Regulation of gene expression in human mammary epithelium: effect of breast pumping

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Abstract

Little is known of the molecular regulation of human milk production because of limitations in obtaining mammary tissue from lactating women. Our objectives were to evaluate whether RNA isolated from breast milk fat globules (MFGs) could be an alternative to mammary biopsies and to determine whether intense breast pumping, which increases prolactin (PRL) secretion, will upregulate α-lactalbumin (α-LA, a major determinant of lactose synthesis) transcription. RNA was isolated from MFG and transcripts of interest were identified and quantitated by real-time RT-PCR using an external standard for normalization. In addition, we performed microarray studies to determine MFG RNA gene expression profile. Ten lactating women were studied using two protocols: protocol A with intense pumping from 0800 to 0814 h followed by short pumping and protocol B with intense pumping from 1200 to 1214 h preceded by short pumping. Plasma PRL and MFG α-LA mRNA expression were measured. During protocol A, plasma PRL (61 ± 7–248 ± 43 μg/l by 14 min) and α-LA (3.5 ± 0.9-fold by 6 h; P < 0.03) increased. During protocol B, PRL gradually increased over 4 h from 69 ± 14 to 205 ± 28 μg/l, and further to 329 ± 23 μg/l by 12 min of intense pumping; α-LA mRNA expression did not increase significantly. We conclude that MFGs provide a unique source to study the in vivo regulation of gene expression in mammary epithelial cells. α-LA mRNA is abundant in the MFG and its expression may be regulated by hormonal and temporal factors.


Introduction

The establishment and maintenance of lactation require the concerted regulation by hormones, genes, and local factors. However, little is known about the molecular regulation of milk production in humans due to limitations in obtaining mammary tissue. Therefore, a non-invasive technique permitting the analysis of gene expression in mammary epithelial cells would provide insight into the complex processes of milk production in humans.

Milk fat is secreted by an apocrine mechanism unique to mammary epithelial cells (McManaman et al. 2004). Cyttoplasmic lipid droplets are enveloped in plasma membrane, and pinched off, resulting in the secretion of milk fat globules (MFGs). Intracellular components of the mammary epithelial cells become trapped within the MFG as a cyttoplasmic crescent containing cytoplasmic material except the nucleus (Huston & Patton 1990). Thus, the MFGs represent a potential source to repetitively sample the cytoplasm of mammary epithelial cells.

α-Lactalbumin (α-LA), the regulatory subunit of the lactose synthetase enzyme complex, is abundantly expressed de novo only in the epithelial cells of the mammary gland (Lo et al. 1998) and drives this enzyme complex to synthesize lactose (Jagoda & Rillema 1991, Stacey et al. 1995, Ramakrishnan et al. 2001). Lactose, in turn, is the primary osmotic agent in milk and, therefore, is thought to be the primary determinant of milk volume.

We report here a non-invasive method for the isolation and quantitation of RNA from human MFG, the steps taken to validate its specificity for the mammary epithelial cell, and the steps to find a reference gene. Quantitative real-time reverse transcription PCR (QRT-PCR) was used to assess gene expression in the MFG RNA; and microarray studies were utilized to examine the MFG RNA transcriptome. We have utilized this new technique to test the hypothesis that increased plasma PRL resulting from a period of intense pumping will upregulate α-LA mRNA expression.

Materials and Methods

Subjects

All women were healthy, 18–35 years old, between 6 and 12 weeks post partum, had singleton uncomplicated pregnancies and delivered at term (≥37 weeks). Their infants were healthy and being exclusively breastfed at the time of the study. Written consent was obtained from each woman prior to enrollment.
Milk samples

Milk samples were obtained from women participating in several lactation protocols (for method development and validation) and in our specific breast pumping protocol; all of which were approved by the Institutional Review Board for Human Subject Research and the Scientific Advisory Committee of the General Clinical Research Center (GCRC) at Baylor College of Medicine (Houston, TX, USA). Breast milk was collected simultaneously from both breasts into sterile milk bottles (Ross Products, Columbus, OH, USA) using a standard breast pump (Playtex Embrace, Dover, DE, USA). Milk bottles were weighed before and after milk collection on a Mettler AE50 balance (Mettler-Toledo, Greifensee, Switzerland) and kept on ice prior to storing at −80°C. Ten milliliters of milk was transferred into sterile, RNase-free tubes, tightly sealed, and then centrifuged (Sorvall Legend T, Germany) at 2680 g for 10 min at 4°C. The supernatant fat layer was transferred using a sterile spatula to a new tube. One milliliter of Trizol (Invitrogen Life Technology) was added prior to storing at −80°C for samples that were used for the Trizol method of isolation.

