

Rainbow trout cytochrome *P*-450_{c17} (17 α -hydroxylase/17,20-lyase)

cDNA cloning, enzymatic properties and temporal pattern of ovarian *P*-450_{c17} mRNA expression during oogenesis

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A cDNA clone encoding cytochrome *P*-450_{c17} (17 α -hydroxylase/17,20-lyase) was isolated from a rainbow trout ovarian follicle cDNA library. The cDNA contained an open reading frame of 1,542 nucleotides encoding a protein of 514 amino acid residues. The amino acid sequence of trout *P*-450_{c17} shows a much greater homology with chicken *P*-450_{c17} than with that of human, bovine and rat. The trout *P*-450_{c17} expressed in non-steroidogenic mammalian COS-1 cells showed both 17 α -hydroxylase and 17,20-lyase activities. The cDNA only hybridized to a single species of mRNA (2.4 kb) isolated from rainbow trout ovaries; the 2.4 kb transcripts were abundant in trout ovaries during the later stages of oogenesis.

Rainbow trout; Cytochrome *P*-450_{c17}; cDNA cloning; Expression in COS-1 cell

1. INTRODUCTION

In vertebrates, the actions of gonadotropins on regulating germ cell development and maturation are considered to be mediated predominantly by gonadal steroid hormones. In salmonid fishes, two biologically important steroidal mediators of oocyte growth (estradiol-17 β) and maturation (17 α ,20 β -dihydroxy-4-pregnen-3-one; 17,20-DP) have been identified. It is now established that ovarian granulosa cells are the site of production of these two steroidal mediators, but production by the ovarian follicle depends on the provision of precursor steroids by the thecal cell (two-cell type model) [1–4]. A dramatic switch in the salmonid steroidogenesis from testosterone to 17 α -hydroxyprogesterone occurs only in the thecal cell layers immediately prior to oocyte maturation [5]. The formation of testosterone requires the activities of both 17 α -hydroxylase and 17,20-lyase, whereas 17 α -hydroxyprogesterone requires only 17 α -hydroxylase. Recent studies of mammalian cytochrome *P*-450_{c17} have shown that *P*-450_{c17} is a single enzyme mediating both 17 α -hydroxylase and 17,20-lyase activities in the synthesis of steroid hormones [6–11]. Therefore, it is of great interest to investigate the molecular mechanisms responsible for the differential regulation of these two enzymatic activ-

ities of *P*-450_{c17} in thecal cell layers immediately prior to oocyte maturation.

To initiate these studies in salmonid fish, we cloned a full-length cDNA encoding cytochrome *P*-450_{c17} from a rainbow trout (*Oncorhynchus mykiss*) ovarian thecal cell layer cDNA library. The enzymatic activities catalyzed by rainbow trout *P*-450_{c17} were determined by expressing the cDNA in transiently transfected non-steroidogenic COS-1 cells. The expression of *P*-450_{c17} mRNA was also examined in trout ovarian follicles at different stages in oogenesis.

2. MATERIALS AND METHODS

2.1. Cloning and sequencing

Three-year-old rainbow trout were obtained from Samegai Trout Hatchery in 1990. Thecal cell layers were isolated from ovarian follicles at the mid-vitellogenic stage (oocyte diameter, 3.54 mm) with fine watchmaker's forceps. A cDNA library from ovarian thecal cell layer poly(A)⁺ RNA was constructed as described previously [12]. A human cytochrome *P*-450_{c17} cDNA [13] was digested at bases 828 and 1,458 with *Nsp*I and *Pvu*II to yield a 630 bp fragment which was subcloned into M13mp19. The human cDNA was labeled as described previously [12] and used to screen the ovarian thecal cell cDNA library of rainbow trout under the following conditions: 5 $\times$ SSC (0.75 M NaCl/0.075 M sodium citrate), 35% (v/v) formamide, 200 μ g/ml of denatured herring sperm DNA, 5 $\times$ Denhardt's solution (0.1% polyvinylpyrrolidone/0.1% ficoll type 400/0.1% bovine serum albumin fraction V), 0.2% SDS, 10% dextran sulfate at 42°C. The cDNA inserts from positively hybridizing clones, were isolated and digested with *Kpn*I. The *Kpn*I fragments were rendered blunt-ended with Klenow polymerase, then cloned into the *Sma*I site of pBluescript KS(–). DNA sequencing was performed by using ExoIII/Mung bean nuclease deletion system (Takara Co.) [14] and a 373A DNA sequencer with Dye

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primer or Dye Deoxy Terminator thermal circular sequencing systems (Applied Biosystems Co.).

