

Targeted Ablation of Gonadotrophs in Transgenic Mice Depresses Prolactin but Not Growth Hormone Gene Expression at Birth as Measured by Quantitative mRNA Detection

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Key Words

Transgenic mouse · Targeted cell ablation · Diphtheria toxin A · Pituitary · Messenger RNA · Quantitative RT-PCR · Gonadotroph · Prolactin · Growth hormone · Luteinizing hormone- β

Abstract

We previously reported that transgenic ablation of gonadotrophs results in impaired development of cells immunostainable for prolactin (PRL) but not of cells immunostainable for growth hormone (GH) or pro-opiomelanocortin (POMC) in pituitary of newborn mice. The question remained whether this reduction in PRL protein is a reflection of reduced PRL mRNA expression, or whether this regulation is only situated at the translational level. We therefore generated a new series of transgenic mice in which gonadotrophs were ablated by diphtheria toxin A targeting, and analyzed hormone mRNA levels instead of hormone protein around the day of birth. Pituitary mRNA expression levels of luteinizing hormone- β (LH β), PRL and GH were quantified using real-time TaqMan RT-PCR. Of the 13 transgenic mice obtained, 8 showed a clear-cut reduction (ranging from 62 to 98%) in LH β mRNA levels. PRL mRNA values were significantly reduced in the transgenic mice ($p = 0.0034$),

while GH mRNA expression was unaffected ($p = 0.93$). An additional observation was that female newborn mice produce 5 times more LH β mRNA than male mice whereas no sex difference was observed for expression levels of PRL and GH mRNA. Moreover, in the wild-type mice, LH β mRNA expression was 20-fold higher than GH mRNA expression which in turn was 500- to 1,000-fold higher than PRL mRNA expression, suggesting a low expression level of the PRL gene at birth. In conclusion, the present data support the hypothesis that embryonic development of PRL gene expression is stimulated by gonadotrophs.

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Introduction

Various in vitro observations suggest a paracrine stimulatory action of gonadotrophs on lactotroph secretion, cell growth and PRL gene expression [2, 3, 15, 33, 34]. In recent work, we obtained experimental data suggesting a developmental interaction between gonadotrophs and lactotrophs also in vivo [31]. Transgenic ablation of gonadotrophs in mice by targeted expression of diphtheria toxin A (DTA) in gonadotrophs using the glycoprotein hormone α -subunit (α SU) promoter, reduces embryonic

development of cells expressing PRL (lactotrophs), but not of cells expressing GH (somatotrophs) or pro-opiomelanocortin (POMC) (corticotrophs), assessed at the level of hormone protein immunoreactivity. The study was performed on newborn mice because estrogen secretion in blood is negligible at that developmental stage, ruling out interference of estrogens in the observed effect of gonadotroph ablation [31].

The question remained whether control of PRL gene expression through gonadotrophs *in vivo* was at the translational or mRNA expression level. Recent new findings emphasized the relevance of the latter question. By means of reverse-transcription polymerase chain reaction (RT-PCR) analysis for hormone mRNA content in single pituitary cells from P1 (postnatal day 1) mice, it was found that classic PRL cells (monohormonal PRL cells) are very rare in newborn mice and that most cells expressing PRL mRNA in newborn mice (more than 70% of all PRL mRNA-expressing cells) also express mRNA of other hormones, including growth hormone (GH) and POMC, in different combinations [30]. In view of these findings, it was not understood why the decrease in number of lactotrophs by gonadotroph ablation reported previously, was not accompanied by a decrease in the number of somatotrophs and corticotrophs, except when it was assumed that there was a selective effect on PRL gene expression. Thus, it seemed important to reexamine the role of gonadotrophs on lactotroph development by means of detection of hormone mRNA instead of immunostaining of the hormone protein. Therefore, new gonadotroph-ablated transgenic mice were produced and PRL, GH and luteinizing hormone- β (LH β) mRNA levels in pituitary RNA extracts were quantified by real-time TaqMan RT-PCR. In addition, this analysis would give information as to whether control by gonadotrophs is exerted at the mRNA expression and/or translational level.

