

Short Commentary

HLA-E Gene from *Ophiocomina Nigra* (Echinodermata-Invertebrates): Bioinformatics Data

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ABSTRACT

HLA-E gene from MHC system has been recently discovered, in our laboratory, in Invertebrates. Blasts were performed against different species to find or not homologies. Results were given in the precedent communication.

INTRODUCTION

In 2020, we discovered for the first time, MHC genes in Invertebrates and particularly in Echinodermata [1,2]. More recently, in 2022 a biosynthesis of HLA-E (Class I, MHC) gene from *O. nigra* was performed [3].

The aim of this work is to analyze HLA-E DNA sequence.

MATERIAL AND METHODS

Starting material: DNA sequence of HLA-E transcriptome

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TGTAATCCCAGCACTTTGGGAGGCCGAGGCGGGCGG
GATCACGAGGTCAGGAGATCGAGACCATCCTGGCT
AACACAGTCAAACCCCGTCTCTACTAAAAATACAA
AAAATTAGCCGGGCGTGGTGGCGGGCGCCTGTAGT
CCCAGCTACTCGGGAGGCTGAGGCAGGAGAATGGC
GTGAACCCGGGAGGCGGAGCTTGCAGTGAGCCGAG
ATCGCGCCACTGCACTCCAGCCTGGGCGACAGAGC
GAGACTCTGTCTCAAAAAAAAAAAAAAAAAAAAAAA
AA
```

RESULTS AND CONCLUSION

1. Blastn original sequence

Database: Standard databases were used

We also optimize for: Highly similar sequences (mega blast)

We recall that Molecule type is DNA

Its query length is 281

We find more than 100 sequences producing significant alignments.

First results appear in the table below **Table 1**.

2. BlastX original sequence: The_Molecule type is again DNA with a query length of 281

The Database which is used consists in: non-redundant protein sequences (nr)

We obtain more than 100 sequences producing significant alignments

The table is recapitulated as following in **Table 2**.

CONCLUSION

Results summarized in the tables show homologies between the *Ophiocomina nigra* HLA-E gene and various proteins issued from *Staphylococcus aureus* to human Chromosome 13 which is sometimes implicated in human trisomy We note also a strong homology with *Macaca fascicularis*: 91,86% of identity.

Mainly we retain that *O. nigra* HLA-E gene exists in “its own right” and in its amplification in plasmid [3].

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Table 1. Results of Blastn original sequence.

Description	Scientific name	Max score	Total score	Query cover	E. Value	Per. Ident	Acc Len	Accession
Pan troglodytes' chromosomes unknown clone CH251-153M19, complete sequence	Pan troglodytes	514	9982	100%	2e-141	99.64%	184578	AC280142.1
Pan troglodytes BAC clone CH251-501A13 from chromosomes unknow, complete sequence	Pan troglodytes	514	10636	100%	2e-141	99.64%	181275	AC185293.4
Homo sapiens clone RP11-92L24 from 2 from chromosomes unknow, complete sequence	Homo sapiens	514	2329	100%	9e-141	99.64%	137248	AC019051.8
Eukaryotic synthetic construct chromosome 13	Homo sapiens	508	1.314e+06	100%	9e-140	99.29%	96089878	CP034516.1

Table 2. Recapitulated of BlastX original sequence.

Description	Scientific name	Max score	Total score	Query cover	E. Value	Per. Ident	Acc Len	Accession
Hypothetical protein EGM_09670	<i>Macaca fascicularis</i>	149	149	91%	1e-44	91.86%	89	EHH59533.1
hCG2030582	Homo sapiens	135	135	90%	5e-39	83.53%	102	EAW48014.1
Low quality protein: histone demethylase UTY	<i>Chlorocebus sabaesus</i>	129	219	91%	7e-36	87.50%	166	XP_037863302.1
Hypothetical protein CRU82_14500	<i>Staphylococcus aureus</i>	124	124	71%	7e-35	92.54%	72	PGG78133.1

REFERENCES

1. Leclerc M (2020) Evidence of MHC Class I and Class II Genes in Echinodermata. *Proteomics Bioinformatics* 2(1): 59-61
2. Leclerc M (2021) Biosynthesis « De Novo » of the Ophurid *Ophiocomina Nigra* Igkappa Gene. *J Clin Class Immunol* 1(1): 1-4.
3. Leclerc M (2022) to be published.