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A mRNA for Membrane Form of Guanylyl Cyclase Is Expressed Exclusively in the Testis of the Sea Urchin Hemicentrotus pulcherrimus

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ABSTRACT—A cDNA clone encoding the membrane form of guanylyl cyclase was isolated from a Hemicentrotus pulcherrimus testis cDNA library and its nucleotide sequence was determined. The cDNA was 4123 bp long and an open reading frame predicted a protein of 1125 amino acids including an apparent signal peptide of 21 residues; a single transmembrane domain of 25 amino acids which divides the mature protein into an amino-terminal, extracellular domain of 485 amino acids and a carboxyl-terminal, intracellular domain of 594 amino acids. Three potential N-linked glycosylation sites were present in the extracellular domain. Northern blot analysis of poly(A)⁺RNA from testes, ovaries, eggs and embryos at various developmental stages showed that the cDNA encoding guanylyl cyclase hybridized to a mRNA of 4.4 kb from the testes.

We developed a large scale purification method of the phosphorylated (131 kDa) and dephosphorylated (128 kDa) forms of the membrane-bound guanylyl cyclase from H. pulcherrimus spermatozoa. The purified 131 kDa and 128 kDa forms of the guanylyl cyclase contained 26.0 ± 1.3 and 4.3 ± 0.7 moles of phosphate per mol protein (mean ± S.D.; n=6), respectively. The amino-terminal amino acids of both the 131 kDa and 128 kDa forms of the guanylyl cyclase could not be detected, suggesting that they were blocked.

INTRODUCTION

Guanylyl cyclase [GTP pyrophosphate-lyase (cycling), EC 4.6.1.2] is found in various cellular compartments as soluble and/or particulate forms and catalyzes the formation of cGMP and inorganic pyrophosphate from GTP (Mittal and Murad, 1982). cGMP concentrations in cells have long been known to increase in response to a wide variety of agents (Goldberg and Haddox, 1977). Critical functions for cGMP have been described in phototransduction (Stryer, 1986) and in mediating the actions of several peptide factors (Hamet et al., 1984; Waldman et al., 1984; Winquist et al., 1984). The binding of sperm-activating peptides, which were originally isolated from sea urchin egg jelly by measuring the respiration-stimulating activity toward sea urchin spermatozoa (Garbers et al., 1982; Suzuki et al., 1981, 1984), to the sperm surface receptor causes a marked and rapid increase and subsequent rapid decrease in cGMP concentrations in sperm cells. The transient increases in cGMP concentrations have been explained by transient activation and subsequent inactivation of the guanylyl cyclase, which is closely linked to the state of phosphorylation of the enzyme (Garbers, 1989). It has been reported that in sea urchin spermatozoa most or all of the guanylyl cyclase activity were recovered in particulate fractions (Garbers et al., 1974; Radany et al., 1983). This suggests that sea urchin sperm guanylyl cyclase is bound to the membrane. The membrane form of guanylyl cyclases contains an extracellular domain, a single transmembrane domain, and an intracellular protein kinase-like regulatory and cyclase catalytic domains which are highly conserved among invertebrates and vertebrates (Garbers, 1992; Garbers and Lowe, 1994).

In the previous study, we purified both the phosphorylated and dephosphorylated forms of guanylyl cyclase from spermatozoa of the sea urchin Hemicentrotus pulcherrimus and showed that the enzyme was bound to sperm membranes and the phosphorylated form of the enzyme had higher activity than the dephosphorylated form (Harumi et al., 1992). In the study, we suggested that the phosphorylated form of H. pulcherrimus sperm guanylyl cyclase might be associated with a 71 kDa sperm-activating peptide-I (SAP-I)-binding protein which was localized in H. pulcherrimus sperm tails. Recently, we reported that a mRNA encoding the 71 kDa SAP-I-binding protein was ex-
pressed exclusively in the testis of *H. pulcherrimus* (Shimizu et al., 1994). In this study, we purified the membrane form of guanylyl cyclase in large amounts from *H. pulcherrimus* spermatozoa and isolated a cDNA clone encoding the guanylyl cyclase from a *H. pulcherrimus* testis cDNA library. We also show that the mRNA for the guanylyl cyclase was expressed in the testis but not in the ovary and eggs nor developing embryos.

