

Comparisons Between 3 Invertebrates Igkappa Genes : From the Less Evolved to the Most One. Bioinformatic Data.

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Abstract

We attempt to establish, in the present paper, comparisons between 3 classes of Echinodermata (Asterids, Ophuirids, Crinoïds) out of 5 classes, at the level of genomes.

Mainly we compare the IGKappa genes of these 3 classes which belong to Invertebrates.

The Ophuirid IGKappa gene from *Ophiocomina nigra* seems to be the most evolved, in terms of immune functions, when compared to the two other ones.

Keywords: Invertebrates; Echinodermata; Immunoglobulins; Evolution

Introduction:

We recall that biosynthesis of 3 IGKappa genes have been performed [1, 2, 3]. They belong to Echinodermata, first Asterids with *Asterias rubens* as a model of study in 2014, second Ophuirids (*Ophiocomina nigra*) and Crinoïds (*Antedon bifida*) in 2021 [2, 3].

We try now to compare them.

Methods:

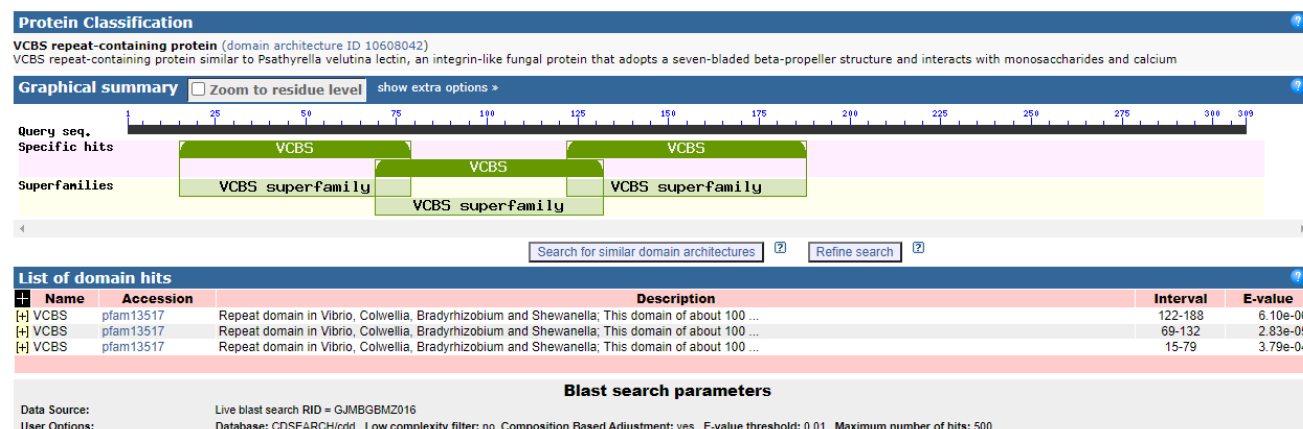
We performed bioinformatic assays according to the method of Marchler-Bauer [4,5] (by the use of various blasts directed against Vertebrate IG genes).

Results:

1) *Antedon bifida* (Crinoïds)

BlastP of the two predicted amino acids sequences

Conserved domains on:





2) Asterias rubens: Two region features as shown below (Fig.1)

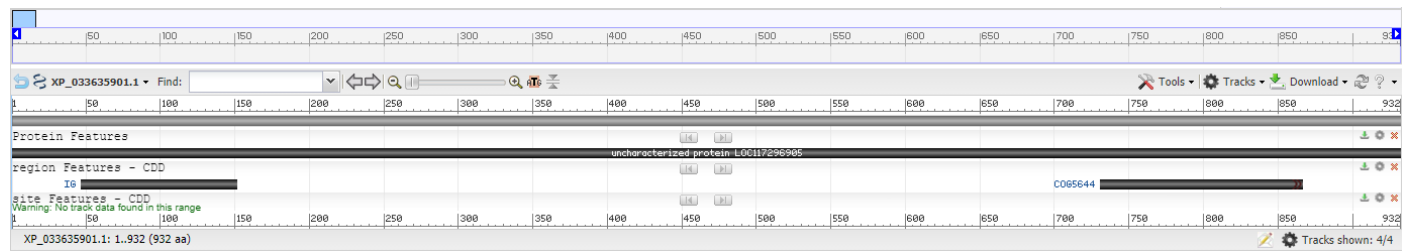


Fig.1. Predicted: Asterias rubens uncharacterized LOC117296905 (LOC117296905)

