

Increased mRNA Related Ovarian Maturation during Induction of Maturation Competence in Red Seabream, *Pagrus major*

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참돔, *Pagrus major*의 성숙능력 유도시 증가된 난성숙 관련 mRNA

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ABSTRACT: This study has used differential display-PCR, to amplify genes transcribed during the ovarian maturation induced by human chorionic gonadotropin (hCG). The cDNA expressed at the times of acquisition of oocyte maturation competence in red seabream (*Pagrus major*) following treatment with hCG was amplified and cloned. A full-length of cDNA for *P. major* was isolated using differential display-PCR and 5'RACE. This cDNA clone contained 2,662 nucleotides including the open reading frame that encoded 434 amino acids. Homology analyses, using the GenBank and EMBL general database searches, indicated that the nucleotides sequence of the cDNA does not have high homology with any other genes. This cDNA was judged to be a gene, which induction of maturation competence coincides with increase of mRNA related ovarian maturation. Consensus sequences which were consistent with protein kinase C phosphorylation sites and casein kinase II phosphorylation sites were identified. *In vitro*, the transcription level of mRNA related ovarian maturation increased between 9 hr and 24 hr following treatment of ovarian follicles with hCG. It was also increased after GtH-II (300 ng/ml) stimulation. Furthermore, *in vivo*, mRNA related ovarian maturation was rarely expressed prior to the acquisition of oocyte maturation competence, but was strongly expressed after the acquisition of oocyte maturation competence, suggesting that the hCG induction of maturation competence is brought about by the *de novo* synthesis of the mRNA related ovarian maturation in *P. major*.

Key words: Red seabream, *Pagrus major*, mRNA related ovarian maturation, Maturation competence.

요 약: Differential display-PCR 방법을 이용하여, hCG 처리에 의한 참돔, *Pagrus major*의 난성숙 능력의 획득 경과시간에 따라 새롭게 발현하는 cDNA를 해석하였다. Differential display-PCR과 5'RACE 방법을 이용하여, 2,662 염기와 434개의 아미노산을 코드하고 있는 cDNA의 전염기배열을 결정하였다. DNA의 데이터베이스인 GenBank 및 EMBL을 이용하여 상동성을 검색한 결과, 본 cDNA와 높은 상동성을 나타낸 유전자는 검색되지 않았다. 따라서 본 cDNA는 참돔의 난성숙 능력 유도과 함께 그 발현량이 증가하는 난성숙 관련 유전자로 판단되었다. 또한 본 cDNA에서는 protein kinase C 인산화 및 casein kinase II 인산화 consensus 배열의 존재가 확인되었다. 본 연구에서 cloning된 난성숙 관련 유전자는 난여포에 hCG 처리 9~24시간 후에 그 발현량이 증가하였으며, GtH-II (300 ng/ml)로 배양한 난여포에서 특이적으로 증가하였다. 또한 *in vivo* 실험에서 난성숙 관련 유전자는 난성숙 능력 획득 이전의 난소에서는 거의 발현하지 않았으나, 난성숙 능력을 획득한 난소에서 강하게 발현된 점으로 보아, hCG에 의한 난성숙 능력 유도에 성숙기간 중 새롭게 합성되는 난성숙 관련 유전자가 관여할 가능성이 높다.

INTRODUCTION

In teleost fishes, oocyte maturation is induced by maturation-inducing steroids (MIS), such as 17α , 20β -dihydroxy-4-pregnen-3-one (DHP) (Nagahama, 1987) and 17α , 20β , 21 -trihydroxy-4-pregnen-3-one (20β -S) (Trant & Thomas, 1988). These steroids are produced by the follicular layer surrounding oocytes under stimulation of gonadotropic hormone (GtH)