Materials and Methods

Reagents

AmpliTag Gold and PCR reagents were obtained from Applied Biosystems (Foster City, Calif., USA), first-strand buffer, DTT, Moloney murine leukemia virus (M-MLV) reverse transcriptase, and RNase-free DNase I from Life Technologies (Grand Island, N.Y., USA), recombinant RNasin ribonuclease inhibitor from Promega (Madison, Wisc., USA), and TaqMan probes from Eurogentec (Seraing, Belgium). Oligonucleotide primers were bought from AP Biotech (Uppsala, Sweden), and Tripure reagent from Roche Diagnostics (Mannheim, Germany). RiboGreen RNA quantitation kit came from Molecular Probes (Eugene, Oreg., USA).

Transgenic Mice

Transgenic mice were produced using the α SU-DTA construct by zygote microinjection as described in detail before [31]. The construct contains DTA under control of the -313/+48 bovine α SU promoter shown to target expression of a transgene to gonadotrophs but not to thyrotrophs [4, 13, 17, 24, 31]. F₀ ('founder') α SU-DTA mice were studied since gonadotroph ablation precludes the establishment of a transgenic line due to infertility. All animal experiments were conducted in accord with the 'Guidelines for Care and Use of Experimental Animals' as signed by the Endocrine Society, and approved by the University Ethical Committee.

Quantitative Real-Time RT-PCR (TaqMan) on Pituitary RNA from Transgenic α SU-DTA Mice and Wild-Type Control Mice

Pups from microinjected zygotes were killed by decapitation around the day of birth (= P1, postnatal day 1), i.e. between P0 (= delivery by cesarian section on the calculated day of birth) and P3. Different perinatal ages were analyzed to explore possible rapid changes in hormone mRNA expression levels. Delivery by cesarian section was sometimes done to prevent the pups from being killed by the mother immediately after birth, thus being lost for analysis. The pituitary gland was isolated under the dissecting microscope, and transferred to 500 μ l Tripure reagent for RNA isolation. The final RNA extract (4 μ l) was treated with DNase (0.5 U) for 20 min at 25°C followed by enzyme inactivation at 65°C for 10 min in the presence of 2.5 mM EDTA. 0.5 μ l of RNA extract (out of 5.5 μ l) was used for RNA quantification using the Ribogreen Quantitation reagent. Completeness of DNase treatment was checked by RT-PCR of GH with and without M-MLV reverse transcriptase in each sample. In all tests, GH amplicons were not observed when M-MLV reverse transcriptase was omitted from the RT step. An additional safeguard to exclude genomic DNA amplification during the real-time PCR step was provided by choosing primers or probes spanning an intron (table 1).

100 ng of total pituitary RNA, or the whole RNA sample if less than 100 ng was available, was reverse-transcribed in a final volume of 20 μ l using the following conditions: 1 \times first-strand buffer, 1 nM DTT, 20 U of RNasin, 500 μ M of each dNTP, 5 μ M random hexamers, and 200 U of M-MLV reverse transcriptase. Part of this mixture was heated for 10 min at 70°C and immediately cooled on ice. Then, dNTPs, random hexamers and M-MLV reverse transcriptase were added, and the final mixture subjected to the following cycle: 15 min at 25°C, 50 min at 42°C, and 10 min at 95°C before cooling down to 4°C. Samples were kept at -20°C, or immediately processed by TaqMan PCR. Samples were assayed in tri- or quadruplicate, and reactions without target cDNA were used as negative controls. 18S rRNA (TaqMan Ribosomal RNA Control Reagents - VIC Probe; Applied Biosystems) was used as an internal standard for normalization of hormone mRNA amount in each reaction. Primers and TaqMan probes were designed from GenBank sequences using Primer Express 1.0 Software (Applied Biosystems), and are summarized in table 1. The principles of the technique are described in Orlando et al. [22]. Reaction mixtures (final volume: 25 μ l) containing between 0.002 and 15 ng reverse-transcribed RNA, oligonucleotide primers at a final concentration of 900 nM for hormones and 50 nM for 18S rRNA (following the manufacturer's recommendations), TaqMan probe at a final concentration of 200 nM and 1 \times TaqMan Universal PCR Master Mix (Applied Biosystems) were incubated in a 96-well plate on an ABI PRISM 7700 Sequence Detector (Applied Biosystems) using the following temperature cycling: 10 min at 95°C for

