The Complement System in *Echinodermata* Includes the Lectin Pathway: Genomic Aspects

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Abstract

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

Keywords: Echinodermata; Invertebrates; Complement; Lectin Pathway

Complement component genes of the classical and alternate pathway have been described in Asterids [1] then in Ophuirids [2] at last in Crinoïds [3]. The aim of this work is to look for MBL2 gene and MASP1 gene which characterize the well-known: Lectin Pathway, in *Echinodermata*.

Materials and Methods

Animals: Ophiocomina nigra (Ophuirid) Antedon bifida (Crinoïd) were obtained at the station "Of Biologie Marine of Roscoff" France.

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 [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+ [5] with parameter word_size 7.

Results

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

Query ID	Query Name	Subject ID	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'GTTGAATTAAATATAAAAATATAAACCAGAACTACTAGCAAAGCTCTGAGCAAGTTGCA
TCTACCTGGATGCAATTGTGTTGTTAGCTTTCAACAGGCTGATATTATACCCAATCTATT
CCCATATTTAAAAGCAGTGACCTGGCTATATCATACGCAGCACATTGTAGGGTATTCTCT
TCAAAATGCAGAGAAAGAAAATATGAATAAATAAAATATGATTTCAATTTTCAGCAGCAT
ACCACAAGTTATTTTTTTCTACTGTAGAGATACAATATCAATCATCATCTTGTTTCTACA3'

>TRINITY_DN55866_c0_g1_i1

5'TATCAAACTTGAAAACTAGTAAAATATTCACTAGTTTTTAACGCCATTCAATCAATAGCC
AGTCTGGTGTCCATCGGACGTTTATTGTTTGACATTTAAAAACAGTCGAGATAAGTGTTA
AAATTCGAAAGAAAATCATGAAAAAAAATGTATGTGACACTGAAAAAAACACCACTTTC
TTAAGTATTGATTATAAATAATGCGTAATAATTTTTTAACAAAAATCTAAATAATAAAAT
CTAAACAACTAGATCATTGAAGAATTAATCAAAATGGAATAAATAAAATAAATAAAAAGA
TTACCGTATTAAAAGTACAAAATAGTAAATATGAG3'

The table 2 and appropriate sequences concerning the transcriptomes of Crinoïds genes are following.

Query ID	Query Name	Subject ID	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	MASP1	TRINITY_DN20737_c10_g1_i2	92	25	2	0	1	7,80E-01	36,2

Table 2

>TRINITY_DN19440_c3_g1_i1

5'AAATAATATATTTGGAGGGTCACCCTTATCTATACTCTAAATATATAACTATAATTAATA
TAATTTTGTACAAAATAAATAATTTATCTATATAGTATTAATTTACAATAGTTTTTATTT
ATATAATTATCAAAACCTATAAAATATACAATAGTTGATCACCTATATATACATAAAATC
CATTATTATTGCACACATTCTGTTTAAACTCTCAAACAAGTCCATATAAATACATTTTCA
AATATTGATTGAACATCTACTCTATCAGAATTATACCAAATATAGTTCACCCAAAGAAAA
TGTTAGTGATATTAAAGCGTAGCTCCGGGGTTAAAGACATTGATGATAGCCCCACTTAAT
TTTCGACAGAAGTTAAGCCGAAAGTATTGTGAACAAAATGTGGTGGCAGAGGAATTTATT
ATTCATGATTTTATATCAAATGAATTGAAAACAGTCATTCTGGCAAAATATAAGTGGGGT
TATTATCATTTGTAAATGTTTATATTTTTATAAAACAATAGAAACTTTATGACTGGTACT
CTTTAAACAATTTTCTCTTCACTAATCTTTCAGTTCAGTTCAAAACTGTCTATTACAAAC
TAGTACTAGCTCTAATTTAAATTAAAATCCTTATTCACCAGAAACGTTTTTAGGCCTACT
ACTACTACTACTATTATTGCAATAACATCAAATGTGTTTTAAGAAAAAAAATCAGAGGTA
AAAGTAAATACATATAGCACTATTATTGGTGGTGATACTTCAGAATAGTCTTAGAAATAA
TAACAACTTTATTATACCTGAGGTAAAAAAGTGGTAGCTACCTATAGAATAATATTTAAC