Two region features:

- | | |
|-----------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------|
| <p>a. Region Ig Comment: Immunoglobulin Location: 47...151 Length: 105 aa CDD: 214652</p> | <p>b. COG5644 Comment: U3 small nucleolar RNA-associated protein 14 (function unknown) Location: 731...866 Length: 136 aa CDD: 227931</p> |
|-----------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------|

3) Ophiocomina nigra: 2 Immunoglobulin domains as seen below (Fig.2)

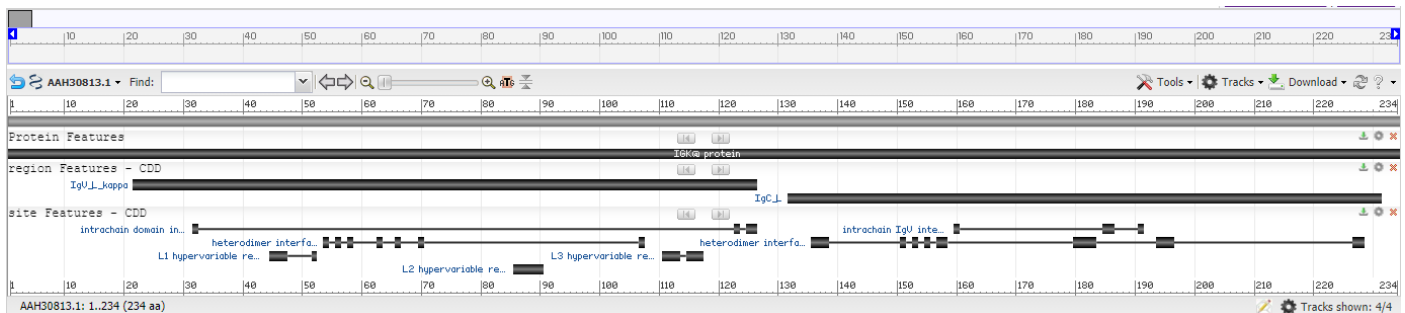


Fig.2: IGHK @ protein [Homo sapiens] graphic by NCBI [Ref]

GenBank: AAH30813.1

The AAH30813.1 protein has two immunoglobulin domains:

- c. Region 1
Region: IgV_L_kappa
Comment: Immunoglobulin (Ig) light chain, kappa type, Variable (V) domain
Location: 22...126
Length 105 aa
1. Region 2
Region: IgC_L
Comment: Immunoglobulin constant domain
Location: 132...231
Length 100 aa

Conclusion, Discussion:

As previously described, we observe something which recalls as an evolution between these 3 Echinodermata (Invertebrates):

- 1) Antedon bifida (Crinoids)
- 2) Asterias rubens (Asterids)

3) Ophiocomina nigra (Ophurids)

The Antedon bifida IGHKappa gene with its two predicted amino-acids sequence presents no Immunoglobulin site; the Asterias rubens IGHKappa gene: 1 Immunoglobulin Domain; the Ophiocomina nigra IGHKappa gene: 2 Immunoglobulin Domains at the level of constant part and the variable part of Immunoglobulins (entiere homology with human IGHK) [6]. At our knowledge it seems highly important to give that data in terms of emergence of Immunoglobulins in Invertebrates when compared to Vertebrates.

References:

- 1) Vincent N, Osteras M, Otten P, Leclerc M. (2014). A new gene in A. rubens: A sea star Ig kappa gene. Meta gene 2: 320-322.
- 2) Leclerc M. (2021). Biosynthesis « De Novo » of the Ophurid Ophiocomina Nigra Ighkappa Gene. J Clin Class Immunol. 1(1).
- 3) Leclerc M (2021) Acad J Clin Health Rep Med Sci.



4) Marchler-Bauer A, Lu S, Anderson JB, Chitsaz F, Derbyshire MK, et al. (2011) CDD: a Conserved Domain Database for the functional annotation of proteins. *Nucleic Acid Res.* 39(D): 225-229.

5) Marchler-Bauer A, Bo Y, Han L, He J, Lanczycki CJ, et al. (2017) CDD/SPARCLE: functional classification of proteins via subfamily domain architectures. *Nucleic Acid.Res.* 45(D): 200-203.

6) Leclerc M (2021) Genomic submitted.