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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.*

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). 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 (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

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

Table 1. *summarizes the obtained results with first Ophuirids*

Query ID	Query Name	SubjectID	Identity (%)	Length	Mis match	Gap open	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

The transcriptomes of MBL2 and MASP1 genes are the following:

TRINITY_DN15627_c0_g1_i1

5’GTTGAAATTAAATATAAAAATATAAACCAGAACTACTAGCAAAGCTCTGAGCAAGTTGCA

TCTACCTGGATGCAATTGTGTTGTTAGCTTTCAACAGGCTGATATTATACCCAATCTATT

CCCATATTTAAAAGCAGTGACCTGGCTATATCATACGCAGCACATTGTAGGGTATTCTCT

TCAAAATGCAGAGAAAGAAAATATGAATAAATAAAATATGATTTCAATTTTCAGCAGCAT

ACCACAAGTTATTTTTTCTACTGTAGAGATACAATATCAATCATCATCTTGTTTCTACA3’

>TRINITY_DN55866_c0_g1_i1

5’TATCAAACTTGAAAACTAGTAAAATATTCACTAGTTTTTAACGCCATTCAATCAATAGCC

AGTCTGGTGTCCATCGGACGTTTATTGTTTGACATTTAAAAACAGTCGAGATAAGTGTTA

AAATTCGAAAGAAAATCATGAAAAAAAAATGTATGTGACACTGAAAAAAACACCACTTTC

TTAAGTATTGATTATAAATAATGCGTAATAATTTTTTAACAAAAATCTAAATAATAAAAT

CTAAACAACTAGATCATTGAAGAATTAATCAAAATGGAATAAATAAAATAAATAAAAAGA

TTACCGTATTAAAAGTACAAAATAGTAAATATGAG3’

Table 2. *Appropriate sequences concerning the transcriptomes of Crinoïds genes are following*

Query ID	Query Name	SubjectID	Identity (%)	Length	Mis match	Gap open	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

