Oxytocin receptor gene expression in rat mammary gland: structural characterization and regulation

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ABSTRACT
The differential, tissue-specific regulation of oxytocin (OT) binding sites allows the neurohypophysial nonapeptide OT to fulfill a dual role: to induce uterine contractions at parturition and to mediate milk ejection during lactation. Whereas uterine OT binding sites are up-regulated prior to parturition and are rapidly down-regulated thereafter, mammary gland OT binding sites gradually increase throughout gestation and remain up-regulated during the ensuing lactation period. Here, we structurally characterized OT receptor (OTR) mRNA in mammary gland and analyzed its expression during gestation and lactation and in response to steroid treatment. In mammary gland tissues, we found a 6.7 and a 5.4 kb OTR mRNA species, and both species were further analyzed by RACE (rapid amplification of cDNA ends). The 6.7 kb mRNA was found to be common to mammary gland and uterus and to extend 618 nucleotides beyond the published sequence of the rat OTR gene. The 5.4 kb mRNA species is unique to the mammary gland and terminates at a mammary gland-specific polyadenylation site that is not preceded by a classical polyadenylation signal. RT-PCR analysis did not provide any evidence for differences in the coding regions, suggesting that both uterine and mammary gland OTR mRNAs encode the same receptor protein. Furthermore, primer extension experiments showed that no differences exist in the specific transcriptional initiation sites of the OTR gene in the two tissues. During pregnancy, OTR mRNA per mammary gland increased approximately 150-fold and remained high during lactation, consistent with the previously identified regulation of OT binding sites and the role of OT during lactation. Whereas estrogen administration strongly induced the uterine OTR mRNA levels (>5-fold), mammary gland remained unaffected by steroid treatment. Moreover, tamoxifen had no effect on the mammary gland OTR mRNA level. In summary, our data demonstrate a differential control of OTR expression during gestation and lactation and in response to steroid treatment. INTRODUCTION
Oxytocin (OT) is a hypothalamic neuropeptide that mediates various reproductive functions. A large body of evidence supports the notion that, as a circulating hormone, this nonapeptide plays a key role in mammals as a mediator of milk ejection from the lactating mammary gland. This has been most convincingly shown by gene ablation studies. Mice in which the OT gene has been inactivated by gene targeting have normal milk production but are unable to deliver the milk to their offspring due to the inability to eject the milk from the glands (Nishimori et al. 1996, Young et al. 1996). Milk ejection is however fully restored in these mice by exogenous OT administration (Nishimori et al.)
1996, Young et al. 1996). In response to the sucking stimulus, OT is released from the neurohypophysis as a result of the synchronous activation of hypothalamic magnocellular OT producing neurons (Belin et al. 1984, Fuchs et al. 1984, Higuchi et al. 1985). Administration of the OT antagonist atosiban inhibits milk ejection and this inhibition is abolished by OT injection (Bruckmaier et al. 1997, Neumann et al. 1994).

OT causes milk ejection by eliciting contractions of the myoepithelial cell network that surrounds the alveoli and milk ducts in the mammary gland (Solo et al. 1980, Ruberti et al. 1983). In myoepithelial cells, activation of the OT receptor (OTR) was shown to induce intracellular calcium release (Moore et al. 1987). OT was also shown to enhance myoepithelial cell differentiation and proliferation in mammary gland (Sapino et al. 1993). Autoradiographic studies performed in the rat confirmed the presence of OT binding sites on myoepithelial cells (van Leeuwen et al. 1985, Soloff et al. 1975).

Binding studies indicate that uterine and mammary gland OT binding sites are differentially regulated. Uterine binding sites increase dramatically at term, reaching a maximum during labor, and return to baseline during the lactation period. In contrast, mammary gland binding sites undergo a gradual increase throughout gestation and reach a maximum during lactation (Soloff et al. 1979).

The structure of the OTR has been elucidated by molecular cloning in different mammalian species (Kimura et al. 1992, Gorbulev et al. 1993, Bathgate et al. 1995, Riley et al. 1995, Rozen et al. 1995, Kubota et al. 1996). The deduced amino acid sequences indicated that this receptor belongs to the G protein-coupled receptor family. Despite the availability of specific OTR cDNA probes, little is known of the molecular structure and the mechanisms of regulation of mammary gland OTR. Although binding studies suggest a similarity of uterine and mammary gland OTRs, they also indicate that the expression of OTRs is differentially controlled in these two tissues (Soloff et al. 1977, 1979, 1988, Shymala & Ferenczy 1982, Soloff & Grzonka 1986, Soloff & Fernstrom 1987). This notion raises the question whether the tissue-specific regulation is caused by the presence of different OTR subtypes, by differential promoter usage, by different tissue-specific factors interacting at the level of the promoter or by differences in the steroid responsiveness of the OTR-expressing cells in these tissues.

We have previously characterized OTR transcripts in uterus (Larcher et al. 1995), pituitary gland (Breton et al. 1995), kidney (Breton et al. 1996) and brain regions (Breton & Zingg 1997) and shown that estradiol (E2) is a important factor in controlling OTR gene expression. In the present study we have analyzed the molecular structure of the mammary gland and uterine OTR mRNA, determined transcriptional start sites and polyadenylation sites in both tissues, and assessed semi-quantitatively mammary gland OTR transcript levels throughout gestation, lactation and in response to gonadal steroid administration.