**MATERIALS AND METHODS**

**Materials**

The sea urchins, *H. pulcherrimus* were collected at the coast near Noto Marine Laboratory, Kanazawa University. Spermatozoa and eggs were obtained by intracoelomic injection of 0.5 M KCl. Spermatozoa were collected as “dry sperm” at room temperature and stored on ice or at −70°C until use. The cDNA Synthesis Kit, Hybond-N membrane, [γ-32P]ATP (111 TBq/mmole) and [α-32P]dCTP (110 TBq/mmole) were products of Amersham International plc. (Amersham, UK). 7-DEAZA Sequencing Kit ver. 2.0 was from Takara Biomedicals (Kyoto, Japan). Sequenase ver. 2.0 DNA Sequencing Kit was from United States Biochemical Co. (Cleveland, OH, USA).

Restriction enzymes, T4 DNA ligase, and other enzymes were purchased from Takara Biomedicals Co. or Toyobo Co. (Osaka, Japan). The Random-Primed DNA Labeling Kit was purchased from Boehringer-Mannheim (Indianapolis, IN, USA). The plasmid pBluescript II KS(+) pBluescript II KS(−) and M13K07 helper phage were generously provided by Professor Yoshitaka Nagahama at the National Institute for Basic Biology, Okazaki, Japan. Rabbit anti-serum against a synthetic peptide (KPPQKTLQEAIEAANRVPDDV) which corresponds to the carboxy-terminal portion of *Strongylocentrotus purpuratus* sperm guanylyl cyclase was a generous gift of Dr. Tim Quill in Professor David L. Garbers laboratory at University of Texas Southwestern Medical Center, Dallas, Texas, and rabbit anti-serum against a synthetic peptide (KPPQKTLQEAIEAANRVPDDV) corresponding to the carboxyl-terminal portion (residue numbers from 1102 to 1125) of *H. pulcherrimus* sperm guanylyl cyclase was made in our laboratory. Other chemicals of analytical grade were obtained from Wako Pure Chemical Industries, Ltd (Osaka, Japan), Nacalai Tesque Inc. (Kyoto, Japan) or Sigma Chemical Co. (St. Louis, MO, USA).

**Fertilization and embryo culture**

The collected and washed eggs were fertilized and cultured at a population density of about 2x10⁴ embryos/ml of Millipore-filtered (0.45 µm) seawater at 20°C. A 10 ml-aliquot of the egg suspension was transferred to a centrifuge tube at 0, 3, 6, 8, 10, 12, 14, and 16 hr after fertilization, and then centrifuged at 2,000g for 10 min at room temperature. The resultant precipitate was frozen in liquid nitrogen and kept at −70°C until use.

**Preparation of RNA**

The testes and ovaries were dissected out from the adult *H. pulcherrimus* as described previously (Suzuki et al., 1982). Total RNA was prepared from samples of *H. pulcherrimus* ovaries, testes, eggs and embryos at various developmental stages by the LCI method (Cathala et al., 1983). Poly(A)⁺RNA was then purified by two passage of the total RNA over a column of oligo(dT)-cellulose (Pharmacia) (Davis et al., 1986).