Table 1. Nucleotide sequence of TaqMan PCR primers and probes used in real-time PCR to quantify GH, PRL and LH β cDNA levels

| cDNA | TaqMan PCR primers and probes Sequence ^a | Position in GenBank sequence | |
|------------|--|------------------------------|----------|
| | | accession No. | position |
| GH | S: 5'-TAATGCTGTGCTCCGAGCC-3' | X02891 | 172-190 |
| | AS: 5'-GAATGGAATAGCGCTGTCCC-3' | | 253-272 |
| | P: 5'-TGACACCTACAAAGAGTTCGAGCGTGCCT-3' | | 214-242 |
| PRL | S: 5'-GGGTCAGCCCAGAAAGCAG-3' | X04418 | 67-85 |
| | AS: 5'-CAGTCACCAGCGGAACAGATT-3' | | 147-167 |
| | P: 5'-CTGCTGTTCTGCCAAAATGTTTCAGCCTCT-3' | | 115-143 |
| LH β | S: 5'-CGGCCTGTCAACGCAACT-3' | Y10418 | 39-56 |
| | AS: 5'-GGCAGTACTCGGACCATGCT-3' | | 129-148 |
| | P: 5'-TGAGTTCTGCCAGTCTGCATCACCTTC-3' | | 71-98 |

^a S = Sense primer; AS = antisense primer; P = probe, labeled at the 5' end with 6-FAM (6-carboxyfluorescein), and at the 3' end with TAMRA (6-carboxytetramethylrhodamine).

activation of AmpliTaq Gold DNA polymerase, followed by 40 cycles of 15 s at 95 °C for denaturation and 1 min at 60 °C for annealing and amplification. In each plate, serial dilutions of adult mouse pituitary cDNA were used as template under the same conditions (same sets of primers and probe) to generate standard curves relating the threshold cycle (C_t) to the log input amount of cDNA. The relative amounts of hormone mRNA (cDNA) in each sample were determined using the standard curve method, as described in detail in ABI PRISM Sequence Detection System User Bulletin 2 (Applied Biosystems) and in Fink et al. [10], and were then normalized to 18S rRNA (cDNA) levels.

Real-time RT-PCRs were done to measure LH β , PRL and GH mRNA levels. The amount of RNA recovered from a neonatal pituitary was limited and did not allow quantification of additional hormone mRNAs.

Conversion factors, based on the amount of template included in the reaction and on the sensitivity of the assays for the individual hormones, were applied to the values obtained in order to compare (normalized) expression levels of the three hormones. Standard curves with serial dilutions of purified hormone cDNA revealed that the TaqMan PCR for GH was 50-times more sensitive than for PRL and LH β (data not shown).

Statistical Analysis

Linear mixed models were used to compare the hormone expression levels in control and transgenic mice [35]. All mice were included in the analysis, also the transgenic mice in which no ablation had occurred (evident from absence of a significant decrease in LH β mRNA values). The model takes into account the dependence between mice from the same litter, and contains group (control/transgenic), age and gender as fixed effects. Approximate F-tests were used to evaluate the effect of group, age and gender. For LH β mRNA, a logarithmic transformation was needed to meet the assumptions of the analysis.

