



Hla-E Gene from Ophiocomina Nigra (Echinodermata-Invertebrates) Bioinformatics Data

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Short Communication

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Abstract

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

Keywords: Chromosome; Homologies

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 (ClassI, 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 Transcript to me

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TGTAATCCCAGCACTTTGGGAGGCCGAGGCGGGCGGATCACGAGGTCAGGAG
ATCGAGACCATCCTGGCTAACACAGTGAACCCCGTCTCTACTAAAAATACA
AAAAATTAGCCGGCGTGGTGGCGGGCCCTGTAGTCCAGCTACTCGGGAG
GCTGAGGCAGGAGAATGGCGTGAACCCGGGAGGCGGAGCTTGCACTGAGCCG
AGATCGGCCACTGCACTCCAGCCTGGGCGACAGAGCGAGACTCTGTCTCAA
AAAAAAAAAAAAAAAAAAAA
```

Results and conclusion

Blastn Original Sequence:

Data base: Standard data bases 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

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 chromosome unknown clone CH251-153M19, complete sequence	Pan troglodytes	514	9982	100%	2.00E-141	99.64%	184578	AC280142.1
Pan troglodytes BAC clone CH251-501A13 from chromosomes unknown, complete sequence	Pan troglodytes	514	10636	100%	2.00E-141	99.64%	181275	AC185293.4
Homo sapiens clone RP11-92L24 from 2 from chromosomes unknow, complete sequence	Homo sapiens	514	2329	100%	9.00E-141	99.64%	137248	AC019051.8
Eukaryotic synthetic construct chromosome 13	Homo sapiens	508	1.31E+06	100%	9.00E-140	99.29%	96089878	CP034516.1

Table 1: Blastn original sequence.

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:

Description	Scientific Name	Max score	Total score	Query cover	E. Value	Per. Ident	Acc Len	Accession
Hypothetical protein EGM_09670 [Macaca fascicularis]	Macaca fascicularis	149	149	91%	1.00E-44	91.86%	89	EHH59533.1
hCG2030582 [Homo sapiens]	Homo sapiens	135	135	90%	5.00E-39	83.53%	102	EAW48014.1
Low quality protein: histone demethylase UTY [Chlorocebus sabaeus]	Chlorocebus sabaeus	129	219	91%	7.00E-36	87.50%	166	XP_037863302.1
hypothetical protein CRU82_14500 [Staphylococcus aureus]	Staphylococcus aureus	124	124	71%	7.00E-35	92.54%	72	PGG78133.1

Table 2: BlastX original sequence.

Conclusion

Results summarized in the 2 Tables show homologies between the *Ophiocoma nigrum* HLA-E gene and various proteins which lead to human Chromosome 13. This chromosome is sometimes implicated in human trisomy. We note also a strong homology with *Macaca fascicularis*: 91,86% of identity with the: Hypothetical protein: EGM 09670. Mainly we retain that *O. nigrum* HLA-E gene exists in "its own right" and can be amplified in plasmid PUC-GW-Kan.

References

1. Leclerc M (2020) Proteomics Bioinformatics 2(1): 59-61.
2. Leclerc M (2021) Biosynthesis « De Novo » of the Ophiurid *Ophiocoma Nigrum* Igkappa Gene. J Clin Class. Immunol 1(1): 1-4.