**MATERIALS AND METHODS**

**Animals**

Timed-pregnant, lactating or bilaterally ovariectomized Sprague–Dawley female rats (200–250 g) were obtained from Charles River Laboratories (Saint-Constant, Quebec, Canada). Animals were injected on four consecutive days with vehicle (oil), estradiol benzoate (E2) (0·1 mg/kg), progesterone (P) (10 mg/kg), tamoxifen (TAM) (10 mg/kg), or a combination of E2 and P or E2 and TAM. Three hours after the last injection, the animals were killed by decapitation under light ether anesthesia. In ovariecotomized animals, treatment was started 1 week after ovariectomy. All procedures were approved by the Bioethics Committee of the Royal Victoria Hospital Research Institute. Tissues were removed, frozen on dry ice and kept at −70 °C before RNA extraction.

**Northern blot analysis**

Total RNA was extracted from mammary gland or total rat uterus with 4 M guanidinium thiocyanate and purified by ultracentrifugation through 5·7 M CsCl. Total RNA was enriched for polyadenylated RNA by absorption to oligo-d(T) cellulose. Twenty µg of poly(A)+ mRNA was subjected to Northern blot analysis before RNA extraction.

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**In situ hybridization**

Mammary glands of female rats at day 21 of pregnancy were rapidly dissected out and frozen in dry ice-cooled isopentane and stored at −20 °C until sectioning. Adjacent 20 µm thick sections were cut on a cryostat, thaw-mounted on gelatin-coated slides and stored at −80 °C. Sense and antisense riboprobes were synthesized using 35S-radiolabeled-UTP and a partial rat OTR cDNA subcloned into pGEM-7Zf+ (provided by Dr P. Burbach, Utrecht; Adan et al. 1995). The frozen sections were thawed and air-dried before fixation in 4% paraformaldehyde in 0·1 M phosphate buffer for 5 min at room temperature. After washing in PBS, sections were permeabilized with proteinase K (10 µg/ml) for 10 min, then postfixed in 4% paraformaldehyde in 0·1 M phosphate buffer for 5 min, treated with acetic anhydride for 10 min, rinsed, dehydrated and delipidated in a series of graded ethanol solutions followed by immersion in chloroform for 5 min. Sections were covered with either sense or antisense probes (30 000 c.p.m./µl) in hybridization buffer and kept for 22 h in a humid chamber at 56 °C. Sections were washed four times for 5 min in saline-sodium citrate buffer (SSC) and incubated in a 20 µg/ml RNase solution at 37 °C for 30 min, followed by a series of washes in decreasing concentrations of SSC (4 × , 2 × , 1 × , 0·5 × SSC for 5 min each, twice in 0·1 × SSC at 65 °C for 30 min). Sections were dehydrated in graded alcohol solutions containing 300 mM ammonium acetate and 1 mM dithiothreitol (DTT), dried and coated with K5 emulsion (Ilford). After 35 days exposure at 4 °C, the slides were developed for 5 min in Kodak D19 at 18 °C, stained with thionin and mounted with Permount.

**RT-PCR**

For the coding region analysis of mammary gland OTR mRNA, two different primer pairs (F3/R8 and F1C/R9) were used as previously described (Breton et al. 1995). The first pair was designed to amplify a 1103 bp cDNA fragment encompassing the coding region of the rat OTR. The second pair amplified a 373 bp region of the coding region, which encompasses the splice site of intron 2.

For the analysis of the 5′ untranslated region, three different primer pairs were used. The common forward primer (F1) consisted of a 24-mer corresponding to nucleotides 1612–1635 and the reverse primers R1 (30-mer), R2 (30-mer) and R3 (27-mer) were complementary to nucleotides 1710–1739, 1910–1949 and 2095–2121 respectively, according to the published gene sequence (Rozen et al. 1995).

The semi-quantitative RT-PCR method used here has been described and validated earlier (Breton et al. 1995). Briefly, 2 µg of total RNA were used for cDNA synthesis with 200 U M-MLV (Moloney murine leukaemia virus) reverse transcriptase, primed with 2 µg of random primers in 20 µl 50 mM KCl (pH 8·3), 50 mM Tris HCl (pH 8·3), 10 mM MgCl2, 2 mM of each dNTP and 20 U RNasin. The reaction mix was incubated for 1 h at 42 °C. Negative controls were performed for the first strand synthesis that contained the above reagents but either no RNA or no reverse transcriptase. One-sixth of the first strand synthesis reaction or negative control were then amplified for 35 cycles for OTR cDNA and 25 cycles for glyceraldehyde-3-phosphate dehydrogenase (GAPDH) cDNA. After amplification, the samples were separated on a 1% agarose gel and transferred to nylon membrane. The blots were hybridized to a radiolabeled oligonucleotide probe that corresponded to the region encoding residues 316–322 of the rat OTR or to residues 157–164 of rat GAPDH. The resulting autoradiograms were scanned densitometrically.