In a further analysis, an attempt was made to explore the relation between the 'change' in LH β mRNA levels and the 'change' in PRL

or GH mRNA levels. As 'change', we used the difference in hormone mRNA expression level between a transgenic mouse and its control mice (paired as grouped in table 2), since a 'real change' (i.e. difference between hormone mRNA expression level before and after ablation in a transgenic mouse) obviously could not be measured. If more than one control mouse was available, the mean of the measurements of these controls was used to calculate the difference with the measurement of the transgenic mouse. In this way, 13 'changes' in LH β mRNA levels and 13 'changes' in PRL or GH mRNA levels were obtained. A regression model was used to analyze the relation between both 'changes', after correction for the effect of gender. Since the quality of the controls was not the same for each transgenic mouse (e.g. not the same age, not the same litter), conclusions based on this analysis should be considered as tentative. A logarithmic transformation of the 'change' in LH β mRNA was needed to fit in the regression model.

To compare the levels of LH β , PRL and GH mRNA in the control mice, the hormone mRNA expression value was treated as a repeated factor. This statistical technique was needed to take into account the dependence of the three hormone mRNA expression values which are measured in each (individual) mouse and, therefore, are not independent. A logarithmic transformation of the hormone mRNA expression levels was needed.

All analyses were performed with the statistical package SAS (version 8.1).

Results

Gonadotroph depletion was achieved in transgenic α SU-DTA mice. LH β mRNA levels were quantified in pituitary RNA from perinatal (P0-P3) pups obtained by zygote microinjection to score the degree of gonadotroph ablation. Of the 13 transgenic mice obtained (out of 158

Table 2. Overview of pituitary LH β , PRL and GH mRNA expression levels in perinatal transgenic α SU-DTA mice and their wild-type controls

| Mouse No. | Sex | Wt/tg ^b | Age ^c | Hormone mRNA levels ^d | | |
|--------------------|-----|--------------------|------------------|----------------------------------|--------|-------|
| | | | | LH β | PRL | GH |
| 47,1 | m | wt | P0 | 96.7 | 0.0190 | 11.01 |
| 43,1 | m | wt | P0 | 81.5 | 0.0111 | 9.75 |
| 43,3 ^a | m | tg | P0 | 9.6 | 0.0019 | 10.18 |
| 91,2 | m | wt | P1 | 113.6 | 0.0255 | 15.08 |
| 91,4 | m | wt | P1 | 96.9 | 0.0277 | 20.12 |
| 91,1 | m | tg | P1 | 113.3 | 0.0261 | 21.12 |
| 107,3 | m | wt | P1 | 143.6 | 0.0284 | 14.56 |
| 107,4 | m | wt | P1 | 122.0 | 0.0260 | 21.05 |
| 107,5 ^a | m | tg | P1 | 31.2 | 0.0101 | 17.12 |
| 83,1 | m | wt | P1 | 128.6 | 0.0233 | 15.16 |
| 83,4 | m | wt | P1 | 111.0 | 0.0206 | 21.99 |
| 112,1 | m | tg | P1 | 126.0 | 0.0200 | 16.02 |
| 67,1 | m | wt | P1–P2 | 239.6 | 0.0186 | 13.34 |
| 67,2 | m | wt | P1–P2 | 241.6 | 0.0232 | 12.66 |
| 68,1 ^a | m | tg | P1–P2 | 8.1 | 0.0042 | 14.66 |
| 11,2 | m | wt | P2 | 217.6 | 0.0622 | 12.20 |
| 11,1 | m | tg | P2 | 164.8 | 0.0275 | 15.01 |
| 26,1 | m | wt | P2 | 27.0 | 0.0102 | 29.01 |
| 26,2 ^a | m | tg | P2 | 3.4 | 0.0024 | 24.40 |
| 40,3 | m | wt | P2 | 215.3 | 0.0717 | 10.01 |
| 40,4 | m | wt | P2 | 248.6 | 0.0792 | 9.56 |
| 95,2 ^a | m | tg | P2 | 5.5 | 0.0208 | 10.95 |
| 47,3 | f | wt | P0 | 1291.1 | 0.0291 | 7.08 |
| 47,2 ^a | f | tg | P0 | 492.0 | 0.0080 | 6.83 |
| 51,6 | f | wt | P1 | 416.0 | 0.0063 | 19.51 |
| 51,7 | f | wt | P1 | 421.6 | 0.0062 | 18.82 |
| 51,5 | f | tg | P1 | 296.7 | 0.0052 | 19.05 |
| 115,1 | f | wt | P1 | 1148.7 | 0.0293 | 20.49 |
| 115,2 | f | wt | P1 | 1129.2 | 0.0248 | 26.23 |
| 115,4 ^a | f | tg | P1 | 165.5 | 0.0045 | 24.06 |
| 115,5 | f | tg | P1 | 887.6 | 0.0215 | 20.39 |
| 38,1 | f | wt | P3 | 604.7 | 0.0292 | 11.07 |
| 38,2 ^a | f | tg | P3 | 172.5 | 0.0059 | 13.85 |