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(Nagahama, 1987; 1990). It is known that priming with an injection of GtH influences the induction of oocyte maturation, *in vitro* (Patino & Thomas, 1990; Degani & Boker, 1992). However, this general concept does not always hold true as shown by studies of the oocyte maturational competence of daily spawners, such as kisu (*Sillago japonica*) (Kobayashi et al., 1988; Zhu et al., 1994), tobinumeri-dragonet (*Repomucenus beniteguri*) (Zhu et al., 1989; 1994), Atlantic croaker (*Micropogonias undulatus*) (Patino & Thomas, 1990), olive flounder (*Paralichthys olivaceus*) (Yoshikuni et al., 1992) and red seabream (*Pagrus major*) (Kagawa et al., 1994). The response of the oocytes to DHP could be induced *in vitro* by preincubation with human chorionic gonadotropin (hCG) (Patino & Thomas, 1990; Yoshikuni et al., 1992; Kagawa et al., 1994; Zhu et al., 1994), suggesting that DHP does not act as a mediator of hCG in the development of oocyte maturational competence. Moreover, in the oocytes of *M. undulatus* (Patino & Thomas, 1990) and *P. major* (Kagawa et al., 1994), actinomycin D has been found to inhibit GtH induced germinal vesicle breakdown (GVBD). These reports suggest that the production of new proteins through a mechanism of GtH-stimulated RNA synthesis is essential for the development of oocyte maturational competence (Patino & Thomas, 1990; Kagawa et al., 1994). Except for *M. undulatus* connexin 32.2 mRNA (Yoshizaki et al., 1994), however, the activities of genes related to oocyte differentiation or maturational competence has not been directly addressed in *P. major* or in any other vertebrate species.

The present study was designed to determine whether the change of mRNA levels in the ovarian follicles of *P. major* following treatment with hCG during the acquisition of oocyte maturational competence, using differential display-PCR. This method potentially amplifies genes transcribed during hCG-induced oocyte maturation.

MATERIALS AND METHODS

1. Fish and Tissue Collection

Mature *P. major* weighing 2.0~3.0 kg were purchased from fishermen in Gokasho Bay, Mie Prefecture, Japan and kept in a flow through outdoor tank (3 ton). The fish were anesthetized with 2-phenoxyethanol (Sigma, St. Louis, MO) and killed by decapitation at 08:00 hr (incompetent ovaries) and 16:00 hr

(competent ovaries). Incompetent ovaries were removed and placed in ice-cold Ringer's solution (pH 7.4, supplemented with 10 g of NaCl, 0.22 g of KCl, 0.25 g of CaCl₂, 0.74 g of MgSO₄·7H₂O, 1.19 g of HEPES, 0.9 g of glucose, 0.1 g of streptomycin, and 100,000 U of penicillin G calcium per liter). Ovaries were cut into small pieces in ice-cold Ringer's solution and the ovarian follicles were dispersed by pipetting the fragments.

2. Incubation Procedures

Clusters of ovarian follicles were removed by passage of the suspension through a stainless-steel wire mesh (pore diameter, 600 μ m), and ovarian follicles at the tertiary yolk stage (about 500 μ m in diameter) (Matsuyama et al., 1988) were collected on a wire mesh (about 420 μ m). Approximately 60 ovarian follicles were transferred to individual wells of 24-well culture plates, each of which contained 1 ml of Leibovitz's L-15 medium (Gibco-BRL, Gaithersburg, MD), pH 7.6, supplemented with 2.4 g of HEPES, 0.1 g of streptomycin, and 100,000 U of penicillin G calcium per liter. The oocytes were preincubated in 1 ml of Leibovitz's L-15 medium in the presence of human chorionic gonadotropin (hCG; Teikoku Zoki Ltd, Tokyo, Japan) at 10 IU/ml. At time 0 (untreated control), 3, 6, 9, 12 and 24 hr after hCG treatment, ovarian follicles were washed 3 times with fresh Leibovitz's L-15 medium, transferred to Leibovitz's L-15 medium containing 17 α , 20 β -dihydroxy-4-pregnen-3-one (DHP; 10 ng/ml; Sigma) and/or actinomycin D (1 μ g/ml; Sigma) and incubated for 24 hr at 20°C. In addition, some ovarian follicles were preincubated with DHP (10 ng/ml), human insulin-like growth factor-I (IGF-I; 10 nM; human recombinant, Bachem Inc., Torrance, CA), *P. major* GtH-I (100 ng/ml, 300 ng/ml) (Tanaka et al., 1993), or *P. major* GtH-II (100 ng/ml, 300 ng/ml) (Tanaka et al., 1993) for 0 (untreated control), 3, 6, 9, 12 and 24 hr, transferred to medium containing DHP (10 ng/ml) and/or actinomycin D (1 μ g/ml) and incubated for 24 hr at 20°C. After incubation, all the ovarian follicles were stored at -80°C until used.

