A GPI-anchored Sea Urchin Sperm Membrane Protein Containing EGF Domains is Related to Human Uromodulin

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Abstract. An M_r 63-kD sea urchin sperm flagellar membrane protein has been previously implicated as a possible receptor for egg jelly ligand(s) that trigger the sperm acrosome reaction (AR). The cDNA and deduced amino acid sequences of the 63-kD protein are presented. The open reading frame codes for a protein of 470 amino acids which contains a putative signal sequence of 25 residues. Western blots using antibodies to two synthetic peptides confirm the sequence to be that of the 63-kD protein. The mRNA is ~2,300 bases in length and the gene appears to be single copy. The protein is released from sperm membrane vesicles by treatment with phosphatidylinositol-specific phospholipase C, showing that it is anchored to the flagellar membrane by glycosylphosphatidyl inositol (GPI). Although we cannot demonstrate involvement of the 63-kD protein in the AR, it is of potential interest because it shares significant similarity with the developmentally expressed proteins crumbs, notch and xotch as well as human uromodulin over a region that includes two separate EGF repeats.

SPERM-EGG interactions during fertilization provide important models for studying such basic cellular phenomena as chemotaxis (Ward et al., 1985; Ralt et al., 1991), cell–cell recognition and adhesion (Wasserman, 1990; Foltz and Lennarz, 1992), membrane fusion (Hong and Vacquier, 1986; Blobel et al., 1992; White, 1992), oxidative stress (Shapiro, 1990), and ionic (Epel, 1990) and second messenger (Garbers, 1989)-mediated cellular activation. When exposed to the extracellular jelly layer of the unfertilized egg, sea urchin sperm undergo the acrosome reaction (AR[1]) in which the acrosomal vesicle is exocytosed and an acrosomal process of filamentous actin is extended from the tip of the sperm head (Dan, 1967). The AR is an absolute prerequisite for fertilization; it is induced by the opening of ligand-gated ion channels, resulting in the net influx of Ca^{2+} and Na^+, and the net efflux of H^+ and K^+ (Vacquier, 1986; Babcock et al., 1992; Gonzalez-Martinez et al., 1992).

mAb J18/29 induces the AR in sea urchin sperm (Trimmer et al., 1987). Based on reaction with this mAb, sperm membrane proteins of approximate M_r, 320 kD, 210 kD, 170 kD and 63 kD have been implicated as potential receptors for the egg jelly ligand(s) mediating the ion channel events underlying the AR (Trimmer et al., 1987). Additionally, a 63-kD sperm membrane protein has been implicated as a receptor for the egg jelly peptide speract that activates sperm respiration and motility (Harumi et al., 1991). Another mAb, J17/30, reacts exclusively with the 63-kD protein and localizes it to the sperm flagellum and midpiece (Nishioka et al., 1987).

To gain a deeper understanding of the sperm membrane proteins mediating the AR, we utilized molecular techniques to characterize the 63-kD protein. Here we report the cDNA and deduced amino acid sequences of the 63-kD protein of *Strongylocentrotus purpuratus* sperm. We show that the protein is anchored to the membrane by glycosylphosphatidyl inositol (GPI) and that it shares significant similarity with proteins of the EGF superfamily, including human uromodulin (Hession et al., 1987), and the developmentally regulated proteins crumbs (Tepass et al., 1990), notch (Wharton et al., 1985) and xotch (Coffman et al., 1990).

Materials and Methods

Cloning and Sequencing the cDNA Encoding the 63-kD Protein

A 1.9-kb cDNA coding for the 63-kD protein was isolated from a λgt 11 sea urchin (*S. purpuratus*) testis library using mAb J17/30 (Nishioka et al., 1987; Trimmer et al., 1987) after standard procedures for antibody screening (Young and Davis, 1983). The *Eco RI* insert was cloned into pBluescript (Stratagene Corp., La Jolla, CA) and single stranded DNA (M13) was isolated. The sequences of both strands were determined by the dideoxy chain termination method using Sequenase 2.0 (United States Biochemical,

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1. *Abbreviations used in this paper*: AR, acrosome reaction; GPI, glycosylphosphatidyl inositol.

Cleveland, OH). This clone was then used to isolate several overlapping cDNAs from an *S. purpuratus* testis cDNA λZAP II library (Stratagene Corp.). Hybridizations were at 65°C in 6× SSPE (1× SSPE: 150 mM NaCl, 1 mM EDTA, 10 mM NaH_2PO_4 pH 7.4), 5× Denhardt's (50× Denhardt's: 1% ficoll, 1% polyvinylpyrrolidone, 1% BSA), 0.5% SDS and 100 μg/ml yeast tRNA (Sigma Chemical Co., St. Louis, MO) overnight. Initial washes were at 23°C for 15 min (2×) in 1× SSC, 0.1% SDS with a final wash at 68°C in 1× SSC, 0.1% SDS for 1 h.