^a Mice showing a clear-cut reduction of pituitary LH β mRNA expression.

^b Wt = Wild type; tg = transgenic.

^c P1 = day of birth (= postnatal day 1); P0 = delivery by cesarian section on the prospective day of birth; P1–P2 means that day of birth is uncertain for 1 day.

^d Hormone mRNA levels in the pituitary were quantified by real-time TaqMan RT-PCR, and normalized to 18S rRNA levels. Ratios were multiplied by 1,000. In addition, conversion factors were applied to the values obtained in order to compare expression levels of the three hormones.

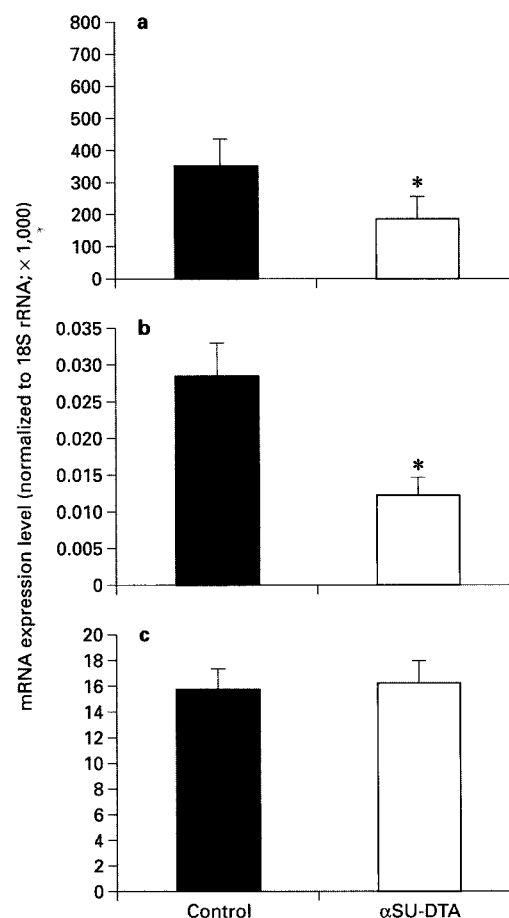


Fig. 1. Effect of transgenic gonadotroph ablation on pituitary LH β (a), PRL (b) and GH (c) mRNA expression levels in perinatal mice. Gonadotroph ablation in α SU-DTA mice causes a significant reduction in both LH β mRNA levels and PRL mRNA expression. GH mRNA expression levels are not affected. Control mice, n = 20; α SU-DTA mice, n = 13. Bars represent SE. * Statistically significant difference in α SU-DTA versus control mice (for p values, see Results).

mice born), 8 mice (marked with an asterisk in table 2) showed a 62–98% reduction in LH β mRNA levels. Statistical analysis using linear mixed models [35] revealed significantly lower LH β mRNA levels in transgenic mice ($p = 0.002$ after correction for gender; fig. 1). PRL mRNA levels were also significantly reduced in α SU-DTA mice ($p = 0.0034$; fig. 1), while GH mRNA expression was unaffected ($p = 0.93$; fig. 1). These differences were neither influenced by age of the animals (i.e. P0 to P3; for