A A T T A C C A G C A T A T C G T T A T T A A T A G T A A C A A G A T T T T T A T T A A A G A A A A T G A C A T A T T A
G A C A T T G T T T T A C T A C A C A T A A C A A A A A G T A T G A A G T A A C A G A A C G C A A C A A G C A T T T G G
A C A T G C A T T C A T C A C A G A C C G T A T C A T T C A C A T A C T G T A G C T A T G G A A G A C A A C A T T G G
A A G A C A G A G A G A C C A A A G A A G C A A T A T A T A A T A T T A T A A A G A A T C A C C A A A A T A C A A T A A
A G A C A A A T A A A C A C A A A G A A T T A T T G C A G T A T C A C C A T C A T C A T C A T C A T A A A T C A A T C T
T T A A A A T G A T A A A A A T A A T G A A A T A G A G A T T C T A G A T T C C T A A A T G T A A A T T T T G A G A A T
A T G C A T C T G T A A A A A T C A G T A T T T C T C T G T A T A T A T G G C T T A T G A G C T A T A C A G T A T T T A
T A G C A C G T A A C T C T G T A C A C T C T C C C T G T C C A C T C T G G C T G C T A T G A T C T C A A C A T C T T C
T G C A C C A C A G A A T A G C A A T A G A G A G C T T T C G A A A G A G G T G A G T T G G T G A T G C G A C G C G C A
A C T G A G C A T G C G G A T A C A A G A A A A C T T C T G C A G A C C G A A C G C G A T T T G A A G G A A G A T A A C
A C G A G G C T G T T T C T G A C T T G C T T G T C T C T C C T A A C C T G T A T C A C T A T T T C G T A A G C T C T C
T A T T G A A C A C C T A T A A G G G G C A A C A G C C T T C A T T A T C A A T T C T T T G T T C C A C T A A A T T C A
C A G A C T T T T C A A T T T C T T T A T C T T C T T T T T C C A G C A A G A A T C G T C C G A T A A T A T A C A T A G
CTCTTAGTACATTATCA3'

>TRINITY_DN20737_c10_g1_i2

5 ' A T T G A T T G A T A A T T A A T A T C T T T T A T A T T A A T A C G T T T A A T A T G G T A C C A T G T G A T T T G T
T T T T T G T T G A T T T T T T T T T C A G G T G A A G A C C T T T A C C A A A C C T C A T G A A A T A G T G T C A T T
G T C A G G A A C T C T T T C A C A A G A T G C A T T C C A T C T T C A T G C T T C T A T A T C A G A T G A G A A T T C
T A T G G T C T T T G G A G G T C A C G T G A T G G A G G T A A T G G A G A C G T A T A C A A C T A T A G A G C T C G T
G G T T G G T G A A C T C A A A A G C C T G A A A T T T A C A A G A G A A T T T G A C T C G A G T T C T G G A T A C A A
G G A G C T T G T C A T A C G A A A C A G A G A A C A A T C A T C T A C T A C A A C A G A T A C A T A A T G A T A T T G
T C T G T G A G T T A A C A A C A C T A A T A A T T G G T A T T A T A A A G C A T A T C T T G T A T A G A C A C T A C A
G T G C G T A A C A A G A T A T G G T A T G C C C A A A G A G G T T A T A T A A T A A A T A G C G A C C A T T T T G T G
G A G A C T T C G C T C T C G T C T A G T T A C C C C T G T A G T T A A T T A T A T A A C C T C T T T G T G G T A T T A
T A T G C T G T A C A A C A A G A C A A T A T A C T G T A C A A C A A A A A T C T A A T T T T A T T A A A T T T C T A
C T T T C T A A A T A G T A T A A T T G T A G A A G T G T T T A A C T A A C A C C C G G G T T T T A T T T T G A A A C G
A C G C C T C T T C A G T T T T T G A G C A A T G T C A A A C A T T T T C T G T G A T G T C T G A G G T A G A G A A A A
G G G G T A A T A T T G G G T A A T A T T T T A T C T C T T A A A A T A G G C C T A A A C A T G C A C A G A G C T A G G
C T C T T T C T A C A C T A T C A A A C A A A A T G T G A C A A A A A A T G T G A T G A T G A T G A T G T C A T A T C A
C T A C C A C C A T A T T G G G G C A C A T C A C A C T T T C A T C A G T A A T C T G C C C T C T A T T C C A T A A A T
T A A T G A A A A A A C T A G A T G T T T G A A G A A G G T T T T C A A T C T T T T G T G A G T A G C T A T A A A T G
A A T G A A A G T G A G T T G A A C A G T G A T T A C A T A T G T G C A T G G C T T C T G A T A T T A G T G C C A T A G
T A T T C T T C A T A T T C A G C A C A T A C T C A C T A A T T G T A A A T A A T G T G T A C A T T A C A G T T T A T A
CACTATTTATATGTATTACAATAGTTG3'

Conclusion

MBL2 genes and MASP1 genes which initiate the Complement Lectin Pathway are present in two classes of *Echinodermata* (Ophuirids and Crinoïds) with a high significant e-value, a significant identity.Is this pathway functional? We think so, but, it has to be demonstrated at the level of future researchs.

Bibliography

1. Leclerc M. "Complement Genes in the Asterids Comparisons with the Echinids (Echinoderma)". *American Journal of Immunology* 9.1 (2013): 26-29.

2. Leclerc M.. *et al*. "Evidence of Complement Genes in the Crinoïd:antedon Bifida. Comparisons with other Echinodermata". *International Journal of Biotechnology and Bioengineering* 4.1 (2018): 7-10.

3. Leclerc M., *et al*. "Evidence of Complement Genes in the Crinoïd: Antedon Bifida. Comparisons with other Echinodermata". *Archives of Immunology and Allergy* 1.1 (2018): 6-7.

4. Grabherr MG., *et al*. "Full-length transcriptome assembly from RNA-Seq data without a reference genome". *Nature Biotechnology* 29 (2011): 644-652.

5. Altschul SF., *et al*. "Basic local alignment search tool". *Journal of Molecular Biology* 215.3 (1990): 403-410.

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