2.2. COS-1 cell expression

The rainbow trout *P-450_{c17}* expression vector was constructed by ligating the 2,081 bp cDNA fragment which was cut from the *KpnI* fragment by digestion with *SacI* into pSVL, an expression vector using the SV40 late promoter (Pharmacia LKB). 15 µg of the recombinant plasmid were transfected to 3×10^5 COS-1 cells plated onto a 60 mm tissue culture dish in 3 ml culture medium according to Tanaka et al. [12]. Thin layer chromatography (TLC) analysis of catalytic properties of trout *P-450_{c17}* was carried out using ¹⁴C-labelled pregnenolone or progesterone as substrate as described previously [15].

2.3. Northern blot analysis

Northern blot analysis was carried out as described previously [12]. The 2,081 bp cDNA fragment as a probe was labelled by Multiprime DNA labelling systems (Amersham), and hybridization was per-

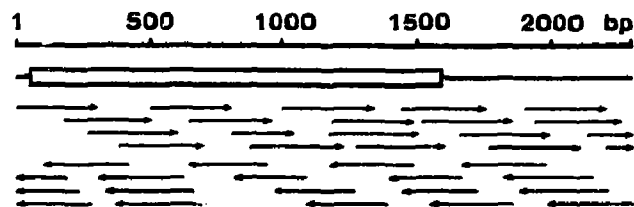


Fig. 1. Sequencing strategy for λh3-7. Location of the open reading frame is shown by an open box. Each arrow indicates the direction and extent of sequencing.

formed under the following conditions: 5× SSC, 50% formamide, 200 µg/ml of denatured herring sperm DNA, 5× Denhardt's solution, 0.2% SDS at 42°C.

GTGACACTCTGATAACGACGCCAGCCCCCTCTCGGCCCAACATACAGCATGGCGTGGT	89
CTGGGTCTACTGCTCTTGCAGGTGAAACTTCGAAGGTCCCTGGAGACGAGGGGGCCCTCCGAGCCTGCCCGTGTCCCACTCATCGGG	179
AGCCTGTGTGACCTGCGAAGCAATCAGGCACCGCATGTCTCTTCCAGAAGCTGCAGCAGAAATATGGACATACCTATTCTCTAATGATG	269
GGCCCCACACACATCATCTTGTCTCAACACCCAGCAGCGCAAGAGGTCCTTAAAAAGGGGAAATCTTTGCAGGAAGACCCAGA	359
ACAGTAACACAGACCTGTTGACGAGGGACGGTAAAGATATTGCCTTTGCAGACTACGGTGCACATTGGAGATTTCATCGTAAAAACAGTG	449
CATGGAGCCTTGTGTATGTTTGGTGAGGGCTCTGCCTCCATCGAGAGATATCTGTAGGGAAGCTCTCTCCCTGTGTGACACTCTGCGA	539
GAGTCAGGAAGTGACATCTTGGACTTGTCTCCAGAGCTGACAAGAGCTGTACCAACGCTGGTCTGCTCTCTCTCAGTCTCTCTCTAT	629