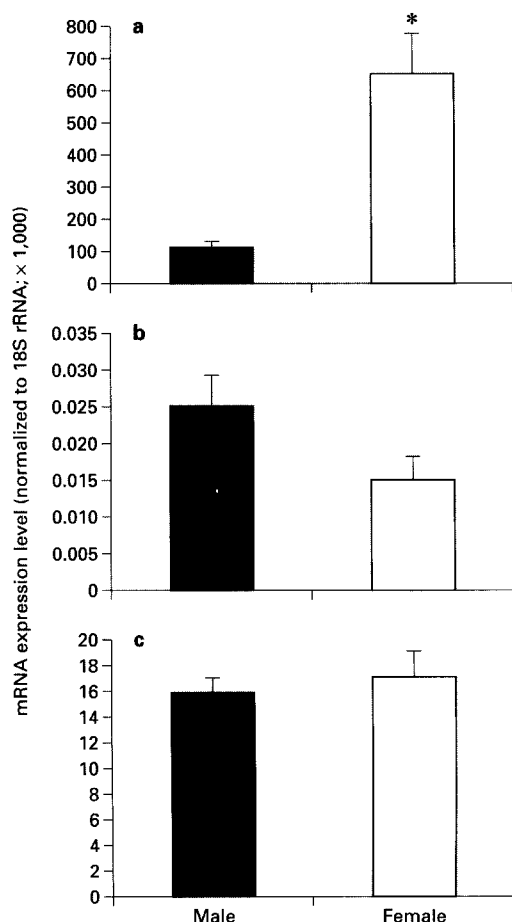


Fig. 2. Pituitary LHβ (a), PRL (b) and GH (c) mRNA expression levels in female and male perinatal mice. LHβ mRNA expression levels in female pituitaries are 5-fold higher than in male pituitaries. No significant differences are measured for PRL and GH mRNA expression levels. Male mice (control + αSU-DTA), n = 22; female mice (control + αSU-DTA), n = 11. Bars represent SE. * Statistically significant difference in female versus male mice (for p values, see Results).

PRL: $p = 0.23$; for GH: $p = 0.96$), nor by gender (for PRL: $p = 0.48$, and GH: $p = 0.94$). The extent of PRL mRNA reduction in the transgenic mice was correlated with the degree of LHβ mRNA reduction; 'changes' in LHβ mRNA levels (i.e. differences between control and transgenic mice) were positively related ($p = 0.001$ after correction for gender) to 'changes' in PRL mRNA values (partial correlation coefficient = 0.71), whereas no significant relation ($p = 0.78$ after correction for gender) was ob-

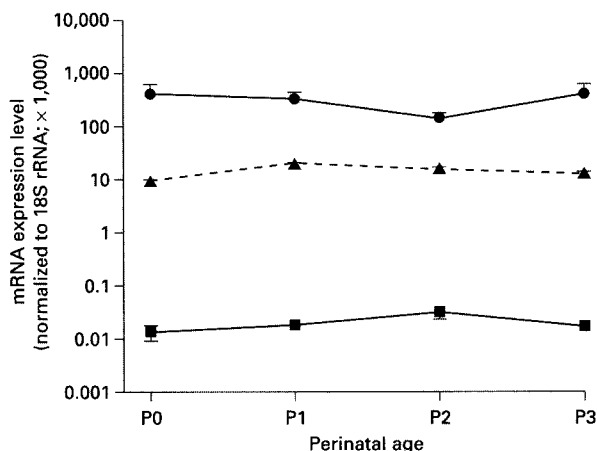


Fig. 3. Pituitary LHβ, PRL and GH mRNA expression levels in mice at different perinatal ages. Expression levels of LHβ (●), PRL (■) and GH (▲) mRNA do not significantly change between the day of birth (P0 = delivery by cesarian section on the prospective day of birth; P1 = day of birth or postnatal day 1) and postnatal day 2 or 3 (P2 and P3, respectively). Values of P1–P2 (table 2) were included in the mean of P2. mRNA expression levels are shown on a log scale. Control + αSU-DTA mice: P0, n = 5; P1, n = 16; P2, n = 10; P3, n = 2. Bars represent SE.

served between 'changes' in LHβ and GH mRNA levels (partial correlation coefficient = -0.11).