Analysis of Sequences

The deduced amino acid sequence of the 63-kD cDNA was compared to all protein libraries available on the Pearson FAST88 package using FASTA (Pearson, 1990). An optimal alignment of homologous sequences was derived using the programs RELATE and ALIGN from the Protein Identification Resource (National Biomedical Research Foundation, Washington, DC). A hydropathy profile of the deduced amino acid sequence was obtained using TGREASE on the Pearson FAST88 package using the Kyte-Doolittle algorithm (Kyte and Doolittle, 1982). All computer programs used were accessed on the VAX/VMS system (Smith, 1988).

Peptide Antigen/Antibody Production and Immunoblotting

Peptides 1 and 2 were synthesized based on the deduced amino acid sequence of the 63-kD protein from residues 237–248 and 382–393 (Fig. 1; *underlines*). Both peptides had an additional lysine at the amino terminus and were coupled to BSA by the glutaraldehyde method (Doolittle, 1987). The peptide antigens (BSA-peptide) were used to generate antisera in rabbits (Cocalico Biologicals, Reamstown, PA). Peptide-specific IgG was purified by affinity chromatography using an ImmunoPure Ag/Ab Immobilization Kit No. 1 (Pierce Chemical Co., Rockford, IL). First, BSA-specific IgG was removed on a BSA affinity column, followed by purification of peptide-specific IgG on a BSA-peptide column. Immunoblotting of sperm membrane proteins isolated by the method of Podell et al. (1984) with peptide-specific IgG, and with mAb J17/30 IgG was detected with an alkaline phosphatase-conjugated secondary antibody (Calbiochem Corp., La Jolla, CA).

Southern Blot Analysis

Sperm DNA (5 μg) was digested with 20 U of *Pst I*, 15 U of *Bst XI*, 20 U of *Xba I*, and 10 U of *Nde I*, and electrophoresed in a 0.6% agarose gel. The DNA was transferred to a nylon membrane (Schleicher and Schuell, Inc., Keene, NH) and the blot probed with pL29-E, a 1,550-bp 63-kD cDNA fragment that was random-prime labeled with [^{32}P]dCTP (Amersham Corp., Arlington Heights, IL) to a specific activity of 7×10^8 cpm/μg. Hybridization was at 68°C in 6× SSPE, 5× Denhardt's, 0.5% SDS, and 200 μg/ml yeast tRNA (Sigma Chemical Co.) overnight. Initial washes were at 23°C for 15 min (2×) in 0.1× SSPE, 1.0% SDS with a final wash at 68°C in 0.1× SSPE, 1.0% SDS for 1 h.

Northern Blot Analysis

Total RNA was isolated from spermatogenically active *S. purpuratus* testes by the guanidinium thiocyanate method (Chomczynski and Sacchi, 1987). Poly A^+ mRNA was isolated with the polyATtract mRNA isolation system (Promega Corp., Madison, WI). The mRNA was electrophoresed and transferred to a nylon membrane (Schleicher and Schuell, Inc.). Blots were hybridized at 68°C with the pL29-E cDNA fragment (random-prime labeled to a specific activity of 7×10^8 cpm/μg) in 5× SSPE, 5× Denhardt's, 0.1% SDS, and 100 μg/ml yeast tRNA for 48 h. Initial washes were at 23°C for 15 min (2×) in 1× SSPE, 0.1% SDS with a final wash at 68°C in 1× SSPE, 0.1% SDS for 1 h.

Gamete Collection, Iodination, and Enzymatic Release of the 63-kD Protein

Sea urchins were spawned by intracoelomic injection of 0.5 M KCl. Semen was collected undiluted and stored on ice. Just before iodination semen was diluted into millipore-filtered sea water, pH 6.5, and pigment cells removed by centrifugation at 250 *g* for 12 min at 4°C. Spermatozoa were washed twice by sedimentation at 1,000 *g* for 15 min and resuspension in millipore-filtered sea water (4°C). Washed spermatozoa (8×10^8) were vectorially labeled with ^{125}I using iodobeads (Pierce Chemical Co.; Lopo and Vacquier, 1980*a*). Labeled cells were washed free of ^{125}I and sea water salts by layering 1 ml of iodination mixture on top of a 13 ml density step made by mixing one volume of 1.0 M sucrose/10 mM NaN_3 with 3 vol of 1.1 M glycerol/20 mM Hepes pH 7.5 (buffer G). After centrifugation (4°C) at 2,000 *g* for 20 min, the supernatant was removed by aspiration and the sperm cell pellet was resuspended in 1 ml of buffer G.