**Primer extension**

To determine the initiation sites of OTR gene transcription in uterus and mammary gland, two different primers were used. We found earlier that the main transcriptional initiation site of uterine OTR gene expression was around position 1593 according to the numbering of Rozen et al. (1995). The primers R4 (30-mer) and R5 (30-mer) were complementary to nucleotides 1618–1647 and 1648–1677 respectively (according to Rozen et al. 1995). The antisense primer was labeled at its 5′ end using [32P]γATP and T4 polynucleotide kinase. The radiolabeled primer was annealed to 1 µg of poly(A)+ enriched RNA and subsequently extended with 200 U M-MLV reverse transcriptase for 30 min at 37 °C. The extension products were analyzed on a 6% sequencing gel. The sequencing ladder was obtained using the same oligonucleotide as a primer in a dideoxy sequencing reaction of the corresponding OTR genomic DNA.

**Rapid Amplification of cDNA Ends (RACE)**

For both tissues, 3′-rapid amplification of cDNA ends (RACE) was performed using the SMART RACE cDNA Amplification Kit (Clontech, Palo Alto, CA, USA) as described by the manufacturer. Briefly, first-strand cDNA was synthesized using
5 µg total RNA, extracted either from rat lactating mammary gland or parturient rat uterus, 200 U M-MLV RT and 10 pmol of a poly(dT) primer adapter (3’CDS). The cDNAs were amplified in two rounds of 25 cycles each. In the first round, two gene-specific outer primers were used which corresponded to sequence regions located upstream of potential polyadenylylation sites (primer 481: CATTTGTGTGATGCCCAGTGTC and primer 671: TGGTGATCTCTGTGAGTTCCAG, corresponding to nucleotides 7030–7052 and 8943–8965 of the published rat OTR sequence respectively (Rozen et al. 1995)). In the second round, the corresponding cDNA generated in the first round of PCR amplification were used as templates, in conjunction with two gene-specific inner primers (primer 482: CAGCTGCTTGATAAATGGTGCAC and primer 672: AGGACA GCCAGGGCTCTGTTACA, corresponding to nucleotides 7089–7111 and 9022–9044 of the published OTR sequence respectively). In both rounds, the unique 3’ primer consisted of a sequence complementary to a portion of the 5’ end of the poly(dT) primer adapter used for first strand synthesis. The cycling parameters were: 94°C for 30 s, 60°C for 30 s and 72°C for 180 s. PCR products were separated on a 2% agarose gel, visualized by ethidium bromide staining and photographed under u.v. light. DNA markers were run in parallel to estimate the size of the amplified products. After purification, the PCR products resulting from the second round of PCR amplification were subcloned using the ‘pGEM-T Easy Vector Systems’ (Promega, Madison, WI, USA) and sequenced on both strands.

DNA sequencing

The subcloned PCR products were sequenced on both strands using an automated DNA sequencer (ABI PRISM 377 DNA Sequencer, Applied Biosystems, Foster City, CA, USA) and the ABI PRISM Original dRhodamine Terminator Cycle Sequencing Kit (Applied Biosystems). In each reaction, 0.8 µg double-stranded DNA was used in conjunction with pUC/M13 forward and reverse primers (Promega) and rat OTR gene-specific oligonucleotide primers. The novel 3’ sequence presented here (nucleotides 5872–6489) was derived from two different clones, each sequenced twice in the forward and twice in the reverse direction (using two different forward and two different reverse primers) resulting in a full eightfold sequence coverage. Sequence alignment revealed an average of 3·3 mismatches per raw sequence obtained within the 618 nucleotides of new sequence analyzed. In each case, the mismatch was confined to one out of the eight sequences and was therefore considered to be a sequencing error.

RESULTS

Northern blot analysis

Mammary gland OTR mRNA was characterized by Northern blotting. As shown in Fig. 1, the mammary gland expresses two mRNA species that hybridize to a rat OTR cDNA probe. They were estimated at 6·7 and 5·4 kb. We have shown earlier that the rat uterus contains three different OTR mRNA species that correspond in size to 6·7, 4·8 and 2·9 kb and that differ with respect to the length of their 3’ untranslated regions due to differential selection of polyadenylation sites (Rozen et al.)
Thus, the larger transcript identified here in mammary gland is identical in size to the largest OTR transcript present in uterus. As shown earlier, this transcript is also expressed in many other OTR-expressing tissues, including the pituitary gland (Breton et al. 1995), the kidney (Breton et al. 1996) and the brain (Breton & Zingg 1997). The lower 5.4 kb band present in mammary gland is not detected in any other tissues expressing OTR mRNA. It is therefore mammary gland-specific.