**Cloning and sequencing of cDNAs**

A cDNA library (4.9x10⁵ pfu) from poly(A)⁺RNA isolated from *H. pulcherrimus* growing testes was constructed in λgt10 using the cDNA Synthesis System and the cDNA Cloning System λgt10 (Amersham). Approximately 7.1x10⁶ plaques were screened on replicable Hybond-N membranes with 32P-end-labeled, mixed antisense synthetic oligonucleotide probes which correspond to a part of the extracellular domain (nucleotide numbers from 760 to 803) (probe II, 44 mer; 3'-TCTAAGACGTTGCTCATGATGCGCCTAAGCTA-GTAGCCTGT-5') and the intracellular domain (nucleotide numbers from 2689 to 2731) (probe I, 45 mer; 3'-TTGTAATGCGGTAGT-ACCTGGCAGTTGTTATACCTCCTG-5') of the membrane form of guanylyl cyclase of *Arabida punctulata* spermatozoa (Singh et al., 1988). Finally 8 positive clones were obtained and the phage DNA was purified. Digestion of the DNA with *Aprl* showed that four of them contained inserts of 4.0 kbp and two of them contained inserts of 4.3 kbp. Restriction mapping showed that two clones with inserts of 4.3 kbp were identical. The 4.3 kbp cDNA insert from an isolated clone λGC4-7-1 was subcloned into the plasmid vector pBluescript II KS(+) (Stratagene). Serial deletion mutants of subclones were made according to the method described by Yanisch-Perron et al. (1985). Nucleotide sequence was determined by the dideoxy chain termination method (Sanger et al., 1977) using the 7-DEAZA Sequencing Kit ver. 2.0 and the Sequenase ver. 2.0 DNA Sequencing Kit using [α-32P]dCTP and analyzed on DNANIS software (Hitachi Software Engineering Co., Yokohama, Japan).

**Northern blot analysis**

Northern blot analysis was carried out as follows: A 1.6 µg of poly(A)⁺RNA was denatured with 2.1 M formaldehyde, electro-phoresed on a 1% agarose gel in the presence of 2.2 M formaldehyde, and transferred onto a Hybond-N membrane. The RNA on the membrane was then hybridized to the random-primed, [α-32P]dCTP-labeled 2249 bp cDNA insert (nucleotide numbers from 1 to 2249 of the λGC4-7-1 cDNA insert) at 65°C for 18 hr. The membrane was washed with 6 x SSC and 0.1% SDS at room temperature for 30 min, followed by final wash with 0.5 x SSC and 0.1% SDS at 65°C for 30 min. The size of RNA was estimated using 0.24–9.5 kb RNA Ladder (GIBCO BRL, Gaithersburg, MD, USA) as markers.

**Purification and proteolytic digestion of the membrane form of guanylyl cyclase from *H. pulcherrimus* spermatozoa**

Three test tubes, each of which contains 10 g wet weight of dry sperm were placed in a boiling water bath at 100°C for 10 min and then the test tubes were cooled down by placing in an ice bath for 10 min. The boiled dry sperm (total 30 g wet weight) were pooled, suspended in 35 ml of distilled water and kept in a freezer until use. Two ml of the suspension were mixed with 2 ml of 20% SDS and vortexed with heating. The suspension was centrifuged, and the resulting supernatant, after being mixed with an equal volume of the SDS-PAGE sample buffer without SDS, was applied on a preparative SDS-PAGE system model 491 Prep-Cell (BioRad Laboratories, Richmond, CA, USA) using a 6% polyacrylamide gel. Five hundred microliter of fractions were collected. Every three fractions were analyzed for presence of guanylyl cyclase by Western blotting using anti- *S. purpuratus* guanylyl cyclase antiserum. Fractions containing guanylyl cyclase were pooled and used for further experiments. For purification of the dephosphorylated form of *H. pulcherrimus* guanylyl cyclase, dry sperm were suspended in seawater and then 2 µl of sperm-activating peptide I (SAP-I) was added to the sperm suspension. After 1 min incubation at 20°C, the mixture was centrifuged at 10,000g for 30 min at 4°C. The resulting sperm pellet was treated as described above.