20 μl of 50 mM triethanolamine pH 7.5/10 mM EDTA/10 mM NaN_3, with or without 1 U of phosphatidylinositol-specific phospholipase C (PI-PLC; Boehringer Mannheim Corp., Indianapolis, IN), was incubated with 380 μl of ^{125}I-labeled sperm for 3 h at 23°C. The digests were centrifuged in an airfuge at 150,000 *g* for 1 h and the protein components of the supernatants and pellets separated on a 10% SDS-PAGE gel (Laemmli, 1970). The gels were stained with Coomassie blue, dried, and prepared for autoradiography.

Results

Deduced Amino Acid Sequence

Overlapping cDNA fragments of the two libraries yielded the full-length sequence encoding the 63-kD protein (Fig. 1). The start of the putative open reading frame is the methionine designated number 1. A putative signal sequence of 25 amino acids (Von Heijne, 1986) is followed by the putative amino-terminal amino acid, glutamine (△). The mature sequence contains five sites for potential N-linked glycosyla-

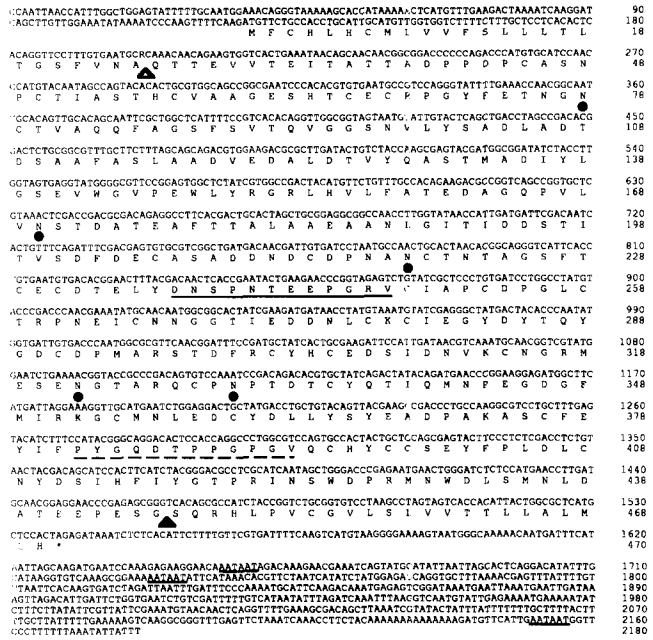

Figure 1. The cDNA and deduced amino acid sequences of the 63-kD protein. Numbers on the right margin indicate either amino acid position where the putative start methionine is designated 1, or nucleotide sequence position. The numbers in each row correspond to the sequence position of the last amino acid/nucleotide in that row. A signal sequence of 25 amino acids is followed by the putative amino-terminal amino acid, glutamine (△). The mature sequence contains five sites for potential N-linked glycosylation (●). Synthetic peptide 1 is underlined with a solid line and peptide 2 with a dashed line. The stop codon (*) yields an open reading frame of 470 amino acids followed by a 3′ untranslated region of 641 nucleotides containing three modified signal sequences for polyadenylation (AATAAT). Glycine 446 (▲) is tentatively assigned as the site of GPI attachment. These sequence data are available from EMBL/GenBank/DDBJ under accession number M99584.

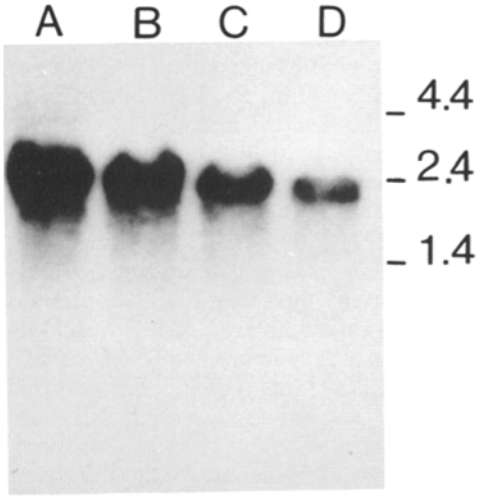

Figure 2. Northern blot analysis of *S. purpuratus* testis. Various amounts of poly A^+ RNA were electrophoresed on a formaldehyde-denatured gel and blotted onto a nylon membrane, hybridized with clone pL29-E at 7×10^8 cpm/μg and washed at high stringency followed by autoradiography. RNA load (lane *A*) 22 μg; (lane *B*) 11 μg; (lane *C*) 5.5 μg; (lane *D*) 2.8 μg. Kilobase size markers are on the right.

tion (•). The stop codon (*; TAG) is followed by a 3′ untranslated region of 641 nucleotides containing three modified signal sequences for polyadenylation (AATAAT).