An additional observation was that LHβ mRNA levels were significantly higher (~5-fold) in female than in male perinatal mice (statistical analysis within the whole group of transgenic and control mice; $p < 0.0001$ after correction for group, i.e. transgenic or control; fig. 2). PRL and GH mRNA levels were not different between newborn male and female mice ($p = 0.63$ and 0.61 , respectively; fig. 2). Differences in PRL mRNA expression levels measured at the different ages P0 to P3 were at the border of non-significance ($p = 0.05$; fig. 3). There was no significant difference in GH mRNA level between the different ages ($p = 0.21$; fig. 3), neither was there a significant difference in LHβ mRNA content (after correction for gender and group; $p = 0.64$; fig. 3).

Analyses within the group of control mice proper further revealed that at the perinatal age LHβ mRNA expression levels were significantly higher (~20-fold) than GH mRNA expression levels ($p < 0.0001$; fig. 4), and GH mRNA levels were 500- to 1,000-fold higher than PRL mRNA levels ($p < 0.0001$; fig. 4).

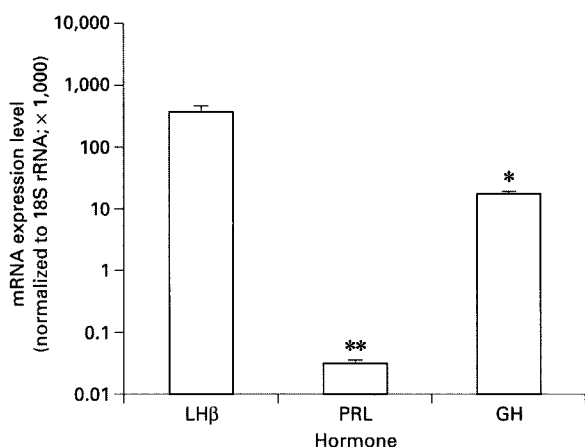


Fig. 4. Pituitary LH β , PRL and GH mRNA expression levels in normal (wild-type) perinatal mice. In the pituitaries of perinatal wild-type mice, LH β mRNA expression levels are 20-fold higher than GH mRNA expression levels. PRL mRNA levels are 500- to 1,000-fold lower than GH mRNA levels. mRNA expression levels are shown on a log scale. For all hormones, $n = 20$ (wild-type mice = control mice). Bars represent SE. * $p < 0.0001$ for GH versus LH β mRNA level; ** $p < 0.0001$ for PRL versus GH mRNA level.

Discussion

In the present study we show that ablation of gonadotrophs during embryonic development results in a reduced PRL, but not GH, mRNA expression level in the pituitary of perinatal mice. These results are an extension to our previous study [31] in which impaired development of PRL cells, scored by immunoreactivity to anti-PRL antiserum, was found in transgenic mice with gonadotroph ablation.

Previous immunocytochemical findings were challenged by more recent observations. We found that in normal pituitary, a substantial number of cells express different pituitary hormone genes at the mRNA level, including PRL, GH and POMC, not only in adult life but also during fetal and neonatal life [25, 30]. The proportion of cells with specific combinations of hormone mRNA was particularly high compared with monohormonal PRL mRNA cells in P1 mice. If most cells containing PRL mRNA also contain either GH and/or POMC mRNA during early life, it is unclear why in the gonadotroph-ablated mice only the PRL-immunoreactive cells were decreased and not the number of GH- and POMC/ACTH-immunoreactive cells. The present findings show

