

Short Commentary

Fc Receptor Genes in *Asterias Rubens* (Echinodermata) when Compared to Mammals

Michel Leclerc*

*556 rue Isabelle Romée, 45640 SANDILLON, Immunology of Invertebrates, France.

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ABSTRACT

The Fc receptor gene of *Asterias rubens* (Echinodermata, Invertebrates) present at least 33 % identities with 7 Fc receptor Mammal genes by using the following method of Compositional matrix adjust. The e-values are highly significative.

Keywords: *Asterias Rubens*, Invertebrates, Fc receptor gene, Mammal Fc genes

INTRODUCTION

In 2016, we have isolated the *Asterias rubens* Fc receptor gene [1]. It was the first time such discovery, in Invertebrates was performed.

In the present work we analyzed the identities between this gene and mammal Fc receptor genes by the use of Compositional matrix adjust [2] and blasts against mammal's protein.

The *A. rubens* starting material (DNA sequence in 5'-3') is the following:

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TCCATTAGGGCAATGAGTGGGACTGCGCGGCTTGG
CACAGATCATCCCTTTTCTATCACGACACCTCGAGT
CTTTCCACTTGCCGTTGCTAATCTGTAATGCCACAC
AGTTATTCTCCAATGATTGACTCCAGACAGCTCAG
TTTGCTCTTCTTCGATGAAGTTCGTGTAGTTGACGG
GGGAATCGTTTGACCAATTTCCAATCGCTTTCGTTGT
GTGTATCATGGAGCCCGATCCACACGTCCTGTCA
TTAGTTCGGTAAGAAAATCATTAAATTTCTGGTCAG
TGATGGCGACCAGCCTAGCGCCGTCGTATTTAGTGC
ACTTCTGTTCAGCATCGACCCAGCGTGCTACATCGT
CTGGAATCCAGAAGCATTTCATCACGGAAGAGATGG
CCGTTGTTTAGGCAGTACTGTGGTTGACCACGTA
GTTTGAAGAAGATGAGCTGACCCAATAACCATCAT
CATCACGAATGGAATCATTGTGAATTTGTTTGAGAT
ACGTCGGATACGTCCTGTCCTAGATGAAAAAATG
CCGAAGTCTCTCACATAATTCACCAGGCATTGTTG
ATGCCTTGCTGCTATGGTTGATGCTTGGTGCCAG
TCCACGAAAGAATGTGCAGTTAGGGAAAGTCCAGC
TTGTATATCTC
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RESULTS

7 Fc mammal sequences which present high identities with ours [1] are given now with their characteristics:

1) **Predicted:** low affinity immunoglobulin epsilon Fc

receptor [*Dipodomys ordii*]

Sequence ID: XP_012889053.1 Length: 306

Range 1: 172 to 296

Score: 77.8 bits (190), Expect: 7e-13,

Method: Compositional matrix adjust.,

Identities: 43/131(33%), Positives: 69/131(52%), Gaps: 13/131(9%)

Query 387
FRDECFWIPDDVARWVDAEQKCTKYD GARLVAITDQ
EINDFLDLDIRDVWIGLHDTHNE 208

F+ +C++ + RW+ A C+ +G RLV+I QE DFL+ + +D WIGL
D E

Subject 172 FQKCYFEGEGTKRWLQARFACSDLEG-
RLVSIHSQEEQDFLSKHVSKDAWIGLQDL DVE 230

Query 207
SDWKWSNDSPVNYTNFIEEEQTELSGVESLENNCVL
QISNGKWKDSRCRDR-----K 49

++ W + SPV+Y+N+++ E E +CV ++ S G W D+ CR +
+

Subject 231
GEFVWMDGSPVSYSNWLQGEPPNAGSDE----
DCVMMRGS-GHWNDAFCRSQDLDTWVCER 285

Corresponding author: Michel Leclerc, 556 rue Isabelle Romée, 45640 Sandillon, France, Tel: +92219926130; E-mail: mleclerc45@gmail.com

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Query 48 GMICAKPRSPT 16.....C P PT
 Subject 286 LATCGPPALPT 296

2) Low affinity immunoglobulin epsilon Fc receptor [Dipodomys spectabilis]

