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

Michel Leclerc¹, Ariane Jolly² and Pierre de la Grange²

¹Immunology of Invertebrates, Orleans University (France)
²Genosplice, Paris (France)

*Corresponding Author: Michel Leclerc, Immunology of Invertebrates, Orleans University (France)

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 nigra (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:

<table>
<thead>
<tr>
<th>QueryID</th>
<th>Query Name</th>
<th>SubjectID</th>
<th>Identity (%)</th>
<th>Length</th>
<th>Mismatch</th>
<th>Gapopen</th>
<th>Query cover</th>
<th>E-value</th>
<th>Bitscore</th>
</tr>
</thead>
<tbody>
<tr>
<td>NM_000242.2</td>
<td>MBL2</td>
<td>TRINITY_DN15627_c0_g1_i1</td>
<td>100</td>
<td>22</td>
<td>0</td>
<td>0</td>
<td>1</td>
<td>2.30E-02</td>
<td>41.7</td>
</tr>
<tr>
<td>NM_001031849.2</td>
<td>MASP1</td>
<td>TRINITY_DN55866_c0_g1_i1</td>
<td>95.65</td>
<td>23</td>
<td>1</td>
<td>0</td>
<td>1</td>
<td>2.00E-01</td>
<td>38.1</td>
</tr>
</tbody>
</table>

Table 1

The transcriptomes of MBL2 and MASP1 genes are the following

TRINITY_DN15627_c0_g1_i1
5’GTTGAAATATAATATAAAAATATAAAAAGCACATGCTGCTAGCTAGTTC
TGCA
TCTAATCTGGACATTGTTTGTGGTTAAGTT
TCCAATGCTGATATATACCCCATCCTATT
CCCATTTCAGCAGTGACCTGGCTA

ATCATACTCAGCAGCAATTGTAGGGATTTCTCT
TCGTAAGGAAAGAAAGAAATATGAAT
AAATAATAATGTATTTCAATTTCATCGAGCAT
AAGAAAGAAAGAAATATGAAT
AAATAATAATGTATTTCAATTTCATCGAGCAT
AAGAAAGAAAGAAATATGAAT
AAATAATAATGTATTTCAATTTCATCGAGCAT
AAGAAAGAAAGAAATATGAAT
AAATAATAATGTATTTCAATTTCATCGAGCAT
AAGAAAGAAAGAAATATGAAT
AAATAATAATGTATTTCAATTTCATCGAGCAT
AAGAAAGAAAGAAATATGAAT
AAATAATAATGTATTTCAATTTCATCGAGCAT
AAGAAAGAAAGAAATATGAAT
AAATAATAATGTATTTCAATTTCATCGAGCAT
AAGAAAGAAAGAAATATGAAT
AAATAATAATGTATTTCAATTTCATCGAGCAT
AAGAAAGAAAGAAATATGAAT
AAATAATAATGTATTTCAATTTCATCGAGCAT
AAGAAAGAAAGAAATATGAAT
AAATAATAATGTATTTCAATTTCATCGAGCAT
AAGAAAGAAAGAAATATGAAT
AAATAATAATGTATTTCAATTTCATCGAGCAT
AAGAAAGAAAGAAATATGAAT
AAATAATAATGTATTTCAATTTCATCGAGCAT
AAGAAAGAAAGAAATATGAAT
AAATAATAATGTATTTCAATTTCATCGAGCAT
AAGAAAGAAAGAAATATGAAT
AAATAATAATGTATTTCAATTTCATCGAGCAT
AAGAAAGAAAGAAATATGAAT
AAATAATAATGTATTTCAATTTCATCGAGCAT

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.

ABSTRACT


Keywords: Echinodermata; Invertebrates; Complement; Lectin Pathway
The Complement System in Echinodermata. A Third Pathway: A Lectin Pathway

<table>
<thead>
<tr>
<th>QueryID</th>
<th>Query Name</th>
<th>SubjectID</th>
<th>Identity (%)</th>
<th>Length</th>
<th>Mismatch</th>
<th>Gapopen</th>
<th>Query cover</th>
<th>E-value</th>
<th>Bitscore</th>
</tr>
</thead>
<tbody>
<tr>
<td>NM_000242.2</td>
<td>MBL2</td>
<td>TRINITY_DN19440_c3_g1_i1</td>
<td>100</td>
<td>23</td>
<td>0</td>
<td>0</td>
<td>1</td>
<td>7.00E-03</td>
<td>43.6</td>
</tr>
<tr>
<td>NM_001031849.2</td>
<td>MASP1</td>
<td>TRINITY_DN20737_c10_g1_i2</td>
<td>92</td>
<td>25</td>
<td>2</td>
<td>0</td>
<td>1</td>
<td>7.80E-01</td>
<td>36.2</td>
</tr>
</tbody>
</table>

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

<table>
<thead>
<tr>
<th>QueryID</th>
<th>Query Name</th>
<th>SubjectID</th>
<th>Identity (%)</th>
<th>Length</th>
<th>Mismatch</th>
<th>Gapopen</th>
<th>Query cover</th>
<th>E-value</th>
<th>Bitscore</th>
</tr>
</thead>
<tbody>
<tr>
<td>NM_000242.2</td>
<td>MBL2</td>
<td>TRINITY_DN19440_c3_g1_i1</td>
<td>100</td>
<td>23</td>
<td>0</td>
<td>0</td>
<td>1</td>
<td>7.00E-03</td>
<td>43.6</td>
</tr>
<tr>
<td>NM_001031849.2</td>
<td>MASP1</td>
<td>TRINITY_DN20737_c10_g1_i2</td>
<td>92</td>
<td>25</td>
<td>2</td>
<td>0</td>
<td>1</td>
<td>7.80E-01</td>
<td>36.2</td>
</tr>
</tbody>
</table>

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

<table>
<thead>
<tr>
<th>QueryID</th>
<th>Query Name</th>
<th>SubjectID</th>
<th>Identity (%)</th>
<th>Length</th>
<th>Mismatch</th>
<th>Gapopen</th>
<th>Query cover</th>
<th>E-value</th>
<th>Bitscore</th>
</tr>
</thead>
<tbody>
<tr>
<td>NM_000242.2</td>
<td>MBL2</td>
<td>TRINITY_DN19440_c3_g1_i1</td>
<td>100</td>
<td>23</td>
<td>0</td>
<td>0</td>
<td>1</td>
<td>7.00E-03</td>
<td>43.6</td>
</tr>
<tr>
<td>NM_001031849.2</td>
<td>MASP1</td>
<td>TRINITY_DN20737_c10_g1_i2</td>
<td>92</td>
<td>25</td>
<td>2</td>
<td>0</td>
<td>1</td>
<td>7.80E-01</td>
<td>36.2</td>
</tr>
</tbody>
</table>
The Complement System in Echinodermata. A Third Pathway: A Lectin Pathway?

CONCLUSION

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

REFERENCES