To confirm that the size of the mRNA coding for the 63-kD protein corresponds to that of the cDNA presented in Fig. 1, Northern blot analysis of testicular poly A^+ RNA was performed. Fig. 2 shows that ^{32}P-labeled pL29-E, a 1,550 nucleotide fragment of the 63-kD protein cDNA, hybridizes to a single mRNA of ~2,300 nucleotides, quite close to 2,180 nucleotides presented in Fig. 1.

Southern blot analysis was performed with *S. purpuratus*

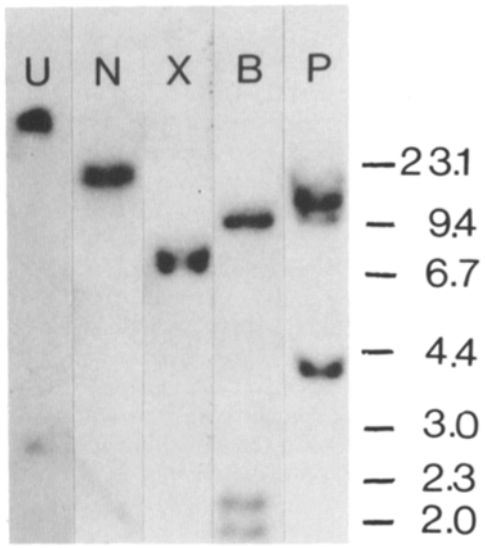

Figure 3. Southern blot analysis. Each lane contains 5 μg of genomic DNA from sperm cells digested with various restriction enzymes (*Nde I, N*; *Xba I, X*; *Bst XI, B*; *Pst I, P*) as well as undigested (*U*) DNA. The blot was hybridized with clone pL29-E. Size markers are shown on the right in kilobases.

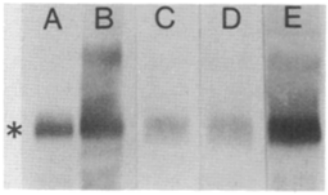

Figure 4. Protein immunoblots with J17/30 and synthetic peptide-specific antibodies. Lanes *A* and *B* are sperm membrane vesicles (SMVs) from *S. purpuratus* (1.0 μg and 5.0 μg) reacted with the 63-kD-specific mAb J17/30 (2.0 μg/ml). Lanes *C–E* contain 20 μg of SMVs. Lane *C* was reacted with peptide 1 IgG at 2.5 μg/ml and lanes *D* and *E* were reacted with 2.5 μg/ml of peptide 2 IgG. Lane *E* was overdeveloped. The asterisk (*) denotes M_r 63 kD.

sperm genomic DNA to determine the copy number of the 63-kD gene. Restriction enzyme digested genomic DNA from sperm cells was hybridized with ^{32}P-labeled pL29-E (Fig. 3). Neither *NdeI* nor *Xba I* restriction sites are present within the pL29-E sequence. Fig. 3 shows that ^{32}P-pL29-E hybridizes with a single band in both *Nde I* (*N*; at 21 kb) and *Xba I* (*X*; at 7 kb) digested genomic DNA, supporting the conclusion that the 63-kD protein is encoded by a single copy gene. Furthermore, both *Bst XI* and *Pst I* restriction sites are present at one site within the 1,550-bp pL29-E cDNA sequence. As expected for a single copy gene, two bands (at 17 and 4 kb) hybridize with ^{32}P-pL29-E in the *Pst I* (*P*) digested genomic DNA. Hybridization of ^{32}P-pL29-E to the *Bst XI* (*B*) digested genomic DNA, however, is more difficult to interpret and suggests the presence of introns within the gene.

To confirm that the deduced amino acid sequence was that of the 63-kD sperm membrane protein recognized by mAb J17/30, rabbit antibodies were prepared against two synthetic peptides made to distinct regions of the deduced sequence (underlines in Fig. 1; shaded zones in Fig. 5). On Western immunoblots of sperm membrane vesicles (*SMVs*), both peptide antisera reacted specifically with an antigen of M_r 63 kD, which comigrated with the sperm membrane protein recognized by mAb J17/30 (Fig. 4). We conclude that the deduced amino acid sequence is that of the 63-kD protein. Neither the two peptide antibodies nor mAb J17/30 induced sperm cells to undergo the AR, and none of the antibodies were capable of inhibiting fertilization or the egg jelly-induced AR.