The purified guanylyl cyclase was digested for 8 hr at 37°C with lysyl endopeptidase (Achromobacter Protease I) in 50 mM Tris-HCl (pH 9.0) containing 0.1% CHAPS at enzyme to substrate ratio of 1:100 (w/w). The peptides generated were separated by HPLC using a Shimadzu model LC6A chromatography system on a reverse-phase column (Unisil QC-18, 5 µm, 6.0x250 mm), which was developed with a linear gradient of 5–60% acetonitrile (ACN) in 0.1% trifluoroacetic acid and then 0–60% ACN in 5 mM sodium phosphate (pH 5.7) at a flow rate of 1 ml/min at 40°C. The column efflu-
Analyses of amino acid composition and amino acid sequence

Peptide samples were hydrolyzed with constant-boiling HCl at 110°C for 20 hr. The hydrolysate was dried and dissolved in 100 µl of coupling solution [ethanol:0.1 M boric acid buffer, pH 9.0:phenylisothiocyanate (PITC), 79:20:1, v/v/v]. The mixture incubated at room temperature (20–25°C) for 15 min. After being dried, 100 µl of sample buffer (3% ACN in 50 mM sodium phosphate buffer, pH 6.5 containing 50 mM sodium perchlorate) was added and submitted to HPLC on a reverse-phase column (TSKgel ODS 80 TM, 5 µm, 4.6x150 mm), which was developed with a linear gradient of 3–38.25% ACN in 50 mM sodium phosphate buffer (pH 6.5) containing 50 mM sodium perchlorate for 20 min at a flow rate of 1 ml/min at 40°C. The column effluent was monitored for an absorbance at 254 nm.

Amino acid sequence analysis was performed on an Applied Biosystems model 476A pulsed-liquid sequencer with an on-line model 120A phenylthiohydantoin amino acid analyzer. To analyze the amino-terminal amino acid sequence of both the phosphorylated and dephosphorylated forms of guanylyl cyclase, both forms of the enzyme purified by the preparative SDS-PAGE system were subjected to slab gel electrophoresis separately and then the protein in the gel was transferred to a PVDF membrane using a Multiphor II NovaBlot terminal amino acid sequence of both the phosphorylated and dephosphorylated protein band corresponding to each form of guanylyl cyclase (131 kDa for the phosphorylated form and 128 kDa for the dephosphorylated form) was cut out and submitted to automated Edman degradation on an Applied Biosystems model 476A pulse-liquid sequencer.

Immunological methods

The sequence KPPPQKLTQEAIEVAANRVIPDDV which corresponds to the carboxyl-terminal portion (residue numbers from 1102 to 1125) of H. pulcherrimus sperm guanylyl cyclase was selected as the antigenic determinant according to Hopp and Woods (1981), and designed to contain a cysteine residue to the amino terminus. The peptide was chemically synthesized with 432A Peptide Synthesizer (Applied Biosystems Inc.) and purified by reversed-phase HPLC on a Unisil QC-18 column (5 µm, 4.6x250 mm). HPLC was carried out with Shimadzu Model LC-6A chromatography system. The column effluent was monitored by absorbance at 225 nm with use of a Shimadzu SPD-6AV spectrophotometer. We used the following program for purification of the peptide. The sample was applied to the column equilibrated with 5% ACN in 0.1% TFA and unabsorbed materials were washed out with the equilibration solvent. Then, peptides were eluted with a linear gradient of ACN from 5 to 60% in 0.1% TFA over a 55-min time period at a flow rate of 1 ml/min. The peptide collected in a major fraction was rechromatographed with the same program.

The peptide (210 nmol) was conjugated to 0.7 nmol of maleimide-activated keyhole limpet hemocyanin according to the manufacturer’s instruction. The protein (100 µg) coupled to the peptide was emulsified in complete Freund’s adjuvant (1/1, v/v) and injected intracutaneously into the back of a Japanese white rabbit. Subsequently the same amount of antigen in incomplete adjuvant was administered at 2 weeks and 4 weeks after the first injection. At 12 days after the last injection, titer of the antiserum was measured by an enzyme-linked immunosorbent assay (ELISA) using the peptide as an antigen according to the procedures of Voller et al. (1976). Then, the rabbit was bled from vein on the ear, and the antiserum was stored at 4°C until use.

