Supplementary Data S1: Amino acid sequences of relaxin/insulin-like peptides in echinoderms

Article Title:

“Aquaculture breeding enhancement: Maturation and spawning in sea cucumbers using a recombinant relaxin-like gonad-stimulating peptide”

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**Abbreviations:**

RGP: Relaxin-like Gonad-stimulating Peptide

IGF: Insulin-like Growth Factor

Hle: *Holothuria leucospilota* (Brandt, 1835)

Hsc: *Holothuria scabra* (Jaeger, 1833)

Hgl: *Holothuria glaberrima* (Selenka, 1867)

Apj: *Apostichopus japonicus* (Selenka, 1867)

Aru: *Asterias rubens* (Linnaeus, 1758)

Aam: *Asterias amurensis* (Lutken, 1871)

Aja: *Aphelasterias japonica* (Bell, 1881)

Apl: *Acanthaster planci* (Linnaeus, 1758)

Ppe: *Patiria pectinifera* (Muller & Troschel, 1842)

Spu: *Strongylocentrotus purpuratus* (Stimpson, 1857)

**Amino acid sequences of RGP/IGF peptides in echinoderms include:**

>Hle-RGP

MASKTIRVVFFAAVCVLLVLEEAASTRLCGRELSRAIYRICSHGKRGYPMVDLEEEDFSQELDTEWDEFLAQALTGLLESRTFAADIESDRYFTIPQRFRRSGGIARRCCASGCSSSDIAKLC

>Hsc-RGP

MASKTTRVVFFAAVCVLLVLEHAASVRLCGADLSRAVYRVCSHGKRGYPMIDIEEDDFSQELDTELDEYLAQALTGFLESRSFAADIESDRYYTIPQRFRRNGGIARRCCASGCSSSDIAKLC

>Hgl-RGP

MASKATRVVFFAAVCVLLVLEEAASVRLCGADLSRAVYRVCSHGKRGYPMVDLEEEDFSQELDTEVDEFLAQALTGFLASRSFAADMESDRYYTLPQRFRRNARGGIARRCCASGCSSSDIAKLC

>Apj-RGP

MTTQSTTVIILRIFCVLIAVREAASIRLCGPDLSRAVYQICSHGKRGYIPPTFNSEDDQLNQEFGTDLEEYLAETIKEYLKPNSLYDDVERELYPSLPRGFRRVTRTGGIARRCCSTGCSSSDIAKLC