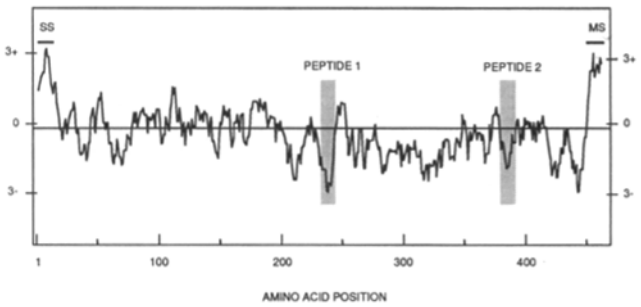

Figure 5. Hydropathy profile of the 63-kD deduced amino acid sequence. Hydrophobicity plotted against amino acid position was obtained with the program TGREASE. Hydropathic index is on the y-axis in arbitrary units. A hydrophobic stretch at the extreme NH_2-terminal end is designated as the signal sequence (*SS*). A single membrane spanning (*MS*) domain at the extreme COOH-terminal end is indicated. The regions of the deduced sequence from which peptides 1 and 2 were designed are shaded.

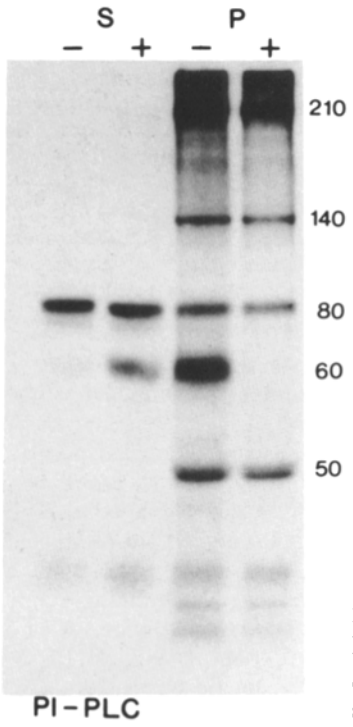

Figure 6. The 63-kD protein was enzymatically released from ^{125}I-labeled sperm with PI-PLC. Spermatozoa were incubated in the presence (+) or absence (−) of 1 U of PI-PLC from *Bacillus cereus*. The digests were centrifuged at 150,000 *g* for 1 h and the protein components of the supernatants (*S*) and pellets (*P*) separated on 10% SDS-PAGE followed by autoradiography. M_r is shown on the right in kilodaltons. The 63-kD protein is freed from the SMVs (*P*+ lane) and appears in the supernatant (*S*+ lane).

GPI-anchorage

Although biochemical evidence indicates that the 63-kD protein is an integral membrane protein (Podell et al., 1984), a hydropathy plot of the deduced sequence (Fig. 5) failed to identify a transmembrane domain. This analysis, however, showed that the COOH-terminal domain consists of 20 hydrophobic residues having the characteristics of a signal sequence for GPI anchor attachment (Ferguson and Williams, 1988). To confirm this hypothesis, ^{125}I-labeled spermatozoa were digested with PI-PLC. The 80-kD membrane protein was released from the cells independent of the presence of PI-PLC. However, the 63-kD protein was released from the cells to the 150,000 *g* supernatant only in the presence of PI-PLC (Fig. 6), confirming that the 63-kD protein is GPI-anchored to the sperm plasma membrane. Following established criteria for the identification of GPI signal sequences (Moran et al., 1991) we tentatively assign glycine 446 (Fig. 1; ▲) as the site of GPI attachment. This assignment would yield a mature protein of 421 amino acids, of mol wt 45,739 D, GPI anchored to the outer surface of the sperm plasma membrane. Digestion of SMVs with Peptide-N-Glycosidase F results in an M_r shift from 63 to 51 kD (not shown) confirming the presence of N-linked oligosaccharides and partially accounting for the discrepancy between the molecular weight predicted for the 421 amino acid protein and the observed M_r of 63 kD. The 63 kD protein is not released from the cells upon induction of the AR by soluble egg jelly.

Homology to the EGF Superfamily

Two regions of the 63-kD protein's deduced amino acid sequence containing EGF-like domains are homologous to several proteins in GenBank. The first region spans ~38 residues, from amino acid position 43 to 81. The second region spans 113 residues, from amino acid position 202 to 315. The proteins identified from the GenBank search include the sea urchin EGF homolog (Hursh et al., 1987), uromodulin (also known as the Tamm-Horsfall protein; Hession et al., 1987) from human, crumbs (Tepass et al., 1990) and notch (Wharton et al., 1985) from *Drosophila*, and xotch (Coffman et al., 1990), the *Xenopus* homolog of notch.