3. Differential Display-PCR

Total RNA was extracted using a total RNA extraction kit (Pharmacia Biotech, Uppsala, Sweden) from each time of hCG-treated ovarian follicles. Differential display-PCR experiments were carried out using an RNA mapTM mRNA differential

display system (GenHunter, Brookline, MA). Total RNA was reverse-transcribed with an anchor primer in the presence of Maloney murine leukemia virus (MMLV) reverse transcriptase (GenHunter) and then amplified with an 5' adaptor primer (5'-AAGCTTCGACGCT-3') and the anchor primer (5'-AAGCTTTTTTTTTTTTA-3') in the presence of Ampli-Taq DNA polymerase (5 U/ μ l; Perkin-Elmer, Norwalk, CT). PCR was carried out for 40 cycles as follows; 94°C for 30 sec for denaturing; 40°C for 2 min for annealing; and 72°C for 30 sec for extension, followed by 1 cycle for 10 min at 70°C for extension. Three μ l loading dye was added to 5.25 μ l the amplification products, heated at 80°C for 2 min and then fractionated on a 6% DNA sequencing gel. The gel was run at 55 W constant powers for 3 hr, dried and then analyzed by staining of DNA silver staining kit (Pharmacia Biotech.). The PCR product which increased particularly during the oocyte maturation was excised from the gel, soaked in 100 μ l of H₂O for 10 min, boiled for 15 min and centrifuged at room temperature (20°C) for 2 min. DNA was precipitated from the supernatant by the addition of 10 μ l of 3 M sodium acetate, 5 μ l of glycogen (10 mg/ml; Sigma) and 350 μ l of 100% ethanol for 15 min at -80°C, and centrifugation for 10 min at 4°C. The pellet was then dissolved in 10 μ l of H₂O. For each band, 4 μ l of the extracted DNA was reamplified using the same primer set and PCR conditions used above. One fragment was isolated and ligated, cloned into pGEM-T Easy Vector (Promega, Madison, WI) and sequenced.

4. Rapid Amplification of cDNA 5'ends (5'RACE)

The PCR production (179 bp) was particularly increased during the development of oocyte maturation. Ovarian follicles from each times of incubation with hCG (10 IU/ml) were found to have an adaptor primer (5'-AAGCTTCGACGCT-3') and the anchor primer (5'-AAGCTTTTTTTTTTTTA-3') included with the RNA mapTM mRNA differential display system. One clone isolated using differential display-PCR did not contain the complete 5'ends. Consequently, a fragment containing the 5'end of the transcript was amplified using a 5'RACE System for Rapid Amplification of cDNA Ends, Version 2.0 kit (Gibco-BRL). The total RNA (1 μ g) was reverse-transcribed according to the kit protocol using a gene specific primer (GSP)1 (5'-ATGTGTGTTATGACAT-3') located within the

coding sequence. Therefore, two GSPs were designed (GSP2; 5'-ACAGACTTTATATCTGAGGTACTACTGGACC-3' and GSP3; 5'-CACCAACATGGCCGCCCACTC-3'). The final PCR product was amplified and cloned and sequenced using the ALFexpress DNA sequencer (Pharmacia Biotech.), and the DNA sequence was analyzed using the GENETYX-WIN (Software Development Co., Japan) software package.

5. Northern Blot Analysis

To clarify whether isolated mRNA from ovarian follicles from each time of incubated with hCG (10 IU/ml) was differentially expressed specifically in the oocyte undergoing developmental maturation, Northern blot analysis was performed. The total RNA (30 μ g) was electrophoresed according to the formaldehyde gel method (Sambrook et al., 1989) and transferred to nylon membranes (Hybond N⁺) (Amersham, Buckinghamshire, U.K.) according to the manufacturer's instructions. The PCR product label used for the Oligolabelling kit (Amersham) with [α -³²P] dCTP. Post-hybridization washing was carried out in 2 \times SSC for 20 min at 65°C, in 1 \times SSC/0.5% SDS for 15 min at 65°C, and finally in 0.1 \times SSC/0.5% SDS for 15 min at 65°C. The hybridization signals were analyzed using FUJIX BAS 1000 Bio-Imaging Analyzer (Fuji Film, Japan).