Immunoblotting experiments were carried out essentially by the method of Towbin et al. (1979) using rabbit anti-H. pulcherrimus or anti-S. purpuratus guanylyl cyclase antiserum.

Other methods

SDS-polyacrylamide gel electrophoresis (SDS-PAGE) was carried out essentially as described by Laemmli (1970). The gel was stained with silver by the method of Morrissey (1981). Phosphate content of the purified guanylyl cyclases was determined by the method described in a paper (Buss and Stull, 1983). To avoid unfavorable influence of SDS derived from the guanylyl cyclase preparation on color development in determination of phosphate, fractions containing low concentration of the guanylyl cyclase were dialyzed exhaustively against distilled water and then concentrated with an Amicon Diaflow Cell RK 52 using a YM100 membrane which passes through substances with molecular weight less than 100,000. This procedure was useful to avoid unnecessary accumulation of SDS in the sample. The concentration of protein was determined by the Lowry method (Lowry et al., 1951) modified by Schacterle and Pollack (1973) or by the method of Bradford (1976) using BSA as a standard.

RESULTS

Isolation and sequence analysis of cDNA clone encoding H. pulcherrimus guanylyl cyclase

A cDNA library representing the mRNA from H. pulcherrimus testis was screened with mixed antisense oligonucleotide probes which were synthesized based on the amino acid sequences of the extracellular and intracellular

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Fig.1. The restriction endonuclease map and sequencing strategy for AGC4-7-1 cDNA insert. The map only shows the relevant restriction sites. The direction and extent of the sequence determination are indicated by arrows. The deduced open reading frame is shown by a solid box.
Fig. 2. Complete nucleotide sequence and deduced amino acid sequence of the AGC4-7-1 cDNA insert. The predicted amino acid sequence of the open reading frame is shown below the nucleotide sequence. Nucleotide and amino acid number are listed on the right hand side. The signal sequence and the putative transmembrane sequence are indicated by shaded-boxes. The potential N-linked carbohydrate binding sites are indicated by open-boxes. Polyadenylation signal sequences at the 3'-untranslated region are underlined.
domains of *A. punctulata* guanylyl cyclase. The analysis of \(7.1 \times 10^4\) recombinants from an amplified cDNA library gave rise to finally 6 positively hybridizing clones. The size of the inserts was determined by agarose gel electrophoresis. Four clones contained approximately 4.0 kbp cDNA insert and two clones (λGC4-7-1 and λGC4-7-2) contained almost the same size cDNA insert (approximately 4.3 kbp). One clone, λGC4-7-1, was used for nucleotide sequence determination. The sequencing strategy for λGC4-7-1 is shown in Fig. 1. The complete nucleotide sequence and the deduced amino acid sequence are presented in Fig. 2. The λGC4-7-1 cDNA insert was 4123 bp in length. The oligonucleotide sequences used for screening the clone were found in the sequence at nucleotide positions 708-751 for probe II and 2656-2700 for probe I, respectively. We have assigned the initiation codon to the ATG at nucleotide position 100 because (1) there is an upstream in-frame stop codon, (2) this ATG is flanked by sequences that fit Kozak's criteria for translation initiation codon (Kozak, 1981) and (3) the 21-amino acid sequence following this ATG possesses the features characteristic of signal sequences (Watson, 1984). The initiation codon is followed by an open reading frame of 3378 bp. An in-frame stop codon occurs at nucleotide position 3475 and the 3'-untranslated region composed of 646 bp includes polyadenylation sites (AATAAA). The deduced amino acid sequence suggests that cleavage of signal peptide would yield a protein of 1104 amino acids with a calculated molecular weight of 124,061. The protein contains three potential N-linked glycosylation sites (NXT) at residues 5-7, 164-166 and 409-411, respectively. The protein also contains a hydrophobic region composed of 25 amino acids at residues 486-510 that is flanked on the carboxyl-terminal side by RKR (Fig. 3). These features are typical of membrane-spanning domain of many membrane proteins.