**RT-PCR**

The structure of mammary gland OTR mRNA was further analyzed by RT-PCR. It is known from the analysis of the rat OTR gene that the OTR coding region is interrupted by one large intron (intron 2) located in the region encoding the putative third extracellular domain of the receptor (Rozen et al. 1995). Two sets of primers were used to investigate the coding region (Fig. 2A). The primer pair F3/R8 amplified the coding region encompassing the intron 2 splice site and, in the uterus, gave rise to a 1.1 kb band (Fig. 2B), in accordance with the known gene structure (Rozen et al. 1995). The F1C/R9 pair amplified a sub-region of the coding region, centered around the intron 2 splice site, resulting, in the uterus, in a 373 bp band. As shown in Fig. 2B, RT-PCR products generated by either set of primers yielded a single band of the predicted size, independent of whether uterus or mammary gland was used as a template. In both cases, the PCR Southern blot (Fig. 2B) and the ethidium bromide stained gels (not shown) exhibited no additional bands that could be indicative of the existence of any splicing variants. These data therefore do not provide any evidence for structural variations, such as alternative splicing of intron 2. The data are thus consistent with the idea that the rat mammary gland and rat uterine OTR transcripts encode the same receptor.

We next analyzed the 5′ untranslated region of uterine and mammary gland OTR mRNA. To this end, RT-PCR experiments were performed with three different sets of primers distributed along this region (Fig. 3A). Based on the reported gene structure (Rozen et al. 1995), application of primer pairs F1/R3 and F1/R2 were predicted to result
in amplification products of 413 bp and 241 bp respectively if intron 1 was spliced out, and of 510 bp and 338 bp respectively if intron 1 was not spliced out. As shown in Fig. 3B, both primer pairs yielded each two bands that were consistent with the presence of two different OTR mRNA types, one containing intron 1 and one in which intron 1 was removed by splicing. The use of a third primer pair, F1/R1, designed to amplify only mRNA containing intron 1, confirmed the presence of mRNA containing intron 1 (Fig. 3C). This situation is analogous to the one described earlier in the uterus (Rozen et al. 1995), where intron 1 is not consistently spliced out, and a portion of OTR mRNA retains the small 97 bp intron. The present observation indicates that the same pertains to mammary gland OTR mRNA. The significance of this observation is unclear, at present. However, the presence of a small open reading frame in intron 1 suggests that presence or absence of intron 1 may have an effect on the translational efficiency of the resulting mRNA (Rozen et al. 1995).

**Determination of transcriptional initiation sites by primer extension analysis**

We next examined and compared the transcriptional initiation sites of uterine and mammary gland OTR mRNA. Primer extension revealed several extension products that identified two major transcriptional initiation sites situated at 326 bp and 318 bp upstream from the translational start codon (Fig. 4). Identical primer extension products were obtained using RNA from either uterus or...
mammary gland. No products were obtained when RNA extracted from liver was used, a tissue that does not express the OTR gene (data not shown). These finding indicate that OTR gene transcription initiates in mammary gland at the same site as in the uterus.

Analysis of the 3’ ends by RACE

The RACE technique was used to further characterize the 3’ end of OTR mRNA detected in mammary gland. As depicted schematically in Fig. 5A, four different sense primers were used in combination with a common reverse primer that hybridized to the different poly(A) tails. Use of the two upstream primers resulted in each case in three bands of ~1·0, 0·20 and 0·16 kb respectively (Fig. 5B, lanes 2–5). Whereas the two lower bands were generated irrespective of whether uterine or mammary gland RNA was used as a starting material, the 1·0 kb band was only generated if RNA extracted from mammary gland was used (lanes 3 and 5 in Fig. 5B). This band, therefore, was indicative of a mammary gland-specific OTR mRNA species. Sequencing of each of these bands determined the sites of polyadenylation in the corresponding template RNA molecules. The deduced sites of polyadenylation are indicated in Fig. 6. Taking into account the transcriptional starting sites determined above and the removal of introns 1, the predicted sizes of the corresponding OTR mRNA are (without the poly(A) tail): 4·69, 4·75 and 5·49 kb. The 5·49 kb mRNA species corresponds to the mammary gland-specific mRNA. This size is compatible with the mammary gland-specific band observed by Northern blotting that was estimated at 5·4 kb, as shown in Fig. 1. Of note is that the mammary gland-specific polyadenylation site is not preceded by a classical AAATAAA polyadenylation signal. Thus it remains to be determined what signals the tissue-specific polyadenylation in this particular tissue.

The other two predicted mRNA species correspond to the 4·8 kb band observed by Northern blotting of uterine-derived RNA. Due to the small size difference of these two mRNAs, they appear as one band in the Northern blot. The detection by RT-PCR of a band corresponding to the 4·8 kb species in mammary gland extracts was surprising, inasmuch as a corresponding band is only detected in Northern blots of uterine extracts. This is likely due to the greater sensitivity of the RT-PCR technique compared with the Northern blot technique. The fact that, in mammary gland, this species is below the detection limit of the Northern blot approach indicates that it must correspond to a very minor component of mammary gland OTR mRNA.

Using the two primers 671 and 672 that correspond to regions further downstream on the

![Fig. 4](https://www.endocrinology.org)
OTR mRNA, a band of \(~1.0\) kb was generated, irrespective of whether uterine or mammary gland RNA was used as a starting material. This size was compatible with the idea that this band corresponded to the \(6.7\) kb mRNA species that was common to uterus and mammary gland. The length of the band also suggested that the corresponding polyadenylation occurred at a site that was located over \(0.5\) kb \(3\)' to the end of the published OTR gene sequence. Sequencing of these bands confirmed this prediction and generated novel sequence information that extends 618 nucleotides beyond the previously published rat OTR gene sequence (Fig. 6). The predicted polyadenylation site is preceded by a classical polyadenylation signal (AAATAAA) located 20 nucleotides upstream of the poly(A) site (Fig. 6, novel sequence is in capitals). The novel \(3\)' sequence contains one A- and U-rich sequence element that is in addition to the five other elements located further upstream in the previously characterized \(3\)' untranslated sequence and may play a role in the regulation of mRNA stability. With the added sequence, the length of the \(3\)' untranslated sequence of the longest OTR mRNA has now been determined to be a total of 6132 nucleotides.