>TRINITY_DN19440_c3_g1_i1

5’AAATAATATATTTGGAGGGTCACCCTTATCTATACTCTAAATATATAACTATAATTAATA

TAATTTTGTACAAAATAAATAATTTATCTATATAGTATTAATTTACAATAGTTTTTATTT

ATATAATTATCAAAACCTATAAAATATACAATAGTTGATCACCTATATATACATAAAATC

CATTATTATTGCACACATTCTGTTTAAACTCTCAAACAAGTCCATATAAATACATTTTCA

AATATTGATTGAACATCTACTCTATCAGAATTATACCAAATATAGTTCACCCAAAGAAAA

TGTTAGTGATATTAAAGCGTAGCTCCGGGGTTAAAGACATTGATGATAGCCCCACTTAAT

TTTCGACAGAAGTTAAGCCGAAAGTATTGTGAACAAAATGTGGTGGCAGAGGAATTTATT

ATTCATGATTTTATATCAAATGAATTGAAAACAGTCATTCTGGCAAAATATAAGTGGGGT

TATTATCATTTGTAAATGTTTATATTTTTATAAAACAATAGAAACTTTATGACTGGTACT

CTTTAAACAATTTTCTCTTCACTAATCTTTCAGTTCAGTTCAAAACTGTCTATTACAAAC

TAGTACTAGCTCTAATTTAAATTAAAATCCTTATTCACCAGAAACGTTTTTAGGCCTACT

ACTACTACTACTATTATTGCAATAACATCAAATGTGTTTTAAGAAAAAAAATCAGAGGTA

AAAGTAAATACATATAGCACTATTATTGGTGGTGATACTTCAGAATAGTCTTAGAAATAA

TAACAACTTTATTATACCTGAGGTAAAAAAGTGGTAGCTACCTATAGAATAATATTTAAC

AATTACCAGCATATCGTTATTAATAGTAACAAGATTTTTATTAAAGAAAATGACATATTA

GACATTGTTTTACTACACATAACAAAAAGTATGAAGTAACAGAACGCAACAAGCATTTGG

ACATGCATTCATACACAGACCGTATCATTCACATACTGTAGCTATGGAAGACAACATTGG

AAGACAGAGAGACCAAAGAAGCAATATATAATATTATAAAGAATCACCAAAATACAATAA

AGACAAATAAACACAAAGAATTATTGCAGTATCACCATCATCATCATCATAAATCAATCT

TTAAAATGATAAAAATAATGAAATAGAGATTCTAGATTCCTAAATGTAAATTTTGAGAAT

ATGCATCTGTAAAAATCAGTATTTCTCTGTATATATGGCTTATGAGCTATACAGTATTTA

TAGCACGTAACTCTGTACACTCTCCCTGTCCACTCTGGCTGCTATGATCTCAACATCTTC

TGCACCACAGAATAGCAATAGAGAGCTTTCGAAAGAGGTGAGTTGGTGATGCGACGCGCA

ACTGAGCATGCGGATACAAGAAAACTTCTGCAGACCGAACGCGATTTGAAGGAAGATAAC

ACGAGGCTGTTTCTGACTTGCTTGTCTCTCCTAACCTGTATCACTATTTCGTAAGCTCTC

TATTGAACACCTATAAGGGGCAACAGCCTTCATTATCAATTCTTTGTTCCACTAAATTCA

CAGACTTTTCAATTTCTTTATCTTCTTTTTCCAGCAAGAATCGTCCGATAATATACATAGCTCTTAGTACATTATCA3’

>TRINITY_DN20737_c10_g1_i2

5’ATTGATTGATAATTAATATCTTTTATATTAATACGTTT AATATGGTACCATGTGATTTGT

TTTTTGTTGATTTTTTTTTCAGGTGAAGACCTTTACCAAACCTCATGAAATAGTGTCATT

GTCAGGAACTCTTTCACAAGATGCATTCCATCTTCATGCTTCTATATCAGATGAGAATTC

TATGGTCTTTGGAGGTCACGTGATGGAGGTAATGGAGACGTATACAACTATAGAGCTCGT

GGTTGGTGAACTCAAAAGCCTGAAATTTACAAGAGAATTTGACTCGAGTTCTGGATACAA

GGAGCTTGTCATACGAAACAGAGAACAATCATCTACTACAACAGATACATAATGATATTG

TCTGTGAGTTAACAACACTAATAATTGGTATTATAAAGCATATCTTGTATAGACACTACA

GTGCGTAACAAGATATGGTATGCCCAAAGAGGTTATATAATAAATAGCGACCATTTTGTG

GAGACTTCGCTCTCGTCTAGTTACCCCTGTAGTTAATTATATAACCTCTTTGTGGTATTA

TATGCTGTACAAACAAGACAATATACTGTACAACAAAAATCTAATTTTATTAAATTTCTA

CTTTCTAAATAGTATAATTGTAGAAGTGTTTAACTAACACCCGGGTTTTATTTTGAAACG

ACGCCTCTTCAGTTTTTGAGCAATGTCAAACATTTTCTGTGATGTCTGAGGTAGAGAAAA

GGGGTAATATTGGGTAATATTTTATCTCTTAAAATAGGCCTAAACATGCACAGAGCTAGG

CTCTTTCTACACTATCAAACAAAATGTGACAAAAAATGTGATGATGATGATGTCATATCA

CTACCACCATATTGGGGCACATCACACTTTCATCAGTAATCTGCCCTCTATTCCATAAAT

TAATGAAAAAAACTAGATGTTTGAAGAAGGTTTTCAATCTTTTGTGAGTAGCTATAAATG

AATGAAAGTGAGTTGAACAGTGATTACATATGTGCATGGCTTCTGATATTAGTGCCATAG

TATTCTTCATATTCAGCACATACTCACTAATTGTAAATAATGTGTACATTACAGTTTATA

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.

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