**Purification and characterization of *H. pulcherrimus* sperm guanylyl cyclase**

In the previous study, we purified the phosphorylated and dephosphorylated forms of *H. pulcherrimus* sperm guanylyl cyclase, which retained enzyme activity (Harumi et al., 1992). However, the method used in the study was not adequate for large scale purification because the guanylyl cyclase purified by the method, which comprised several initial steps using low pH-solutions containing 100 mM NaF that are known to inhibit the activity of protein phosphatases, lost enzyme-bound phosphates gradually during the storage without phosphatase inhibitors. This might be due to action of a protein phosphatase(s) which is associated tightly with the guanylyl cyclase or is contaminated in the enzyme preparation, and under the conditions without inhibitors the protein phosphatase became active to release phosphates from the enzyme. Therefore, we used the boiled spermatozoa, in which almost all enzymes should be inactive, for purification of the guanylyl cyclase. By this improved method, we could obtain 2.6 mg (about 20 nmol) of the guanylyl cyclase from 10 g wet weight of spermatozoa. The phosphorylated
Fig. 4. SDS-PAGE and Western blotting analysis of *H. pulcherrimus* sperm guanylyl cyclase. The phosphorylated (1) and dephosphorylated (2) forms of the guanylyl cyclase were analyzed by SDS-PAGE using a 6% gel. The proteins in the gel were silver-stained (left panel) or transferred onto a nitrocellulose filter. The proteins on the filter were located by the method of Towbin et al. (1979) using site-directed antibody against the carboxy-terminal portion of *S. purpuratus* sperm guanylyl cyclase (right panel). The dephosphorylated form of the guanylyl cyclase was purified from *H. pulcherrimus* spermatozoa which were incubated in seawater containing 2 µM SAP-I for 1 min at 20°C.

and dephosphorylated forms of the guanylyl cyclase thus purified contained 26.0 ± 1.3 and 4.3 ± 0.7 moles of phosphate/mol protein (mean ± S.D., n=6), respectively. These values were comparable to those reported previously (Harumi et al., 1992). Both forms of the guanylyl cyclase reacted with site-directed anti-*H. pulcherrimus* sperm guanylyl cyclase antibody as well as site-directed anti-*S. purpuratus* sperm guanylyl cyclase antibody (Fig. 4). Seven peptides were isolated from lysyl endoprotease-digests of the phosphorylated and dephosphorylated forms of guanylyl cyclase and their amino acid sequences were determined as follows: RAYEAALDSLWVK (peptide 1), VDWSEVQTK (peptide 2), GSLQDILENDDIK (peptide 3), GIVYLSSEIJK (peptide 4), PNILDNMIAMERYTNNEELVDERTQELQK (peptide 5), IHVSPWXK (peptide 6) and GEIHTFWLL-GQDPSYK (peptide 7). These sequences were found in the deduced amino acid sequence for *H. pulcherrimus* guanylyl cyclase as follows: peptide 1, residues 534 - 546; peptide 2, residues 547 - 555; peptide 3, residues 651 - 663; peptide 4, residues 679 - 689; peptide 5, residues 848 - 878; peptide 6, residues 1052 - 1059; and peptide 7, residues 1082 - 1097. The amino-terminal amino acids of both forms of the guanylyl cyclase could not be detected in the sequencing.

Northern blot analysis

To determine the size of the mRNA for the λAGC4-7-1 cDNA insert and to see whether the mRNA exists in testes, ovaries, eggs or developing embryos, poly(A)*"RNA prepared from these tissues and embryos was analyzed by Northern blot hybridization using a part (nucleotide numbers from 1 to 2248 of the λAGC4-7-1) of the λAGC4-7-1 cDNA insert as a probe. A strong hybridization signal at the position corresponding to 4.4 kb was detected only with poly(A)*"RNA from a testis sample (Fig. 5).