Sequence ID: XP_042549638.1 Length: 306
 >low affinity immunoglobulin epsilon Fc receptor [Dipodomys spectabilis]

Sequence ID: XP_042549639.1 Length: 306
 >low affinity immunoglobulin epsilon Fc receptor [Dipodomys spectabilis]

Sequence ID: XP_042549640.1 Length: 306
 Range 1: 172 to 296

Score: 77.8 bits (190), Expect: 8e-13,
 Method: Compositional matrix adjust.,
 Identities: 43/131(33%), Positives: 69/131(52%), Gaps: 13/131(9%)

Query 387
 FRDECFWIPDDVARWVDAEQKCTKYD GARLVAITDQ
 EINDFLDLDLRD V WIGLH DTHNE 208

F+ +C++ + RW+ A C+ +G RLV+I QE DFL+ +
 +D WIGL D E

Sbjct 172 FQKCYFFGEGTKRWLQARFACSDLEG-
 RLVSISHQEEQDFLSKHVSKDAWIGLQDL DVE 230

Query 207
 SDWKWSNDSPVNYTNFIEEEQTELSGVESLENNCVAL
 QISNGKWKDSRCRDR-----K 49

++ W + SPV+Y+N+++ E E +CV ++ S G W
 D+ CR + +

Subject 231
 GEFVWMDGSPVSYSNWLQGE PNNAGSDE----
 DCVMMRGS-GHWND AF CRSQLDTWVCER 285

Query 48 GMICAKPRSPT 16
 C P PT

Subject 286 LATCGPPA

3) Low affinity immunoglobulin epsilon Fc receptor [Microtus ochrogaster]

Sequence ID: XP_005371819.1 Length: 172
 Range 1: 27 to 147

Score: 72.0 bits (175), Expect: 1e-11,
 Method: Compositional matrix adjust.,
 Identities: 42/127(33%), Positives: 67/127(52%), Gaps: 7/127(5%)

Query 408
 CLNNGHLFRDECFWIPDDVARWVDAEQKCTKYDGA
 RLVAITDQEINDFLDLDLRD V WIG 229

C N F+ +C++ +D RW+ A C+ G RLV+I QE +FL
 ++D WIG

Subject 27
 CPKNWLHFQKCYFFGND SKRWI QARFTCS DLKG-
 RLVSISHQEEQNFLMKHTNKDSWIG 85

Query 228
 LHDTHNESDWKWSNDSPVNYTNFIEEEQTELSGVESL
 ENNCVALQISNGKWKDSRCRDR 52

L D + E ++ W + SPV Y+N+ E E +CV ++ S
 G+W D+ C

Subject 86
 LRDLNVEGEFIWMDGSPVGYSNWSPGEPNNAGQGE--
 --DCVMMRGS-GQWND AF CHSFL 140

Query 51 KGMICAK 31
 +G +C +

Subject 141 EGWVCEQ 147

4) Low affinity immunoglobulin epsilon Fc receptor-like, partial [Nannospalax galili]

Sequence ID: XP_008853602.1 Length: 154
 Range 1: 11 to 122

Score: 71.2 bits (173), Expect: 2e-11,
 Method: Compositional matrix adjust.,
 Identities: 42/118(36%), Positives: 61/118(51%), Gaps: 6/118(5%)

Query 408
 CLNNGHLFRDECFWIPDDVARWVDAEQKCTKYDGA
 RLVAITDQEINDFLDLDLRD V WIG 229

C N F+ +C++ +W+ A+ C+ G +LV+I QE DFLT
 I D WIG

Subject 11
 CPKNWLNFQKCYFFGKGSKQWIQAKFTCSNLKG-
 QLVSISHQEEQDFLTKHIKEDSWIG 69

Query 228
 LHDTHNESDWKWSNDSPVNYTNFIEEEQTELSGVESL
 ENNCVALQISNGKWKDSRCRDR 55

L D E ++ W +DSPV Y+N+ E E +CV + S
 G+W D+ CR

Sbjct 70
 LRDLFTEGEFVWMDDSPVGYSNWNPGE PNNGGQGE-
 ---DCVMMWGS-GQWND AF CR 122

5) Fc fragment of IgE receptor II [Rhinolophus ferrumequinum]