6. Statistics

The data were expressed as mean \pm S.E.M. ANOVA followed by Duncan's multiple range tests was as applied for statistical analysis.

RESULTS AND DISCUSSION

In this study, hCG (or GtH-II) induced oocyte maturational competence in the ovarian follicles of *P. major*. Kagawa et al. (1988) reported that GtH-II, but not GtH-I, is involved in the final maturation of *P. major* oocytes. Moreover, in the *M. undulatus* oocytes, actinomycin D blocked GtH-induction of oocyte maturational competence (Patino & Thomas, 1990). Kagawa et al. (1994) reported that hCG induced the oocyte maturational competence of *P. major* via synthesis of RNA and *de novo* protein synthesis. Therefore, newly-synthesized proteins are involved in hCG (or GtH-II)-induction of oocyte maturational competence. However, if hCG (or GtH-II) directly stimulates an

increase in oocyte maturational competence of ovarian follicles, this increase should not require *de novo* protein synthesis. In this study, cDNA expressed in ovarian follicles during the acquisition of oocyte maturational competence after treatment with hCG (or GtH-II) was cloned using differential display-PCR method. The differential display-PCR method was used to identify differences among subsets of mRNA samples, since it allows the amplification of genes the transcription of which is induced under unique conditions (Liang & Pardee, 1992; Liang et al., 1994; Zimmermann & Schultz, 1994). Fig. 1 shows a base sequence of the cloned cDNA. It contained a 2,662 bp insert cDNA with an open reading frame of 1,302 bp that begins with the first ATG codon at position 3 bp and ends with a TGA stop codon at position 1,305 bp. A putative polyadenylation signal, AATAAA (Proudfoot & Brownlee, 1976) was recognized at position 2,634 bp. This open reading frame encodes a polypeptide containing 434 amino acids (Fig. 1). Homology analyses using the GenBank and the EMBL general database searches indicated that the nucleotide sequence of the cDNA did not have a high homology with any other genes. Therefore, this cDNA was judged to be a gene, which induction of maturational competence coincides with increase of mRNA related ovarian maturation. The physiological roles on production of the mRNA related ovarian maturation are not known.

In this study, Northern blot analyses revealed that the transcription level of mRNA related ovarian maturation increased with the time of incubation; the levels at 9 hr and 24 hr were significantly higher ($P < 0.05$) than that at 0 hr (Fig. 2). Effects of hCG on *in vitro* induction of GVBD were examined using the ovarian follicles ($87.76 \pm 3.29\%$) of the oocytes had undergone GVBD at 12 hr (data not shown). Therefore, the processes of oocyte maturational competence and the induction of GVBD of the oocytes are well correlated. Furthermore, Northern blot analysis on transcription levels of mRNA related ovarian maturation, and on the β -actin probe for positive control, was carried out using 30 μ g of total RNA extracted from ovarian follicles cultured for 12 hr in normal medium, DHP (10 ng/ml), human IGF-I (10 mM), *P. major* GtH-I (100 ng/ml, 300 ng/ml) or *P. major* GtH-II (100 ng/ml, 300 ng/ml) (Fig. 3). The mRNA related ovarian maturation was highly expressed in the presence of GtH-II, while DHP and IGF-I had no effect.