To determine the significance of the similarity between these distantly related proteins, and to obtain optimal alignments between them and the 63-kD sea urchin sperm protein, the program ALIGN (Dayhoff et al., 1983) was used. EGF 1 contains six cysteine residues that are conserved between the 63-kD protein and the other EGF-like proteins (Fig. 7 *a*). The second region of similarity (Fig. 7 *b*) includes the two remaining EGF-like domains in the 63-kD protein sequence (EGF 2 and EGF 3). This region is characterized by the alignment of 11–13 cysteine residues with the 63-kD protein over 102–113 amino acids. Table I lists pairwise comparisons of the percent amino acid identity for these domains (above the diagonals) and the alignment score in SD units greater than random (below the diagonals) determined by the program ALIGN. Table I, *a* and *b*, correspond to the regions presented in Fig. 7, *a* and *b*. Both percent identity and alignment scores presented in Table I include only the regions presented in Fig. 7, not the entire protein sequence.

The most significant homology is between the 63-kD protein and uromodulin, a glycoprotein expressed in human kidney on the thick ascending limb of the loop of Henle (Kumar and Muchmore, 1990). The alignment score is 10 SD U above random (Table I *b*) which indicates that the probability of this alignment occurring by chance is <1 in 10^{23}. The least significant alignment score is 4.0 SD units between the 63-kD protein and xotch over the region that includes EGF 2 and 3 (Table I *b*). The probability of this occurring by chance is <1 in 10^5. These data support the conclusion that the sea urchin sperm 63-kD protein is a member of the EGF superfamily.

The 63-kD Protein is not a Speract Receptor

Harumi et al. (1991) have reported that some echinoid sperm possess a 63-kD receptor for the egg jelly decapeptide speract (SAP 1; Suzuki, 1990). The following experiment was performed to determine if the 63-kD protein of *S. purpuratus* sperm was a receptor for this egg-derived peptide. Two speract analogs, GYGG-GFDLNGGGVG (GYGG-speract) and GGGY-speract were iodinated and then cross-linked to live spermatozoa according to the methods described by Harumi et al. (1991). These authors reported the identification of two speract receptors from the Japanese sea urchin *Hemicentrotrus pulcherrimus* of M_r 63 and 71 kD with the GGGY-analog. We found (Fig. 8) that both analogs cross-linked to a single protein of M_r 77 kD of *S. purpuratus* sperm, confirming the results reported by Dangott and Garbers (1984). Although minor cross-linking reactions are apparent in this autoradiogram, at pH 7.8 there is no cross-linking of labeled peptide to proteins in the M_r 63-kD range.

Discussion

Sea urchin sperm are ideal single cells for studying the mechanism of signal transduction underlying exocytosis. They are a uniform population that can be obtained in mass quantities, they have a large cell membrane surface area to