Collection of MFGs

Ten milliliters of milk was transferred into sterile, RNase-free tubes, tightly sealed, and then centrifuged (Sorvall Legend T, Germany) at 2680 g for 10 min at 4°C. The supernatant fat layer was transferred using a sterile spatula to a new tube. One milliliter of Trizol (Invitrogen Life Technology) was added prior to storing at −80°C for samples that were used for the Trizol method of isolation.

Total RNA isolation and assessment of RNA integrity

RNA isolation was performed initially by the RNeasy method (Qiagen Inc.) but later changed to the Trizol method utilizing the manufacturers’ protocols. RNA concentration was measured by reading the absorbance at 260 nm using a Thermospectronic (Biomate 3; Rochester, NY, USA) spectrophotometer (Manchester 1995). RNA integrity was assessed by standard denaturing 1% Seakern ME agarose (Lonza, Basel, Switzerland) gel electrophoresis (Ausubel 1988, Brown et al. 2004) using 5 μg MFG RNA with 1X 3-(N-morpholino) propanesulfonic acid (MOPS) running buffer for 30 min at 80 V in a Bio-Rad MiniSub Cell gel box (Bio-Rad).

Identification of select gene transcripts in MFG by real-time RT-PCR

RNA isolated from random milk samples from two women and a human T-cell line (0.1–10 ng) was used to determine the expression of selected genes of interest by one-step RT-PCR: α-LA, cytosolic phosphoenolpyruvate carboxykinase 1 (PCK1), mitochondrial PCK2, ribosomal 18S (R18S), and colony-stimulating factor 1 (CSF1). Primers for α-LA (cataaatgtgtgccaa-agaagatcct and gccactgttccagcttctcagt) were synthesized in our laboratory, while the probe (6FAMtgactactggttggccca-taagcccctctTAMRA) was synthesized by Applied Biosystems (ABI, Foster City, CA, USA). Primer–probe pairs for PCK1 and PCK2 (Assay ID Hs00159918_m1 and Hs00356436_m1 respectively), CSF1 (Hs00174164_m1), and R18S (Hs9999901_s1), a candidate reference gene, were purchased from ABI. Reverse transcription (48°C for 30 min) and PCR cycling parameters were performed following the instruction manual of the ABI PRISM 7900 (95°C for 10 min, 95°C for 15 s, 60°C for 1 min, 40 cycles). Reactions were carried out in a 96-well plate in a final reaction volume of 50 μl using TaqMan One Step PCR Master Mix Reagents Kit (P/N 4309169, ABI).