TGCCCGGGCGACCCCGAGTTTGAGGCCATGCTGCAGTTCAGCCAGGGCATCGTGGATACGGTCCCTAGGACAGTCTGGTGGACATCTTC	719
CCATGGCTACAGGCTCTCCCAACGACAGACCTGCGTCTCTAAAGCAGTGTGTCAATCAGAGACAAGCTGCTTCAGAAAAAATACGAG	809
GAACACAAGTCGGACTACAGCGATCATGAACAGAGAGACCTGCTGGACGCCCTGCTAAGGGCCAAACGAGTGTGAGAACAACAACACT	899
GCCGAGATCACCATGGAGACCGTGGGCCCTTAGTGAAGACCACCTGCTCATGACCGTGGGTGACATATTGGAGCCGGAGTGGAAACACG	989
TCAACAGTCTTAAATGGGCAATTGCCTACCTCACCACAGGTACACAGGTAACAACGGAATTCAGGAGGAACGGACAGTGTGGTGGGG	1079
GGAGACAGAACCCCCAGCTCAGTGACAGGGGGAGCCCTGCCCTACCTGGAGGCCACCATTAGAGAGGTGCTACGCATCCGGCCTGTTGCC	1169
CCTCTACTCATCCCCCATGAGCCCAACAGACACCAAGTATTGGCAAGTCTGTTAGGAAGGTGCTCGCATCATCATCAACTTGTGG	1259
TCCCTGCTACCATGAGAGAGGAGTGAAGAACCAGAGATGTTTGACCTGGTCTGCTTCCGAAACGAGGAGGGGACAGGTCTGTGCATC	1349
CCCTCGCCAGCTACTTGGCGTTTGGGGCAGGGGTGAGAGTGTGCTGGGGGAGGCCCTGGCTAAGATGGAGATCTTCCCTCTCCCTCTCC	1439
TGGATCTCTCAGCGTTTAACTATGACCGTGTCCCGGGCCAGCCACTGCCAGCCGTGAAGGAAGTTTGGGGTAGTCTCCAGCCGGTC	1529
AAATACAAGGTCAATGCCACACCAAGAGCAGGCTGGGAGAAGAGCCATCTCCAGACCTCTTAGACCCCCCCCCCTCCACCCTTAACGA	1619
ATGACATGCATGGGTGTTAATGTTTAAACACTAATAGTGGTGCATTTGAATTGACCTTGGAACTCTCATAGCTCCAGTTGGTCAAGTTGTG	1709
AAGATGATATAAATGCCCTTCTAGTGTCTTTTGAGGTTGGTACAACTCTACAATGAATTAGATTTTTAGCTAGAGCGCTAAGCAAGATAGTG	1799
TTGCTAATAATAAGTTGGTTAACTAGCTGACAAATGTGTCAAACCATAGACTGTATTGGTCAAAGTAGCTTCTTTATCCACATAGCTAAAG	1889
GCATTGTTTACCATCTTTTGGTCGCAAGGTGACAGGTCAATTGATGAACCGTCAGAACTCGATGATACTCAGGTATCATCATTTCTGGCC	1979
TGAGTTTTCACCTTGAACCTTGGAGGGCATTGACTTGGAGGGCATTGTACTGGCTATTTTGGAGTCGGGAACCTCGTATTTCCACATTTCA	2069
GAGAGCTCTCGAATGCACCATAGAACATGGAACAGGGCGTGAACTAAGTTGTGATACATTACGCAGAGACAGCCCTTGTAATGACTGCT	2159
ATTTTTCACCTGTATTGATGTTGAACAATGCTGTATATTTTTTGGCTTAATGAGCTGTACTAATGTATTCGGTTTCTACAGTTTACATA	2249
ATACTGTCTTTTCAGTGTATGATAAATAATCATATGGCAAAAAAAAAAAAAA	2300