There is currently no information on the functional domain

and consensus sequence of this gene. However, it is noteworthy that mRNA related ovarian maturation possesses the protein kinase C (PKC) phosphorylation site, (S,T)X(R,K) (Kishimoto et al., 1985; Woodget et al., 1986), and the casein protein kinase II phosphorylation site, (S,T)X₂(D,E) (Pinna, 1990) (Fig. 1). These regulate phosphorylation of many systems (Hoh et al., 1991). Takeda et al. (1987) reported that rat connexin (Cx) 32 was phosphorylated by PKC *in vitro*. *M. undulatus* Cx32.2 also has PKC phosphorylation sites, and an increase in ovarian Cx32.2 mRNA production coincided with the induction of oocyte maturational competence (Yoshizaki et al., 1994). Moreover, phorbol 12-myristate 13-acetate (PMA), a PKC activator, inhibited GtH-II inducible oocyte maturational competence (Chang et al., 1999). Furthermore, Yoshizaki et al. (1994) reported that the transcription of Cx32.2 levels were negligible in incompetent ovarian tissue and increased substantially upon induction of competence by treatment with hCG. In the present study, *in vivo* Northern blot analysis was carried out using 30 μ g of total RNA extracted from incompetent and competent ovaries (Fig. 4). The mRNA related ovarian maturation was highly expressed after, but not before, the acquisition of oocyte maturational competence. These results suggest that the gene activation of mRNA related ovarian maturation in *P. major* is related to the selective development of ovarian follicles to completion of oocyte maturational competence.

In summary, the present study found that the induction of oocyte maturational competence by GtH-II requires *de novo* synthesis of ovarian RNA and protein, and coincides with an increase in the production of a novel gene transcript, mRNA related ovarian maturation. On the other hand, the physiological roles of mRNA related ovarian maturation in the acquisition of oocyte maturational competence could not be clarified. Further research is needed to explain the role of steroids and secondmessenger systems in the regulation on the expression of mRNA related ovarian maturation.