**DISCUSSION**

It has been reported that SAP-I caused electrophoretic mobility change of *H. pulcherrimus* sperm guanylyl cyclase from 131 kDa to 128 kDa and this mobility change was due to dephosphorylation of the enzyme (Harumi et al., 1992). In this study, site-directed antibody against *S. purpuratus* sperm guanylyl cyclase reacted with both the phosphorylated (131 kDa) and dephosphorylated (128 kDa) forms of *H.*
Terminal portion of the guanylyl cyclase because the anti-
pulcherrimus sperm guanylyl cyclase (Fig. 4). This suggests
that apparent molecular weight difference between the 131
kDa and 128 kDa forms of H. pulcherrimus sperm guanylyl
cyclase is not due to proteolytic degradation of the carboxyl-
terminal portion of the guanylyl cyclase because the anti-
body was made against the synthetic peptide (KPPP-
QKLTQEAIEVAARNVPDDV) which corresponds to the resi-
dues 1102 to 1125 of S. purpuratus sperm guanylyl cyclase
(Thorpe and Garbers, 1989) and identical to the carboxyl-
terminal sequence (KPPPQKLTQEAIEVAARNVPDDV) of
H. pulcherrimus sperm guanylyl cyclase except underlined
valine residue. On the other hand, the amino-terminal amino
acids of both the 131 kDa and 128 kDa forms of H.
pulcherrimus sperm guanylyl cyclase could not be detected,
suggesting that the amino-terminal amino acid is blocked.
Although there is possibility that after proteolytic degradation
of the amino-terminal portion of the enzyme, the resulting
new amino-terminal amino acid was blocked again, we pre-
sume that the amino-terminal amino acid of H. pulcherrimus
sperm guanylyl cyclase was post-translationally modified.
Therefore, apparent molecular weight change of
H. pulcherrimus sperm guanylyl cyclase from 131 kDa and 128
kDa upon SAP-I treatment of spermatozoa does not seem to be
due to proteolytic degradation of the amino-terminal por-
tion of the enzyme. As with membrane forms of guanylyl
cyclases of H. pulcherrimus, S. purpuratus and A. punctulata
spermatozoa, the loss of phosphates from the enzymes
which is induced at fertilization by a specific sperm-activat-
ing peptide is correlated with a decrease in the enzymatic
activity (Harumi et al., 1992; Ramarao and Garbers, 1985;
Vacquier and Moy, 1986). These facts lead to a model for
the sea urchin sperm guanylyl cyclase: the binding of a ligand
(specific sperm-activating peptide) to the receptors
activates the cyclase and the activated cyclase is dephos-
phorylated by a protein phosphatase activated upon the
ligand-binding or already active protein phosphatases which
became accessible to the cyclase due to its conformational
change induced upon the ligand-binding, and the cyclase is
subsequently desensitized.