Fig. 2. Nucleotide and deduced amino acid sequences of rainbow trout ovarian *P-450_{c17}*. Amino acid sequence deduced from an open reading frame is shown below the nucleotide sequence. The 'AATAAA' polyadenylation signal is underlined.

		82
Tr	MANFLCMCVFSVVGGLGLLLQVKL-RRSLETAGG-----PPSLFVFPFLIGSLLSLRSNQAPHVLFQKLQKKYGHYTSLLMGPHYTVLV	
Ch	MPP-LAVLLALLALALLCAWRLSYSGQPTGTGTGRPRSLPALPLVGSLLQLAGHPQLHLRLWRLQGRYGSLLGLWMSGHYVVVV	
Bv	MWLLLAFLLLTLAYLF-WPKTKHSGAKY-----PRSLPSLPLVGSLLPFLPRGQQHKNFFKLQEKYGPYISFRLGSKTTVMI	
Rt	MWELVGLLLLLILAYFF-WVKSRTFGAKL-----PRSLPSLPLVGSLLPFLPRGQHMHVNFVKLQEKYGPYISRLGTTTTVTI	
Hu	MWELVALLLLTLAYLF-WPKRRCPGAKY-----PKSLSLPLVGSLLPFLPRGQHMHNNFFKLQKKYGPYISVRMGTKTTTVI	
		172
Tr	NHHQHAKEVLLKKGKIFAGRPRTVTTDLLTRDGKDIAFADYGATWRFHRTVHGALCMFGECSASIEKICREALSLCDTLRESGSASLD	
Ch	NSYQHAREVLLKKGKAFAGRPRTVTTDLLSRGQKDIASFASYGPLWKFQKRLVHAALSMFGECSVALEKICREAASLCETLGAAQDMALD	
Bv	GHHQLAREVLLKKGKEFSGRPKVATLDILSDNQKGIADFADHGAHWQLHRKLALNAFALPKDGNLKEKINQEANVLCDFLATQHGEAID	
Rt	GHYQLAREVLLKKGKEFSGRPKVMTQSLSDQGGKGVAFADAGSSNHLHRKLVFSTFSLFKDG-QKLEKLCQEAASLCDDMLAHDKESID	
Hu	GHHQLAKEVLLKKGKDFSGRPQMATLDIASNNRKGIAFADSGAHWQLHRRALMATFALFKDGDQKLEKICQEISTLCDDMLATHNGQSID	
		262
Tr	LSPFLTRAVTNVCSLCFSSSYCRGDPFEFAMLQFSQGIQVDTVAKDSLVDIFPWLQVFPNADLRLLKQCVSIRDKLLQKKYEEHKSDDYS	
Ch	MAPELTRAVTNVCSLCFSSSYRGDPFEFAMLEYSQGIQVDTVAKESLVDIFPWLQIFPNRDLALLKRCCLKVRDQLLQKKFTEHKEAFCG	
Bv	LSEPLSLAVTNIIISFICFNFSFKNEDPALKATQNVNDGILEVLSKEVLDDIFPWLKIFPSKAMERMKGCVQTRNELLNEILEKQCFNFS	
Rt	LSTPIFMSVTNIIICAFCNISYEKNDPKLTAIKTFTGIVDATQDRNLVDIFPWLTIFFPKGLEVIKGYARVRNEVLTGIFERCREKFRS	
Hu	ISFPVFVAVTNVISLICFNTSYKNGDFELNVIQNTYNEGIIIDNLSKDSLVDLVPWLKIFPNKTFLEKLSHVKTIRNLLNKILENYKEKFRS	
		352
Tr	HEQRDLALLAKRASAENNNTAETMETVGLSEDHLLMTVGDIAGAGVETTTSTVLKWAIAIYLIHHPQVQRIQEELDSVVGDRTPQLS	
Ch	DTVRDLMDALLQVRLNAENNSPLEPGL-----LTDDHLLMTVGDIAGAGVETTTSTVLKWAIVLYLLHYPEVQKKIQEEMDQKIGLARHPHLS	
Bv	DSITNLLHILTIQAKVNADNNNAGPDQDS-KLLSNRHHMLATIGDIFGAGVETTTSTVIKWIYAYLLHHPSLKKRIQDDIDQITGFNRTPTIS	
Rt	QSISSLDILTIQAKMNSDNNNSCEGRDP-DVFSDRHILATVGDIAGAGIETTTSTVLKWLAFVLHNPEVKKIQKEIDQYVGFSTRPTTFN	
Hu	DSITNMLDTLMQAKMNSDNGNAGPDQDS-ELSDNHILTTIGDIFGAGVETTTSTVVKWTLAFLHNPQVKKKLYERIDQNVGFSRTPTIS	
		442
Tr	DRGSLFYLEATIREVLRIKRVAPLLIPHVAQTDTSIGKFTVRKGIIRIINLWSLHHDKEWKNPEMFDPGRFLNEEGTGLCIPSPSYLPP	
Ch	DRPLLFYLEATISEGLRIKRVSPLLIPHVSADTSIGEYSIRPKGARVVINLWSVHHDKEWKNPEEFNPGRFDEQGGHHSPPSYLPP	
Bv	DRNRLVLEATIREVLRIKRVAPLTIPIKKAVIDSSIGDLTIDKGTDVVNLWALHHSKEWQHFDLFMPERFLDPTGTQLISPSLSYLPF	
Rt	DRSHLLLEATIREVLRIKRVAPMLIPKKAVIDSSIGFTVVKDTHVVNLWALHHDENEWDQPDQFMPERFLDPTGSHLITPTQSYLFF	
Hu	DRNRLLEATIREVLRIKRVAPMLIPKKAVIDSSIGFAVDKGTVEIINLWALHHDENEWDQPDQFMPERFLNPAQTQLISPSVSYLPF	
Tr	GAGVRVCLQZALAKMETFLFLSWILQRLTMTVSPGQPLPSLEGKFGVVLQPVKYKVNATPRAGWEKSHLQTS	
Ch	GAGIRVCLGEVLAKMELFLFLANVLQRFTELECPDQPLPSLEGKFGVVLQVQKFRVKARLREAWRGEMVR	
Bv	GAGPRSCVGEMLARQELFLFMSRLLRQFNLEIFDDGKLPSLEGHASLVLQIKPFVKVIEVRQAWKEAQAEGSTP	
Rt	GAGPRSCIGELARQELFVFTALLQRFDLVSDDKQLFRLEGDPKVVLIDPFVKVITVRQAWMDAQAEVST	
Hu	GAGPRSCIGELARQELFLIMAWLLQRFDLVSDDKQLPSLEGIPKVVLIDSFVKVITVRQAWREAQAEGST	