**In situ hybridization analysis**

The sites of OTR gene expression in mammary gland were analyzed by *in situ* hybridization, using a specific antisense \(^{35}\)S-labeled cRNA probe. As shown in Fig. 7a, silver grains were found predominantly in an area located outside, but adjacent to, the epithelial layers of milk ducts. This location is compatible with expression in the myoepithelial cell network that surrounds the mammary gland milk ducts. Only background labeling was observed when a similarly labeled sense strand RNA was used as a probe (Fig. 7b).

**Regulation during lactation**

By semi-quantitative Northern blot analysis, we found a non-significant relative 1.14-fold increase of mammary gland OTR mRNA during lactation. However, estimation of mammary gland OTR

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**Figure 5.** Determination of polyadenylation sites of rat mammary gland and uterine OTR mRNA by RACE. (A) Schematic diagram of strategy. A first round of PCR amplification was done using primers 481 and 671 as forward primers and CDS3' as the common reverse primer. The PCR products were used for a second round of amplification using primers 482 and 672 as forward primers and CDS3' as the common reverse primer. The deduced polyadenylation sites are indicated by upward arrows. The mammary gland-specific site is marked by an asterisk. (B) Agarose gel analysis of RACE products. Lane 1: DNA size markers. Target mRNA was extracted from either the uterus of a parturient rat (lanes 2, 4, 6, 8) or a lactating mammary gland (lanes 3, 5, 7, 9). The forward primers used were primer 481 (lanes 2 and 3), 482 (lanes 4 and 5), 671 (lanes 6 and 7), and 672 (lanes 8 and 9). Bands present in lanes 2–5, 8 and 9 were excised from the gel, subcloned and sequenced (see Fig. 6).
OTR gene expression in rat mammary gland

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-------primer 481----→
3550 cattttgtgtgatgcccagtcgctcctgcctcctggtgtgtgacacagccctcctgctttaacc

-------primer 482----→
3610 aagctgtggataaatctgaccttaataaaatgtctttttcttgtatatctatgtgctttttt

3670 tcctcccccacccacccgacacacaagaagtaggtgctttatattagctttcttgccaggc
3730 tctggtgctatctctctggtgctatgacacgtgctggggctgggagggcagagggcgtg
3790 gtattattctctggaggtcattgtctattttgggtgtgataatttcctgaggtgtg
3850 agccaaatgtgtgtgcttgatagttgaatgttaatcagtttcagtttaacctgaaggg
3910 accaggttcttcaacggtggtgatggtggggtgtaatcctggttttactggaacaggtgtg
3970 tctggtttctgggctctggttaagaatggcatcttatattagcttcctggcaggc
4030 tctgcctctcagtcactacactcaacacctggttcctgcagttcatggtttattacggctgg
4090 gttgcgcacaagctgcatgagaaattttagtgttgtttccctcctctgtctgtagccagacag
4150 cgggattctctggggtgtaaagttctggtctgcttctgagccagacag
4210 cagctcaactcagataacacaccctgcctctgcattcatggtttttctctttta
4270 tcatatgggaaacctattataacctcagccagaaacacattcagaggtgctaaactgagaaacactt
4330 tagttctggttttcatattgcagacactgctcagttttcagttttggtttgacctagaaacta
4390 aggacaccaacaccaccaacctacacagacagcagcatatggtttctgtgtgagcagcagccactcct

↓ mammary gland-specific poly(A) site
4450 ttattgcagcacaacctctctcctctggtgctgctctccctagcatagcaggtgacac
4510 gggtctaccccctctagaagactgttggttttggtgtctttacagtacatgtgtgacgcaaa
4570 gccttctgtagactgcctcttaaggaacccctctgcctcagggctgtctgggtgtgtgatcat
4630 gttgtagctgagcagtccctccacactgtgggtctttcttttctttttgtgctctctgcacatgt
4690 acctccatatttgaggtggagaactggaactggaactaattaaagcatgactggtcgccagacgcca
4750 tgtggagcaggccagcttggtgtacacctggtgcctttcctttacacccctttgcaccccctcaca
4810 gcacacgcgcttttagcctctctctctctctcttgagcagcactttataatggtgtgactcgcagacttggc
4870 ccagtgctggcaggccgatcgggtcaggggtgactggtgcttgatagtactgtgtggtgtgta
4930 tgccactgtgtccatcaactcagttgagtctatataatgagggcaccaggggcaacaggtgcaag
4990 aggagataacaccgcacaaagacttccccgacacgagggcagtgtgaacacaccacagtgtgta
5050 gcacagcggcgcgtagcactttgtgagagctggtaagttgggtgtcactcaccctccac
5110 acgcacagcgttcgtaagttggcctcgctgccgcaacatctccttttaaatcctcctgac
5170 aggacacgacaggagaaaagatttaactcagacagcagctgctgggttttttcaggttttgctgc
5230 ttgacctccttcctactgcgaatcctgtggggtgagttcagcggcagctagatggtttagaatggaagaag

primer 481
primer 482
poly(A) site 1
poly(A) site 2
5290 gcacttgtgctttgcagaagacctgagtttgcttcttagcatatacagaatggctaca
5350 gcacccccataatccagttcaggaatctaactctcttttgaattccagggttccc