>Aru-RGP1

MANYRLILEATCLLVLLINTALYAEAAEKYCDEDFHMAVYRTCTEHKRSGRSAFSLNDFFRSNSKRTAGSPRPDDDFFLTMQKRPETYVGMGSYCCLVGCTRDQLSQVC

>Aru-RGP2

MTSCSHQMLALLSAVYILIFFLGGLPAVHARSDHASVKHFCGLEFSYAVVTACGEAKRSIRSAPFFDMFPVFKSPERIPADFDDSSMIHVRKRQDYQGMATYCCTNGCTISQLTNSGIC

>Aam-RGP

MANYRLILEATCLIVLLINTALYAEAAEKYCDEDFHMAVYRTCTEHKRSGRSAFSLNDFFRSNSKRTAGSPRQDDDFFLTMQKRPETYVGMGSYCCLVGCTRDQLSQVC

>Aja-RGP

MANHRLILEATCLLVLLINTALYAEAAPKYCDEDFHMAVYRTCSEHKRSGRSTYSLNDLLTLNRLRSNPKRTVGSLEDDDLYLTMQKRTETYVGMGSYCCTVGCTREELSQVC

>Apl-RGP

MANNLRRRFQATCLALLILQATINTGAVGEKFCDNDFHLAVYQTCSTHKRGDGEPVLSLKDVLTGSRLRGNIKRSFGSTLEDEAFFASRLVKRSEYDGIASYCCIHGCTPSELAVVC

>Ppe-RGP

MTSNNRHLFQATCLVLLLLHAAFHGGALGEKYCDDDFHMAVFRTCAVSKRSQPGMSLSDVLTMNRFRGHNIKRSIDSTLEDNAFFMSGLEKRSEYSGIASYCCLHGCTPSELSVVC

>Spu-IGF1\_SPU\_007203.3

MVCFRYPVAVMSVVLLALLRHVTASFPLLCGQELVKAVAAVCNDRGYYGQPSKRSAGIFELETRAKTFLKSGMSRGETRRSKRGARTGLIVTECCLNRCSVSHLESYCNPLPPDAVHDAEVHIRLEKSAEEDADEGRPQDGPSQLDTATGTVPETDTSETRGRVRIDAVEKVISERLIPTSTTGSSPSPSRKKPRKDKSERRNSSREAKQARREERRRNRERGSGGRSRSGRRKDKDNDRASRAKRHGLNLWRNMFSDKFFSDIPGLENQPNLHPVNGRAPSSTTIDTFQMKSSIPIQDSPEGNGKENFEQSSINQEADKKMRFSALMTKLRTMVLKFPKDR\*

>Spu-IGF2\_SPU\_030139.3

MDPFRVLLYMVTFLLYVVGPISSFRLCGRELADALAVVCKGRGYYIDDSEIAQKDSPIVPHHVASSFLGSSSASAHSRQRRRVRTGQIVNECCDKECSNNIMESYCNRRTPEVPPESAISENPSEEITEDSTLRTDGESTEIRTDTNPATNLEVPSPDANTPDATATSDVEQPRSDNTTAVEKPRKKDNGKGKNSSLESSTKKNRTSKGMSKEDRRRIASDERRASRERKKELSRERRKRLKLQQRKDKKKKKRLESAERNRGTDHMGLSEDSTLLAREPLGIDVRKRFHHTPRSSREQASTATHALDDDPATSRQERRRTQSRPSSRERKTHRTTTATAREEEMQRERRNVMQRLTGLFL\*

>Aru-IGF1\_ ALJ99972.1

MFRNTSTMRALLLLDVIFVALVLPITAWPKICGEQLVETVSLVCSTRGFYSHRDSKRDVEVFQNERAAKSFLGSRIGSRQRRRTGRIATECCDRICSFDIVESYCNPWPVAIESRDPPLSPVAPGRVREDKSADVDYMYNPDVVDVEEANSVIQREEDLIDDIETQEQEIEQDEEQNMQTLPEEDAEDTDIREPEDVEESFPVPVPTKKRRKVEGRRSKESKNKGGKSEGKNKKRSGSREGGRSSRRSRGKSSRSKKQRDGRERSKRWEGLDTSHPVKEPTARSVLGRVDTRPFRNFLYNRYTVDEKRDTERESYRAVAPLTGYNSHRGGSQPDNHPTLAALYNLAVKLA KGLQH

>Aru-IGF2\_ALJ99973.1

MNQYQLIVLFEVLAHASMLNYASPVQLCGRELTETLRSICGDRGYYSPGQSFSRRAPTHDGIATRCCQSLCESSILETYCNLPAPPSQTQPSTAAPTTTTKMAPLTEDRRTKDVVVDYSDQLATEGSQMSRVDGVLTHDTVTNRSKTTTESNEGSYDNEEGAPYDKPDDSSPSERGESIQDEDNEVNKPEPNNIRDNSKERGRNRTHKGVSSERRANNSRRRGLSSERRGSSSSRREEKLRRRRQRHRERELREQRKQSNSKRKSKGDKKDHSVAATTPLAVQERPLKNGGRNSTSGEHSSVNGTETDTAGAGSPEVKKDDLITTITAVLSDMIGFQPDNGNR

>Hgl-IGF

MHLNQMCKILVYLSLSLVSMVLSADGTGQKYCGEALLEALAFICGDRGYYGMTSGIHGRSVSRSPFLSEERANSFLTNDGTRNRRGTGRIVTECCENYCTTSVLESYCNFATELPTELSTERTTTEPSASPRRNSRHAGADITPDGETPRQSNNGRNRGNPNRHSEDNPEDNIDETVTHRTETEDQSRSNENRGNRGKGNRDNQNNCRNSKKKGSKKKGNRKCRPGNEDSASEDGGNRRPPSAATATEGADRSSGSRGGRGSNHQTGRGSDRGSSRSNGGKGKGNRNQDRNQTDAGADITPDGETPRQSNNGRNR