Fig. 3. Comparison of deduced amino acid sequences of rainbow trout (Tr), chicken (Ch) [18], bovine (Bv) [17], rat (Rt) [19] and human (Hu) [13] *P-450_{c17}*. The N-terminal hydrophobic sequence, the conserved *P-450_{c17}* sequence (amino acids 311–335) identified by Ono et al. [15], the conserved (amino acids 361–383) Ozols tridecapeptide region [25], and the conserved (amino acids 449–470) heme binding region [26] are highlighted by both overlining and underlining. Triangles indicate the location of the introns reported in the human *P-450_{c17}* gene [20].

3. RESULTS AND DISCUSSION

Screening of approximately 2.2×10^5 plaques from a rainbow trout ovarian thecal cell library yielded 30 positive clones. The longest of these, λ th3–7, was chosen and sequenced by the strategy shown in Fig. 1. The nucleotide sequence of rainbow trout *P-450_{c17}* contains an open reading frame of 1,542 nucleotides, starting from the first ATG codon and terminating at a TAG stop codon, which is predicted to encode 514 amino acid residues (Fig. 2). A second in a frame ATG codon is 18 bp downstream from the first. Although the CAG-CATGG sequence surrounding the first ATG codon is similar to the consensus sequence proposed by Kozak [16], the ATG codon that initiates translation has not been proven. A typical poly-adenylation signal, AATAAA, was found 13 bp upstream from the poly(A) track.

Comparison of the amino acid sequence of trout *P-450_{c17}* with that of human [13], bovine [17], chicken [18], and rat [19] *P-450_{c17}* is shown in Fig. 3. We found

considerable amino acid identity between trout and chicken *P-450_{c17}* (64%, 318 residues identical in 500 residues), whereas 48% (243/505), 46% (233/505) and 47% (239/504) identity was found when trout *P-450_{c17}* was compared with human, bovine and rat *P-450_{c17}*, respectively. Residues 152–228 of trout *P-450_{c17}* which correspond to the amino acid sequence encoded by exon III of the human *P-450_{c17}* [20], show an extremely high homology with chicken (79%, 61/77), although much lesser homology was found between trout and human (45%, 35/77), bovine (39%, 30/77), rat (47%, 36/77). When the amino acid sequence of exon III in human *P-450_{c17}* was compared with that of other mammalian *P-450_{c17}*, the least homology (38%, 29/77) was found in exons from I to VIII. Residues 106–151 corresponding to exon II of the human *P-450_{c17}* are also more conservative between trout and chicken (72%, 33/46) than between trout and human (39%, 18/46), bovine (46%, 21/46), rat (44%, 20/45).

It has been reported that the *P-450_{c17}* and *P-450_{c21}* genes are evolutionarily more closely related to each