5410 gcattcacagaatgaatatatattttttgggaacagcacttggaagccagaggtgtgga
---primer 671--→
5470 tctcttgagttccaggacagcctggtctacaatgtaagttccaggacagcctggtctac

----primer 672----→
5530 aatgtaagttccagagccagcaggtgcctggctttacactgataataaaacaacaaaaaata
5590 agcaaaacacaaacacaggaaagggaggaaactctgtgtgtagtgctgtgtgagcttcttgat
5650 ggtgtcttgacaggtctaggactgtatcctctaatgtagtgctacatattgacaataaatat
5710 tttctgcagccctctgtcactttgcctatcagctgctataacaggtactctgaacgtctttt
5770 cagcttctctattctatcatgtgtaagagagcactccagagctgtaagacgtgtaagttcaca
5830 tactgcgtagctagtgatctgcagctgtcataatattgcatcTGTAATGTTCCTCAAAGG
5890 CCCACATGTAAAGCTGTTGGGTTCACAACCAGTACTACTGGGAGATGGTGAGATCTTTGA
5950 GGGGTGGGATTTAGTATAGAGAGAAGGGAAGACGTAGGGCATTTGAAAATGTGCTCTGGAGGGGATGCT
6010 GAGAAGCCCTGCTCCATCCATCCTTGATGCTCTGGGCTGCAGCAGACCTGAGGAGCTATTTGCTA
6070 CCATGTGTCCTCTATTACACTGTTCTCTGCTTGACAAAGGACTGAGGAGCACCATACACCT
6130 CCACACCTGTAGGATCAAAAGAATGTGTGTGTGTGTGTGTTATATTTCAGGTGTGGTTT
6190 GTTGTAGAGGTTGAGAGATGACACTGCTAGTGTGCTGGCTAATTGTTAACTTGACACAAG
6250 CTTGAGTCATTTGGGAAGAGGGAAGAGAGGTCCCAGCCCCTTGACGTGGGTATCCCTG
6310 GGCAGGTGGTGTAGGGGTGTACATGAAAGCAGACCAAGCAAGCTAGTGTTCCT
6370 CATGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG
6430 CTTCATGTTGGTGAATATATATTGATTCCTTTGCTAAGATGAAAATACCCCTTCCCTCTCTCTCTCT

6490 AAA...

---poly(A) site 4---

**Figure 6.** Polyadenylation sites of OTR mRNA in rat mammary gland and uterus and novel, additional 3’ sequence. Polyadenylation sites and the novel sequence information was determined by RACE as shown in Fig. 4 and described in Materials and Methods. The forward priming sites corresponding to primers 481, 482, 671, and 672 are indicated as well as the polyadenylation sites, including the mammary gland-specific polyadenylation site. The A- and U-rich elements are italicized and the polyadenylation signals are underlined. The novel sequence that extends beyond the published rat OTR gene sequence is in capitals. The numbering is according to, and in extension of, the previously deposited sequence of exon 3 of the rat OTR gene (GenBank accession number U15280). Nucleotides 5290–5871 of the RNA-derived sequence presented here are identical to the gene-derived sequence deposited earlier under the accession number U15280. The novel additional 3’ sequence (nucleotides 5872–6490) have been deposited to GenBank under the accession number AF380129.
mRNA levels during lactation is complicated by the fact that there is a strong increase in total RNA per mammary gland during this period. During lactation, we found a 13-fold increase in mammary gland total RNA per mg of tissue. In addition, we found a nearly tenfold increase in rat mammary gland weight (Table 1). Taken together, this indicates that a lactating rat mammary gland contains ~130 times more RNA than a non-lactating gland, likely due to the strongly increased expression of a set of genes necessary for milk production, secretion and ejection. Since the relative OTR signal remained essentially unchanged as determined by Northern blot analysis, where equal amounts of RNA are loaded per well, we conclude that OTR mRNA per mammary gland increased at approximately the same rate, i.e.>100-fold, and that the OTR gene forms part of the set of genes that is strongly up-regulated during lactation.

Effects of steroids

We next investigated the effects of in vivo administration of estrogen (E2), progesterone (P), or the E2 receptor antagonist tamoxifen (TAM) on OTR mRNA accumulation in the mammary gland. As shown in Fig. 8 and as described earlier (Larcher et al. 1995), the uterine OTR mRNA levels increased in response to E2 administration. By contrast, OTR mRNA levels in the mammary gland remained unaffected by E2 administration (Fig. 8). P administration alone had no significant effect on OTR mRNA levels in both tissues, nor did it significantly influence the E2-induced rise in uterus. In uterus, TAM alone acted as an E2 agonist but weakly suppressed E2-induced OTR gene expression, if administrated concomitantly with E2. By contrast, OTR mRNA levels in the mammary gland remained unaffected by treatment with TAM alone or by combined E2 and TAM administration (Fig. 8).