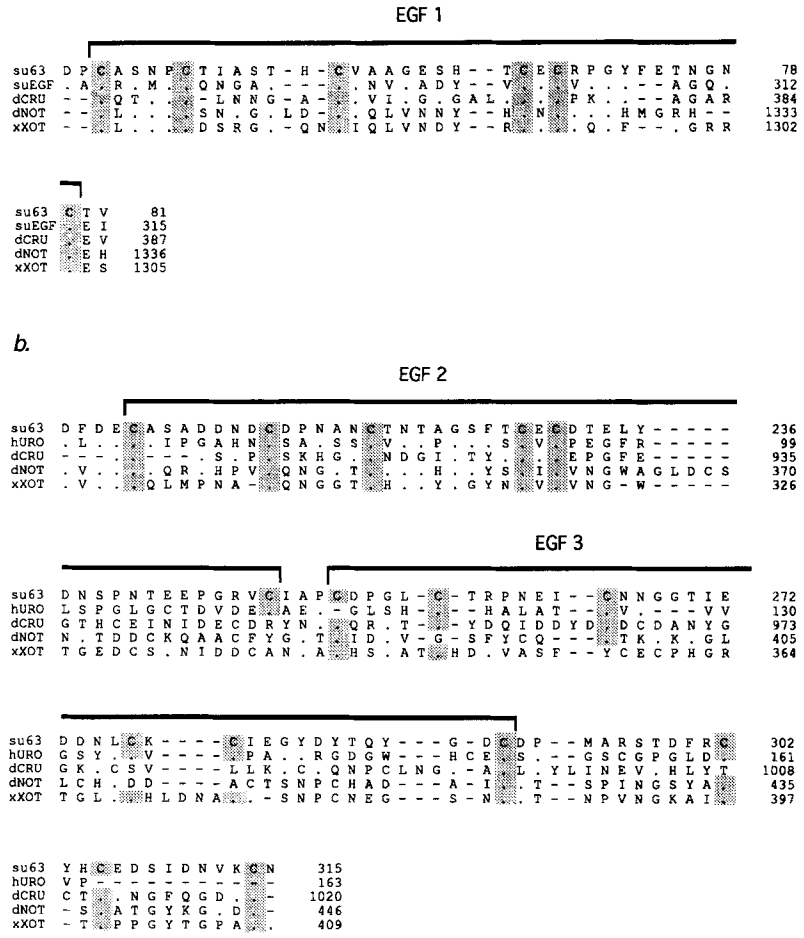

Figure 7. Optimal alignments of sequences homologous to the 63-kD protein were derived using the programs RELATE and ALIGN. The matrix used for the alignment was PAM250; matrix bias was 6; and gap penalty was 12. Dots (·) indicate identical residues and dashes (-) are inserted for alignment. Conserved cysteine residues are shaded. The protein sequences include the sea urchin 63-kD protein (*su63*), the sea urchin EGF homolog (*suEGF*), human uromodulin (*hURO*), *Drosophila* crumbs (*dCRU*) and notch (*dNOT*), and xotch (*xXOT*), the *Xenopus* homolog of notch. Amino acid position within the full-length protein sequence is indicated at the right. EGF-like domains characterized by conserved cysteine residues are indicated above the sequences (*EGF 1; EGF 2; EGF 3*).

Table I. Pairwise Comparisons of % Identity and Alignment Score

a

	su63	suEGF	dCRU	dNOT	xXOT
su63		47	47	43	40
suEGF	7.4		47	47	44
dCRU	6.6	9.0		33	39
dNOT	6.0	9.2	6.7		61
xXOT	6.3	8.3	6.6	11.5	

b

	su63	hURO	dCRU	dNOT	xXOT
su63		29	26	27	25
hURO	10.0		33	37	37
dCRU	5.4	6.5		33	37
dNOT	5.1	7.8	10.7		61
xXOT	4.0	8.1	13.8	25.2	

Pairwise comparisons of percent amino acid identity (above the diagonals) and alignment score (below the diagonals) in SD units above random, as determined by the program ALIGN. The data in *a* and *b* correspond to the regions presented in Fig. 7 *a* and *b*. The matrix used for the alignment was PAM-250; matrix bias was 6; gap penalty was 12.

volume ratio, and they undergo the exocytotic acrosome reaction in a time span of seconds when treated with soluble egg jelly. Evidence that cell surface receptors mediate the AR comes from the finding that protease digestion of sperm renders them unresponsive to egg jelly (Vacquier, V. D., unpublished observations). Also, J18/29, the mAb that reacts with an epitope shared by sperm membrane glycoproteins of M_r 320, 210, 170, and 63 kD, induces the AR in a manner indistinguishable from egg jelly (Trimmer et al., 1987).

The 63-kD protein was first discovered because it is the most heavily labeled protein after vectorial radioiodination of living sea urchin sperm (Lopo and Vacquier, 1980*a*). A high titre rabbit antiserum made to the denatured 63-kD protein reacted strongly with living sperm. Fab fragments of this antibody did not inhibit the egg jelly induced AR (Lopo and Vacquier, 1980*b*). Here we describe the cDNA and deduced amino acid sequences of the 63-kD sperm membrane protein. The protein is GPI-anchored to the cell membrane making it the first such protein discovered in sea urchin sperm. Kabakoff et al. (1992) have identified three GPI-anchored proteins on the surface of primary mesenchyme cells of the developing sea urchin embryo, purported to be involved in embryonic spicule formation. These are the only other sea urchin proteins reported to be GPI-anchored. The

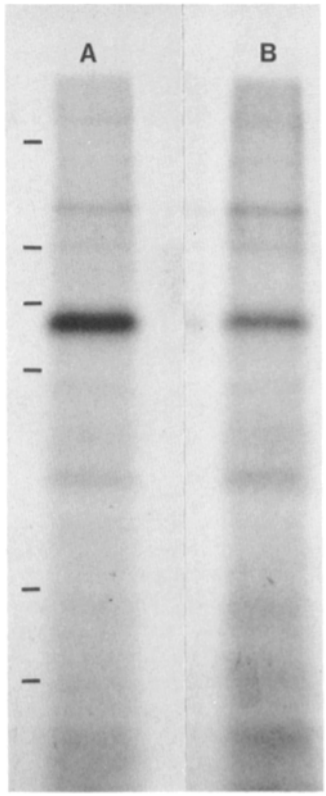

Figure 8. Autoradiogram of a sperm extract after the cross-linking of two radioiodinated speract analogs to living sperm. Lane *A* is with the GYGG-GFDLNGGGVG analog and lane *B* is with the GGGY-GFDLNGGGVG analog. The major cross-linking is with an M_r 77-kD sperm membrane protein as shown previously by Dangott and Garbers, 1984. Molecular weight standards are marked at left: M_r 205 kD, 116 kD, 97 kD, 66 kD, 45 kD, 29 kD.