The predicted molecular weight of mature H.
pulcherrimus guanylyl cyclase (residues 22-1125) was
124,061 which is comparable to the molecular weight of
128,000 for the dephosphorylated form. The apparent small
difference between the values may be attributable to
glycosylation. We presume that at least one of three poten-
tial N-linked glycosylation sites is glycosylated since the H.
pulcherrimus guanylyl cyclase binds to Concanavalin A-
Sepharose. A homology search using NBRF-PIR and
SWISS-PROT databases demonstrated that the deduced
amino acid sequence of cDNA for H. pulcherrimus sperm
guanylyl cyclase showed 98% identity over 1125 amino
acids with that of S. purpuratus spermatozoa (Thorpe and
Garbers, 1989) and 77% identity over 926 amino acids with
that of A. punctulata spermatozoa (Singh et al., 1988). Less
identity with A. punctulata guanylyl cyclase is due to dissimi-
larly in the extracellular domain because the intracellular
domain of H. pulcherrimus guanylyl cyclase has 98% identity
with the intracellular domain of A. punctulata guanylyl cy-
clase (Fig. 6). The predicted primary structure of H.
pulcherrimus guanylyl cyclase bears virtually no resemble-
bance to mammalian receptor/guanylyl cyclase in the extra-
cellular domain (Garbers, 1992). However, the intracellular
domain of H. pulcherrimus guanylyl cyclase had relatively
high similarity to those of mammalian membrane forms of
guanylyl cyclase (30-50% identical) (Fig. 6). As shown in
Fig. 7, a predicted secondary structure of the intracellular
cellular domain of H. pulcherrimus guanylyl cyclase is similar
to that of A. punctulata guanylyl cyclase, although the cata-
ytic domain of A. punctulata is smaller than that of H.
pulcherrimus. Apparent similarity in the predicted secondary
structure of the catalytic domain is seen between H.
pulcherrimus guanylyl cyclase and mammalian receptor/
guanylyl cyclases (Fig. 7). All of the membrane forms of
guanylyl cyclases studied so far possess both a protein ki-
nase-like domain and a cyclase catalytic domain (Garbers
and Low, 1994; Yang et al., 1995). The protein kinase-like
domain contains a majority of the conserved amino acids
identified by Hanks et al. (1988) as conserved or invariant
within the catalytic domain of protein kinases. Although the
protein kinase-like domain shows no protein kinase activity,
it is suggested that the protein kinase-like domain is involved
in regulation of the guanylyl cyclase activity. In mammalian
receptor/guanylyl cyclase (GC-A), ATP-binding to the pro-
tein kinase-like domain has been reported to be a key step
for transduction of the ligand binding signal to activate the
cyclase catalytic domain (Chinkers et al., 1991). Recently, it
has been reported that a novel protein phosphatase binds to
the protein kinase-like domain in mammalian receptor/
guanylyl cyclase, GC-A (Chinkers, 1994). In theory, single-
transmembrane receptors must form dimers, either between
themselves or with other transmembrane proteins, in order
to transduce a signal across the membrane. Both intracellu-
lar and extracellular interactions between receptor subunits
are necessary for this process. In GC-A, a membrane
guanylyl cyclase which is a receptor for atrial natriuretic pep-
tide (Chinkers et al., 1989; Lowe et al., 1989), only a region
composed of 43 amino acids located between the protein
kinase-like domain and the cyclase catalytic domain is nec-
ecessary for dimerization and it is required for guanylyl
cyclase-catalytic activity.

Northern blot analysis demonstrated that the gene en-
coding H. pulcherrimus guanylyl cyclase was expressed only
in the testis. This was also the case for the expression of the
gene for the sperm-activating peptide I (SAP-I)-crosslinked
71 kDa protein (Shimizu et al., 1994). The exclusive expres-
sion of both genes in the testis suggests that apparent co-
expression of both genes in H. pulcherrimus testis may be
due to the necessity of resultant physiological response to
SAP-I and/or its derivatives.
Fig. 6. Sequence comparisons of the intracellular domains of *H. pulcherrimus* guanylyl cyclase (HPGC) and the other membrane forms of guanylyl cyclases. The deduced amino acid sequence of the predicted intracellular domain of *H. pulcherrimus* guanylyl cyclase is compared with the sequences of *S. purpuratus* (Thorpe and Garbers, 1989) and *A. punctulata* (Singh et al., 1988) guanylyl cyclases, rat GC-A (Chinkers et al., 1989), GC-B (Schulz et al., 1989), and GC-C (Schulz et al., 1990). Amino acid identities are shaded, and gaps are represented by dashes.
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Fig. 7. Comparison of the predicted secondary structure of the intracellular domain of *H. pulcherrimus* sperm guanylyl cyclase with those of *A. punctulata* sperm guanylyl cyclase and mammalian receptor/guanylyl cyclases. The secondary structure was estimated according to the method of Chou and Fasman (1978). The secondary structure of the kinase-like domain (residues from 600 to 720) and the catalytic domain (residues 860 to 1090) predicted for *H. pulcherrimus* sperm guanylyl cyclase were similar to the corresponding domains for other membrane form of guanylyl cyclases.

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