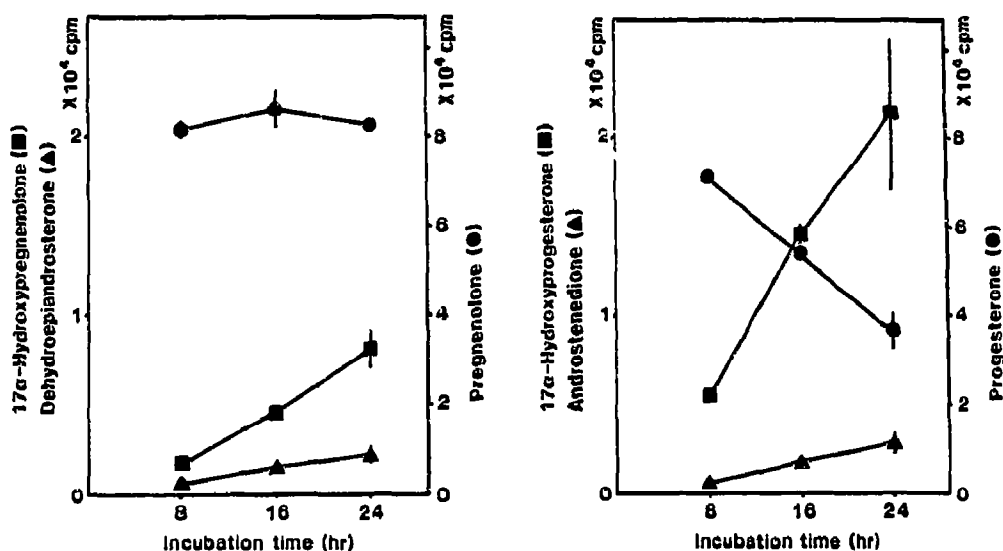


Fig. 4. Activities of 17 α -hydroxylase and 17,20-lyase of trout *P-450_{c17}* in COS-1 cells. ¹⁴C-Labelled pregnenolone (1.4×10^5 cpm) or progesterone (1.3×10^5 cpm) were added to COS-1 cells, and metabolites from each substrate were separated by TLC and identified by recrystallization. The vertical lines represent the means $\pm$ S.E.M. of duplicate measures.

other [20]. When residues 237–265 of trout *P-450_{c17}*, which correspond to exon IV of the human *P-450_{c17}*, were used to search the Swiss Plot data base, the computer detected the amino acid sequence of exon VI of human *P-450_{c17}* (41%, 12/29) [21,22] as well as the exon IV of human *P-450_{c17}* (48%, 14/29) [20]. In bovine, exon IV of *P-450_{c17}* (41%, 12/29) [23,24] rather than the exon IV of *P-450_{c17}* (31%, 9/29) is similar to the region of trout *P-450_{c17}*.

With introduction of the trout *P-450_{c17}* cDNA expression vector into COS-1 cells, exogenous pregnenolone was converted to 17 α -hydroxypregnenolone and dehydroepiandrosterone, and exogenous progesterone was converted to 17 α -hydroxyprogesterone and androstenedione (Fig. 4). The trout *P-450_{c17}* favors conversion

of progesterone to 17 α -hydroxyprogesterone over the conversion of pregnenolone to 17 α -hydroxypregnenolone. However, conversion of pregnenolone to dehydroepiandrosterone and that of progesterone to androstenedione are almost the same. These results indicate that the trout *P-450_{c17}* has more 17,20-lyase activity catalyzing 17 α -hydroxypregnenolone to dehydroepiandrosterone than that catalyzing 17 α -hydroxyprogesterone to androstenedione. Activities of *P-450_{c17}* expressed in COS-1 cells or yeast have been reported in bovine [9,10], human [11] and rat [19]. The 17,20-lyase activity of bovine and human *P-450_{c17}* is greater with 17 α -hydroxypregnenolone than with 17 α -hydroxyprogesterone, whereas rat *P-450_{c17}* has more 17,20-lyase activity catalyzing 17 α -hydroxyprogesterone to androstenedione than that catalyzing 17 α -hydroxypregnenolone to dehydroepiandrosterone. It seems that each *P-450_{c17}* has a slightly different activity in terms of substrate specificity. Thus, it is interesting to determine whether different forms of *P-450_{c17}* express in the trout thecal cell layers during vitellogenesis and oocyte maturation.

By Northern hybridization analysis using a 2,081 bp λ th3–7 cDNA fragment which had excluded 270 bp of 3'-region as a probe, we found the mRNA specific for rainbow trout *P-450_{c17}* to be a single species, approximately 2.4 kb in length. The 2.4 kb transcripts were not found in ovaries during the early vitellogenic stage, barely detected during the mid-vitellogenic stage, and abundant during the post-vitellogenic stage and after ovulation (Fig. 5). These results are consistent with the increasing production of steroid hormones by salmonid ovarian follicles towards the end of the reproductive cycle [5].

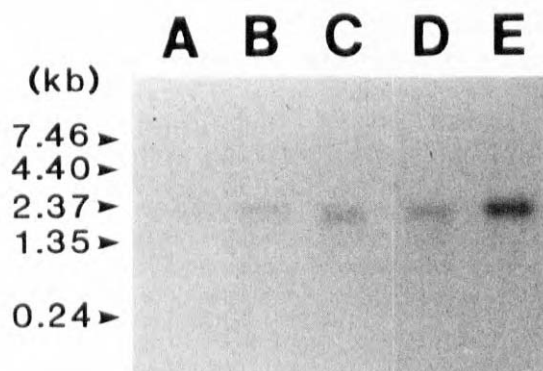


Fig. 5. Northern hybridization of poly(A)⁺ RNA (2 μ g) from various stages of ovarian follicles and isolated thecal cells. A, 1.81 mm diameter of follicle; B, 2.84 mm diameter of follicle; C, 4.68 mm diameter of follicle (immature); D, post-ovulated follicle; E, ovarian thecal cells isolated from 3.54 mm diameter of follicle.

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