63-kD protein is also a member of the EGF superfamily, sharing homology with the developmentally regulated *Drosophila* proteins crumbs (Tepass et al., 1990) and notch (Wharton et al., 1985), *Xenopus* protein xotch (Coffman et al., 1990), and the sea urchin EGF homolog (Hursh et al., 1987), as well as human uromodulin (Hession et al., 1987). The 63-kD protein shows no similarity to the two other cell membrane proteins of known sequence from sea urchin sperm: the speract receptor (Dangott et al., 1989) and guanylate cyclase (Singh et al., 1988).

GPI-anchored proteins are ubiquitous and have been implicated in a variety of physiological processes (Ferguson and Williams, 1988; Low and Saltiel, 1988; Thomas et al., 1990; Robinson, 1991). Of these, protein anchoring is the only clear function that can be assigned. GPI-anchored proteins reside exclusively in the apical membranes of polarized epithelial cells (Lisanti et al., 1988) and have been implicated in signal transduction in which inositol phosphate glycan and myristylated diacylglycerol act as second messengers (Eardley and Koshland, 1991). Some effects of insulin (Saltiel et al., 1987), NGF (Chan et al., 1989; Mahanthappa and Patterson, 1992) and T cell activation (Gaulton et al., 1988) are mediated by GPI-anchored proteins. Others have shown that protein tyrosine kinase activity is associated with GPI-anchored proteins on the surfaces of T cells (Stefanova et al., 1991; Thomas and Samelson, 1992).

GPI-anchoring of the 63-kD sea urchin sperm membrane protein, plus the fact that it contains 20 tyrosine residues are the most probable reasons why it is the most heavily labeled sperm protein when vectorial radioiodination is performed on living cells (Lopo and Vacquier, 1980*a*). The protein does not change location, nor detach from the cell, after the egg jelly induced AR. Significant homology to the developmentally regulated proteins crumbs, notch and xotch, suggests that the 63-kD may function in sperm cell differentiation. The cysteine-rich repeats characteristic of the EGF superfamily in proteins such as urokinase (Apella et al., 1987), laminin (Graf et al., 1987), coagulation factor IX (Rees et al., 1988) and notch (Rebay et al., 1991) are directly involved in protein–protein interactions underlying cell proliferation and differentiation.

Showing the most significant similarity with the sea urchin 63-kD protein is human uromodulin (Tamm-Horsfall protein). The alignment score of 10 SD U (Table I *b*) indicates that the probability of this homology occurring by chance is <1 in 10^{23}. Additionally, like the 63-kD protein, uromodulin utilizes the modified polyadenylation site AATAAT (Hession et al., 1987; Fig. 1) and both proteins are GPI-anchored (Rindler et al., 1990; Fig. 6). The function of the 63-kD sea urchin sperm membrane protein remains unknown; however, it is worth noting that uromodulin, known for four decades to be the most abundant protein in human urine, remains unknown in terms of function (Kumar and Muchmore, 1990). The thick ascending limb of the loop of Henle in human kidney and the sea urchin sperm flagellum share the common attribute of being extremely active in ion flux. Gels of uromodulin can act as an electret, possessing a gross permanent dipole moment that allows the free passage of ions, but restricts the passage of water (Mattey and Naftalin, 1992). This observation is consistent with the observed high ionic and low water permeability of the thick ascending limb of the loop of Henle (Kumar and Muchmore, 1990). Similarly, in sea urchin sperm cells, high ion permeability and low water permeability across the flagellar membrane are crucial for the activation and maintenance of sperm motility (Clapper et al., 1985) and induction of the acrosome reaction (Schackmann and Shapiro, 1981; Shackmann et al., 1981; Christen et al., 1983; Lee, 1985). In relation to general phenomena of cellular homeostasis, protein homologous to the 63-kD protein of the sea urchin sperm flagellar membrane, and human uromodulin, might occur on the membranes of other cells that exist in high ionic strength media and also possess a relatively high rate of ionic flux.

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