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1 GG
 3 ATGGCCCAGAACCAGGTGGTTCTGCAGTTCGCTTTGCCACATTCGGGGACTCCATGCTGCAGAAGATGAACCTCCTACGTCACCAGAGA
 MetAlaGlnAsnGlnValValLeuGlnPheArgPheAlaThrPheGlyAspSerMetLeuGlnLysMetAsnLeuLeuArgHisGlnArg 30
 93 CGCTTCTGTATGTCACCGTACGCATCAACCAGCTGGAGGTCCCGGTCACAAGGTAGTGTGGCCGCTGCTCCTCGTTCTGAGGGAC
 ArgPheCysAspValThrValArgIleAsnGlnLeuGluValProGlyHisLysValValPheAlaAlaGlySerSerPheLeuArgAsp 60
 183 CAGTTCATCCTGCAGCAGGATTCCAGGGCGGTTCCAGATTCCATGATCCAGGAGGCGAGGTGGCCGGCAGCTGTGCTGCTCAGTCC
 GlnPheIleLeuGlnGlnAspSerArgAlaValGlnIleSerMetIleGlnGluAlaGluValGlyArgGlnLeuLeuLeuSerCysTyr 90
 273 ACAGGTACAGTGGAGTTTCCCGAGCTGGAGCTGGTGCATTACCTGACAGTGGCCAGTTTCTCCAAATGGGCCACATTGTGGAGCAATGC
 ThrGlyGlnLeuGluPheProGluLeuGluLeuValHisTyrLeuThrValAlaSerPheLeuGlnMetGlyHisIleValGluGlnCys 120
 363 ACTCAGGCACTCAGCAAGTTCATTAACCCAGGCTGCACGGCAGCTGGAGGTGGAGGTGGAGGTGGATATGAGGAGGGAGAAGAGGAG
 ThrGlnAlaLeuSerLysPheIleLysProGlnAlaAlaArgGlnLeuGluValGluValGluValAspMetArgArgGluLysLysGlu 150
 453 GAGGGTTTATCCTCTCAGGCCAGAGAGGGCAAGAGCACTCTCAGTTCCGACTGTCCATGAGGAAGATGAGGACGTGGAGCATGTTGAG
 GluGlyLeuSerSerGlnAlaGlnArgGlyGlnGluHisSerGlnValArgThrValHisGluGluAspGluAspValGluHisValGlu 180
 543 GACGACAACAATGGTGACGACGAGTATGATGACGATGTGATCATAACGCCCAAGTCCCTCTCCAGATCTTAGGCAGACGTCCAAGG
 AspAspAsnAsnGlyAspAspAspAspAspValIleIleGlnProLysSerProLeuGlnIleLeuGlyArgArgProArg 210
 633 CAGGGTATGGTGGAGAGTGACATCACTATAGTAAAAGTGGAGTCTGTGTCTGACGTAGCAGAAAACCTCCATCACTGGTCAATTTCCCTCC
 GlnGlyMetValGluSerAspIleThrIleValLysValGluSerValSerValAlaGluAsnSerIleThrGlyHisPheProSer 240
 723 AGCCACCTGCTGCCCTGCCTCTCCTGAGCCCCAGCACTCCCTCATCAACTCCACTGTTTACAGTCGTGGCAGTGAGATGGCGGTTCCA
 SerProProAlaAlaLeuHisSerProGluProGlnHisSerLeuIleAsnSerThrValTyrSerArgGlySerGluMetAlaValPro 270
 813 CCTGGCGTGGCCGATACCCGCTCAGTCCGCTCCTCCATCCCTCCTGCGGAGAAACACAGCGGACACCAGGAACTACGACAAACCT
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 1173 TGTGACATGGTTTTCGCTCATAAGCCAGTTCCTCCGCAAGCACCTCAACAGATCCACGGCAAGAAGCCTTCGACAACGCAACGAAAGGC
 CysAspMetValPheAlaHisLysProValLeuArgLysHisLeuLysGlnIleHisGlyLysAsnSerPheAspAsnAlaAsnGluGly 420
 1263 AGCCTGCACGAAGGGGTCTTGACTTTGACTTTCGCCAAATATGAAATCATTGGACCCTTACGTTTTAGTAGCTTTGTTGGAAACCAGCC
 SerLeuHisGluGlyGlyLeuAspPheAspPheArgGlnIle * 434
 1353 GTCATTTAAATGGAAATGGTGGGGCTTCTCTAAGATAGAACTGAAGCTGATACAAAATTTCTTCGGTGGAGAAGCCAGAAATGGCA
 1443 CTATCAACGCTGGCAGATGAGTGAACAGGACATGTGACCTCGTCTGATGAGTTTAACTGGAGAGCATTAAACGAGAAAGAGAGT
 1533 CCTGGTCTAATGTCACCTAGCCTCATTATCGTGGACTGTTTTTATCGTTTTTCTACAATACATTGTAGATGCCTTCATATCATACTT
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 1683 AAAACACAGAGAGCCGAAGTCAAGCCCTTCTGATTTTCTCTGGGAAAAGAGAAAGACAGATAAATTTTTAATGCCATTTGAATGTGT
 1803 CATGAATCACACACATGATGTTTGTGGTGGAGGATGGTTTTCCAAGTCAAGAAAGTCTTAATTTGTGATGAAATTAATGAAATGTGA
 1863 GACTGAAAATACGGAATTACAAACACTATACAGCCAACAGTCTGTTGAACCTTCACAAAACCTGTAACCTTAAACATTTGAGAGCTGCT
 1983 CCTGTATATTAGCAGCTCACTGAACTGACCAGCTCTCCTTTCACATAGCTGCAGTTGTCAATATGACCCGATTTTTTGTGATTTTCATCT
 2043 TTTTGTAGTACCTTCTCTGTGCTGAGTTGGCGCCATGTTGGTGTGTTGTGACGTGTGTTGAGCAAGATGATGATGTTTCACTTATGGCAA
 2163 ACTGCAACTTCTTGACTTGGAAAATATCTTTTAAATGCAAAACATCACAATATCATCACAATGTTAAATACAGCACAATTCATTT
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 2343 ATATATTCAAAATATTTATCATATTTGATATTTGTATATTTGTATACAGTCTACTGTAGCCTTTCTTTCTTACCTGTGTAATATGACAACA
 2403 TCATAACTAAAAGAACTTGAAGAAGCTGGGTTGAAACATATTTTATTGTGGGAAAGCTACGCCGCTGATGGGGATGCCAAAGTGTCT
 2523 ATGTGAACCTGAAATGGTCTTTTATACAGACTTTATATCTGAGGTACTACTGGACCAAAAGTGACATTTGACCTGTCTGTTCATGCAA
 2583 GTCGATGTGTGTATGACATTTAATAAATCTTAATCAGTAAAAAATAA

Fig. 1. Base sequence of gene related ovarian maturation (GROM) in *P. major* and putative amino acid sequence. The nucleotide and amino acid residue number are shown on the left. The polyadenylation signal is boxed. Shaded amino acids show the predicted a casein protein kinase II phosphorylation sites. Underlines show predicted kinase C phosphorylation sites. This sequence data is available from DDBJ/EMBL/GenBank nucleotide sequence databases with the accession number AB036921.