Sequence ID: KAF6306204.1 Length: 290

Range 1: 169 to 284

Score: 73.2 bits (178), Expect: 3e-11,

Method: Compositional matrix adjust.,

Identities: 42/119(35%), Positives: 69/119(57%), Gaps: 5/119(4%)

Query 387
FRDECFWIPDDVARWVDAEQKCTKYD GARLVAITDQ
EINDFLD LIDR-DVWIGLH DTHN 211

F+ +C++ + RW+ A C+K G RLV+I QE DFL I R
WIGL D +

Subject 169 FQRKCYFGE GAKRWIQARLACSKLQG-
RLVSIHSQEEQDFLAKSIHRRG SWIGLRDLNI 227

Query 210
ESDWKWSNDSPVNYTNFIEEEEQTELSGVESLENNCVA
LQISNGKWKDSRCRDR-KGMIC 37

E D+ W +++P++Y+N+ E + G L +CV + +S+G+W
D+ C ++ G +C

Subject 228 EGDVWMDENPLDYSNWRPGEPN-
GGERGLGEDCVMM-LSSGQW NDAFCGNQLDGWVC
284

6) Low affinity immunoglobulin epsilon Fc receptor [*Rhinolophus ferrumequinum*]

Sequence ID: XP_032990569.1 Length: 305

Range 1: 184 to 299

Score: 72.8 bits (177), Expect: 4e-11,

Method: Compositional matrix adjust.,

Identities: 42/119(35%), Positives: 69/119(57%), Gaps: 5/119(4%)

Query 387
FRDECFWIPDDVARWVDAEQKCTKYD GARLVAITDQ
EINDFLD LIDR-DVWIGLH DTHN 211

F+ +C++ + RW+ A C+K G RLV+I QE DFL I R
WIGL D +

Subject 184 FQRKCYFGE GAKRWIQARLACSKLQG-
RLVSIHSQEEQDFLAKSIHRRG SWIGLRDLNI 242

Query 210
ESDWKWSNDSPVNYTNFIEEEEQTELSGVESLENNCVA
LQISNGKWKDSRCRDR-KGMIC 37

E D+ W +++P++Y+N+ E + G L +CV + +S+G+W
D+ C ++ G +C

Subjct 243 EGDVWMDENPLDYSNWRPGEPN-
GGERGLGEDCVMM-LSSGQW NDAFCGNQLDGWVC
299

7) PREDICTED: low affinity immunoglobulin epsilon Fc receptor isoform X1 [*Hipposideros armiger*]

Sequence ID: XP_019523150.1 Length: 385

Range 1: 267 to 381

Score: 73.2 bits (178), Expect: 5e-11,

Method: Compositional matrix adjust.,

Identities: 43/121(36%), Positives: 70/121(57%), Gaps: 8/121(6%)

Query 387
FRDECFWIPDDVARWVDAEQKCTKYD GARLVAITDQ
EINDFLD LIDR-DVWIGLH DTHN 211

F+ +C++ + RW+ A C+K G RLV+I QE DFL I+R
+ WIGL D +

Subject 267 FQRKCYFGE GAKRWIQARLACSKLQG-
RLVSIHSQEEQDFLVKHINRKESWIGLRDLNI 325

Query 210
ESDWKWSNDSPVNYTNFIEEEEQTELSGVESLENNCVA
LQISNGKWKDSRCRDR-RKGMICA 34

E ++ W +++PVNY+N+ E +G E +CV +
+S+G+W D+ C G +C

Subject 326 EGNFVWMDENPVNYSNWRPGEPN--
NGGEG--EDCV-MMLSSGQW NDAFCNSLLNGWVCE
380

Query 33 K 31

+

Subject 381 R 381

CONCLUSION

The sea star *A. rubens* Fc receptor gene shows identities from 33 % To 36 % with 7 Fc receptor mammal genes. We notice just one identity with mammal IgE out of 7.

Mainly, 3 classes of Echinodermata out of 5 present the Fc receptor gene [3,4]: the Asterids, the Ophuirids and the Crinoids. 2 classes have not: the Echinids and the Holothurids. We recall also that the Ophuirids, with the *Ophiocomina nigra* as a model of study, are the most evolved of Echinodermata, since the IgK *O.nigra* shows high similitudes with the Human IgK.

REFERENCES

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