCGTAACAAGATATGGTATGCCCCAA
GAGGTTATATAATAAATAGCGACCATT
TGTG
GAGACTTCGCTCTCGTCTAGTTACCCCTG
TAGTTAATTATATAACCTCTTTGTGGTAT
TA
TATGCTGTACAAACAAGACAATATACTG
TACAACAAAAATCTAATTTTATTAAATTT
CTA
CTTTCTAAATAGTATAATTGTAGAAGTGT
TTAACTAACACCCGGGTTTTATTTTGAAA
CG
ACGCCTCTTCAGTTTTTTGAGCAATGTCAA
ACATTTTCTGTGATGTCTGAGGTAGAGA
AAA
GGGGTAATATTGGGTAATATTTTATCTCT
TAAAATAGGCCTAACATGCACAGAGCT
AGG
CTCTTTCTACACTATCAAACAAAATGTG
ACAAAAAATGTGATGATGATGATGTCAT
ATCA

CTACCACCATATTGGGGCACATCACACT
TTCATCAGTAATCTGCCCTCTATTCCATA
AAT
TAATGAAAAAACTAGATGTTTGAAGAA
GGTTTTCAATCTTTTGTGAGTAGCTATAA
ATG
AATGAAAGTGAGTTGAACAGTGATTACA
TATGTGCATGGCTTCTGATATTAGTGCCA
TAG
TATTCTTCATATTCAGCACATACTCACTA
ATTGTAAATAATGTGTACATTACAGTTTA
TA
CACTATTTATATGTATTACAATAGTTG3'

CONCLUSION

MBL2 genes and MASP1 genes which initiate the Complement Lectin Pathway are present in these two classes of Echinodermata (Ophurids and Crinoids) with a comfortable e-value, a significant identity. Is this pathway functional? It remains enigmatic.

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