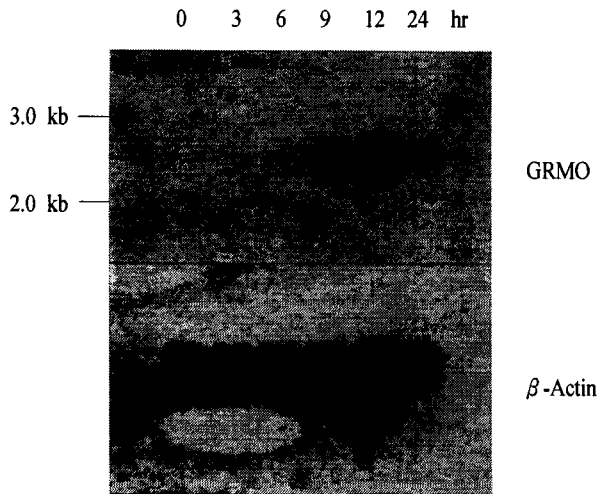


Fig. 2. Effects of hCG (10 IU/ml) on transcription levels of gene related ovarian maturation (GROM). Northern blot analysis of total RNA (30 μ g) extracted from ovarian follicles incubated with hCG for 0, 3, 6, 9, 12 and 24 hr were hybridized with GROM and β -actin probes. The positions (kb) of RNA molecular weight markers are shown on left.

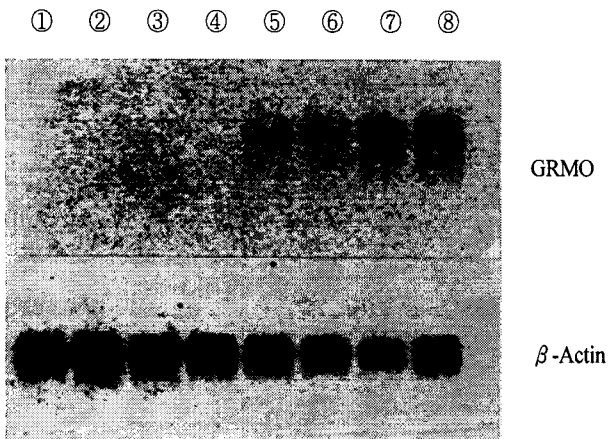


Fig. 3. Effects of 17α , 20β -dihydroxy-4-pregnen-3-one (DHP, 10 ng/ml), human insulin-like growth factor-I (IGF-I, 10 nM), *P. major* GtH-I (100 ng/ml, 300 ng/ml) and *P. major* GtH-II (100 ng/ml, 300 ng/ml) on transcription levels of gene related ovarian maturation (GROM). Northern blot analysis of total RNA (30 μ g) extracted from ovarian follicles was hybridized with *P. major* GROM and β -actin probes.

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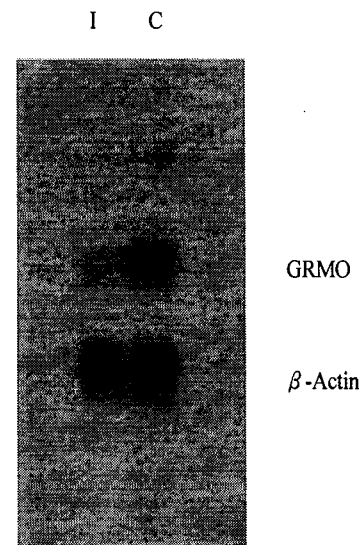


Fig. 4. *In vivo*, Northern blot analysis of total RNA extracted from incompetent (I) and competent ovaries (C). Incompetent and competent ovaries were collected at 08:00 hr and 16:00 hr, respectively. Total RNA (30 μ g) was used for electrophoresis. After transfer to the membrane, the duplicated series of blots were separately used for probing with [α - 32 P] dCTP-labelled gene related ovarian maturation (GROM) and β -actin probes.

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