DISCUSSION

The present study was prompted by earlier findings demonstrating differential regulation of uterine and mammary gland OT binding sites during pregnancy and lactation (Soloff et al. 1979) as well as in response to steroid treatment (Shyamala & Ferency 1982). These findings raised the possibility that the OT effects in the mammary gland are mediated by a different OTR subtype. In the present study, we found by Northern blot analysis, RT-PCR and in situ hybridization that the uterine-type OTR mRNA is expressed in mammary gland and that this transcript is regulated in a fashion that is compatible with the observed regulation of OT binding sites, as described in earlier studies (Soloff et al. 1979). Indeed, this conclusion is compatible with earlier binding studies in the literature, which revealed a single class of OT binding sites in mammary gland with characteristics similar to those of uterine binding sites (Soloff et al. 1977, Soloff & Wieder 1983, Pettibone et al. 1990). Moreover,
studies using specific antibodies against the human uterine-type OTR provided evidence of presence of immunologically identical receptor molecules in the human mammary gland (Bussolati et al. 1996, Ito et al. 1996, Sappino et al. 1998). Although the present and previous studies indicate that the uterine-type OTR gene is expressed in mammary gland, the existence of an additional, very different OTR subtype that is sufficiently different to remain unrecognized by the different probes used here cannot be totally excluded.

Our finding of a 6.7 kb OTR mRNA species that is present in all OTR-expressing tissues examined so far is in support of the idea that the same OTR gene is expressed in all OT-responsive tissues, including the mammary gland. On the other hand, the finding of a 5.4 kb mammary gland-specific OTR mRNA band raised the possibility that this transcript could originate from differential splicing of the primary OTR transcript or by differential transcriptional initiation of OTR gene transcription. This possibility was further explored using RT-PCR in conjunction with several different sets of primers as well as by primer-extension analysis. Our RT-PCR analysis encompassed a primer pair that flanked the coding region of the OTR gene as well as a pair that amplified specifically a region flanking intron 2, the single intron that interrupts the OTR coding region. A third pair was designed to amplify the 5′ untranslated region of the OTR mRNA. Neither of these RT-PCR strategies provided evidence for the existence of any differentially spliced OTR transcript with the exception of variable splicing of intron 1, a small intron present in the 5′ untranslated region. As demonstrated earlier for rat uterine OTR mRNA (Rozen et al. 1995), we found that mammary gland OTR transcripts exist in two forms that differ by the presence or absence of the sequence corresponding to intron 1. The biological significance, if any, of this variable splicing of intron 1 in both tissues

<table>
<thead>
<tr>
<th>Total weight per mammary gland (mg)</th>
<th>Total RNA (ng/mg tissue)</th>
<th>OTR mRNA (arb. units/100 μg total RNA)</th>
<th>Calculated increase of OTR mRNA per mammary gland</th>
</tr>
</thead>
<tbody>
<tr>
<td>Control 598 ± 62</td>
<td>0.351 ± 0.021</td>
<td>83.8 ± 10.0</td>
<td>149-fold</td>
</tr>
<tr>
<td>Lactation 5946 ± 199</td>
<td>4.618 ± 0.112</td>
<td>96.1 ± 15.3</td>
<td></td>
</tr>
</tbody>
</table>

**TABLE 1.** Semi-quantitative analysis of mammary gland OTR mRNA levels during lactation. Mammary glands of non-pregnant control and day 1 lactating rats were dissected and weighed. Total RNA was extracted and quantitated, and OTR mRNA levels were determined semi-quantitatively by densitometric scanning of autoradiographs resulting from Northern blots such as the one shown in Fig. 1. Values are means ± s.e.s of four independent determinations. The overall increase in OTR mRNA (149-fold) per mammary gland was calculated taking into account the increase in weight (9.9-fold), total RNA/mg of tissue (13.1-fold) and densitometric signal obtained from poly(A+) RNA purified from 1 mg of total RNA starting material 1.14-fold

![Figure A](image1.png)

**FIGURE A.** Semi-quantitative analysis of OTR mRNA levels in mammary gland during lactation. The effect of estrogen (E), progesterone (P), both (E+P), tamoxifen (TAM) or estradiol benzoate (E) and tamoxifen (E+TAM) on OTR mRNA levels in mammary gland is shown in panel A. Values are expressed as fold increase over control. The overall increase in OTR mRNA (149-fold) per mammary gland was calculated taking into account the increase in weight (9.9-fold), total RNA/mg of tissue (13.1-fold) and densitometric signal obtained from poly(A+) RNA purified from 1 mg of total RNA starting material 1.14-fold.