that in these gonadotroph-ablated neonatal mice PRL mRNA expression levels are significantly reduced compared to wild-type controls, while GH mRNA levels are unchanged. Therefore, gonadotrophs seem to control the number of developing lactotrophs by selectively stimulating PRL gene expression, not only in monohormonal PRL cells, but also in plurihormonal PRL cells where GH expression is not affected. What may be the basis of the selective interference with PRL mRNA expression? PRL and GH gene activation are both crucially dependent on the POU homeodomain transcription factor GHF-1/Pit-1 [28, 29]. Confinement of expression to the proper cell type requires combinatorial interactions of Pit-1 with other (transcription) factors [28, 29, 32]. Lactotroph-specific expression of PRL needs interaction of Pit-1 with Ets-1 (a widely expressed proto-oncogene product) on the PRL promoter through binding of a composite Ets-1/Pit-1 cis-acting element, not present in the GH gene [6]. Likewise, efficient GH gene expression is dependent on synergistic combinations of Pit-1 with factors such as Zn-15 (member of the Cys/His zinc finger family of transcription factors) [18] and the thyroid hormone receptor [27]. Another Pit-1-dependent hormone gene, TSH β , is activated by cooperative interaction of GATA-2 and Pit-1, which both bind to the TSH β promoter [11]. In addition to these combinatorial codes of transcription factors, recruitment of coactivator – or corepressor – complexes seems to be fundamental to the selective activation or repression of the PRL and the GH gene by Pit-1 in lactotrophs and somatotrophs [28, 29]. The selective effect of the gonadotroph-derived factor(s) on PRL mRNA expression as reported here suggests a unique interference with signaling pathways that lead to PRL gene activation but not to GH gene transcription. One example of such a PRL-specific signal transduction pathway is the Ras-dependent activation of the Ets-1/Pit-1 synergy in PRL (but not GH) gene activation, where essential coactivators are recruited to the PRL gene [5, 6, 16, 28, 29, 36]. Gonadotroph-derived paracrine factors may act through this pathway to selectively affect PRL expression. Candidate paracrine factors that affect lactotroph growth and PRL production are α SU, N-POMC-derived peptides and certain growth factors (EGF, TGF α) (reviewed in [7]). Some of these factors (e.g. EGF) have been demonstrated to act through a Ras-dependent pathway [23].

It remains unclear, however, whether transcription factor combinations that govern specific hormone gene activation in monohormonal cells are identical to the combinatorial codes, if any, used in plurihormonal cells.

In the present study, quantitative RT-PCR revealed some additional findings. It was noted that neonatal PRL mRNA levels were a 1,000 times lower than GH mRNA levels. Low PRL levels at birth are in line with other studies in mice and rats [1, 20]. On the other hand, PRL levels in pigs and sheep have been reported to be rather high around birth [19, 26]. Another interesting finding was that on average female newborn mice produce 5 times more LH β mRNA than males. Sex-dependent differences of LH production in newborn mice have not been documented before. Moreover, pituitary and plasma LH levels in wild-type mice seem to be very low at birth in both sexes [8, 20], which is not in accordance with the high mRNA levels we measured both in female and male mice. Protein levels, however, do not necessarily correlate with mRNA expression levels [12, 14, 21], and our data therefore suggest an interesting difference in regulation of LH β mRNA and protein expression in the neonatal pituitary. High LH gene activation may coincide with the onset of pulsatile GnRH secretion in rodents towards the end of gestation [9].

In conclusion, new data on PRL gene expression in gonadotroph-ablated newborn mice using mRNA levels

as a hallmark confirm our previous observations on selectively impaired development of PRL cells when gonadotrophs are depleted. Gonadotrophs may increase the number of cells expressing PRL mRNA or may increase the PRL mRNA level in already existing cells that express PRL alone (classic lactotrophs) or coexpress PRL together with GH or POMC. Furthermore, the present data indicate that control of lactotroph development by gonadotrophs is at least in part at the PRL mRNA level, and not, or not only, at the PRL protein level.

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