![Figure B](image2.png)

**FIGURE B.** Effects of administration of estrogen, progesterone or tamoxifen on OTR mRNA accumulation in uterus and mammary gland in ovariectomized rats. Animals were injected on four consecutive days with either vehicle (C, control), estradiol benzoate (E), progesterone (P), both estradiol benzoate and progesterone (E+P), tamoxifen (TAM) or estradiol benzoate and tamoxifen (E+TAM). OTR mRNA were determined semi-quantitatively using an RT-PCR assay described previously (Breton et al. 1995). Each bar represents the mean ± s.e. of the results obtained from four different animals, assayed each independently. Means that differ significantly from control (P<0.01) are indicated by an asterisk.
remains unclear. Since an open reading frame consisting of seven codons is present in intron 1, the two types of OTR mRNA may differ with respect to their translational efficiency. Since the two splicing variants only differ by 97 nucleotides, they are not distinguishable by Northern blot analysis.

Differential selection of transcriptional initiation sites represents an alternative mechanism that could underlie the production of differently sized mRNAs. Differential transcriptional initiation resulting in differential promoter usage has indeed been found to occur in genes that encode members of the G-protein coupled receptor family and include the PTH/PTHRP receptor gene (McCuaig et al. 1995) and the α-adrenergic receptor gene (Gao & Kunos 1994). The results from our primer extension studies do not support the hypothesis that such a mechanism underlies the tissue-specific differential regulation of the OTR gene, since we found that OTR transcription initiates at exactly the same positions in mammary gland and uterine tissues.

An alternative explanation for the existence of a mammary gland-specific 5-4 kb OTR mRNA band is differential selection of polyadenylation sites. We have shown earlier that the heterogeneity of uterine OTR mRNA is due to differential selection of polyadenylation sites. Our present data demonstrate that the same applies to OTR gene expression in the mammary gland. In addition, we found that polyadenylation site selection in OTR gene transcripts is also tissue specific, and that the existence of a mammary gland-specific 5-4 kb transcript is due to selection of a distinct, tissue-specific polyadenylation site. The mechanisms and biological significance, if any, of the differential polyadenylation site selection remain to be explored.

Analysis of mammary gland OTR gene expression during pregnancy and lactation demonstrated a distinct pattern that differed from any other tissue in which OTRs are expressed. In kidney, OTR gene expression decreases at term, whereas in certain extra-hypothalamic brain regions, OTR mRNA levels remain constant (Breton et al. 1996, Breton & Zingg 1997). In uterus, pituitary gland and hypothalamus, there is a strong but short-lasting increase in OTR expression around the time of parturition (Breton et al. 1995, Larcher et al. 1995, Breton & Zingg 1997). In contrast, OTR levels per mammary gland undergo an increase during the period of lactation. This distinct pattern of OTR gene regulation is compatible with the function that OT assumes during lactation as well as with earlier OT binding studies (Soloff et al. 1979). Based on our in situ hybridization studies, mammary gland OTR expression is most marked in the milk ducts of the mammary gland and occurs mainly in a layer adjacent to the epithelial cell layer, corresponding to the myoepithelial cell network.

Since the mammary gland is an estrogen-sensitive organ and since we have shown earlier that the OTR is up-regulated in response to estrogens in uterus, kidney, pituitary and hypothalamus (Breton et al. 1995, 1996, Larcher et al. 1995, Breton & Zingg 1997), the absence of any steroid response of mammary gland OTR expression is surprising. There is abundant evidence that the mammary gland is indeed an estrogen sensitive-organ: estrogen administration promotes mammary gland growth and differentiation in vivo (Dilly & Nandi 1968, Hoshiai et al. 1982, Klinge et al. 1987), estrogen binding sites have been demonstrated on mammary gland stroma and epithelial cells (Hsueh et al. 1973, Auricchio et al. 1975, Buell & Tremblay 1984), and transcripts encoding estrogen receptor alpha and beta have been detected in mammary gland (Couse et al. 1997). However, although estrogen administration induces alterations in the myoepithelial cells of the rat mammary gland (Strum 1978), to our knowledge, no direct evidence for the specific presence of estrogen receptors in myoepithelial cells has been provided so far. Although the possible absence of any estrogen receptors from myoepithelial cell remains to be formally excluded, it represents nevertheless an unlikely explanation for the observed results.

A more likely possibility is that the estrogen effect on OTR gene expression is indirect and is either mediated via a paracrine action of an adjacent cell population or, more likely, via the steroid-mediated induction of another gene, expressed in the same cell, that affects OTR gene expression in trans (see Ivell & Walther 1999 for review). The latter hypothesis is strengthened by the finding that the OTR gene does not contain a classical estrogen response element, and that in transient transfection experiments in human mammary gland tumor cells, the existing non-classical response element remains ineffective at its original position in the promoter (Bale & Dorsa 1997). Thus the estrogen induction of the OTR gene is most likely mediated via additional trans-acting gene(s), such as, for example, c-fos, which is involved in mediating the estrogen induction of the prolactin gene in pituitary lactotrophs (Allen et al. 1997). Additional tissue- and cell-specific factors that remain to be identified may further modulate the site- and stage-specific expression of the OTR gene in different tissues.

In conclusion, the present demonstration of tissue-specific differential regulation of a single OTR gene under the control of a single promoter.

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represents an attractive model system for the combinatorial interplay of cell-specific factors that modulate gene expression and allow the hormone OT to assume multiple functions in a physiologically appropriate manner.

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