Microarray analysis

Microarray analysis was performed to evaluate the gene expression profile of the MFG RNA from a single subject enrolled in a lactation protocol where breast milk was collected every 3 h (q3h) for 96 h. After the first 24 h of milk collection, 0.1 mg/kg rhGH (Nutropin AQ, Genentech Inc., South San Francisco, CA, USA) was administered subcutaneously at 0830 h for the next 2 days. For initial analysis, 16 samples from different time points were used. Total RNA (1.5 μl) was quantified using the Nanodrop ND-1000 u.v.–vis spectrophotometer (Nanodrop Technologies, Wilmington, DE, USA), and the RNA quality was assessed using the Experion RNA StdSens Analysis Kit (Bio–Rad Laboratories) on a 2100 Bioanalyzer (Agilent Technologies, Palo Alto, CA, USA). Gene expression analysis was performed using the Sentrix BeadChip and BeadStation system from Illumina Inc. (San Diego, CA, USA). Total RNA between 300 and 500 ng was converted to cDNA by reverse transcription using Supernscript II reverse transcriptase and T7-(dT)24 primers, followed by second-strand synthesis to generate double-stranded cDNA. After purification, the cDNA was converted to biotin-labeled cRNA, hybridized to a human Ref-8 BeadChip array (Illumina Inc.), and stained with streptavidin–Cy3 for visualization. The human Ref-8 BeadChips contain sequences representing ~22 000 curated genes and ESTs. Quality standards for hybridization, labeling, staining, background signal, and basal level of housekeeping gene expression for each chip were verified. After scanning the probe array, the resulting image was analyzed using the BeadStudio software (Illumina Inc.). Samples were normalized using a rank invariant procedure to the baseline sample. Selected genes, casein (CSN3 and CSN2), xanthine dehydrogenase (XDH), growth hormone receptor (GHR), insulin-like growth factor (IGF1), and IGF1 receptor (IGF1-R), were chosen and the fluorescence intensity data (extracted using the manufacturer’s software) were used to determine the expression of these genes. We then used QRT-PCR to confirm the array results for GHR, IGF1, and IGF1-R using the MFG RNA samples from the same subject (10–4000 ng) and compared this with α-LA expression (10–100 ng). Primer–probe pairs were obtained from ABI (Hs00174872_m1, Hs01547656_m1, and Hs00181385_m1 respectively).

Evaluation of candidate reference genes for quantitative real-time RT-PCR

Human R18S RNA The MFG RNA from four subjects was used to determine R18S expression at different time
points in a lactation protocol. One-step QRT-PCR was performed in duplicate 50 μl reactions using 10 ng MFG RNA. R18S expression was calculated as the fold change relative to the baseline sample: fold difference = $2^{-\Delta \Delta C_t}$ (Livak & Schmittgen 2001).

**Human endogenous control array** TaqMan Low Density Human Endogenous Control Array (ABI) was used to determine the expression of 16 commonly used reference genes. Briefly, we reverse-transcribed 100 ng MFG RNA from one subject (taken at five time points in a lactation protocol) using the Reverse Transcription (Livak et al. 1986). No further breastfeeding was performed until the end of the study.

**Protocol A: intense breast pumping at 0800 h** Starting at 0800 h, seven successive 2-min milk collections were performed. In addition, one 2-min milk collection was obtained at 1000 h and then q30 min from 1200 to 1600 h. The milk was immediately placed on ice and processed for collection of MFG.

**Protocol B: intense breast pumping at 1200 h** This protocol was identical to protocol A, except that 2-min breast milk samples were collected q30 min from 0800 to 1200 h, prior to the seven successive 2-min breast milk collections from 1200 to 1214 h. Additional 2-min samples were collected at 1400, 1600, and 1800 h.

Blood (2.5 ml) was collected q30 min from 0400 h until the end of the study, except during the intense pumping, where blood was collected q2 min for measurement of plasma PRL. Subjects were discharged between 1800 and 2000 h after consuming a light snack.

**α-LA quantitation** One-step QRT-PCR using Mm β-actin as a reference gene was used to quantitate α-LA in the MFG RNA. The expression of α-LA was calculated as the fold change relative to the baseline sample (0800 h) according to the $\Delta \Delta C_t$ method (Pfaffl 2001).

**Plasma assays** Blood samples (2.5 ml) were centrifuged at 2680 g for 10 min at 4 °C. The plasma was separated and transferred to a new tube then stored at −80 °C. Plasma PRL was measured using an electrochemiluminescence assay (Elecsys 1010, Roche Diagnostics). The inter-assay mean ± s.d. for the assay control was 7.6 ± 0.7 mg/l with a coefficient of variation (CV) of 9%, while the intra-assay CV among ten replicates was 0.9%.

**Statistical analysis** All data are presented as mean ± s.e.m. Data were compared using Student’s $t$-test and ANOVA followed by Tukey’s HSD post hoc analysis using SPSS for Windows (Version 10.0, SPSS Inc. Chicago, IL, USA).

**Results**

**Total RNA isolation and assessment of RNA integrity**

Total RNA yield with the RNaseasy method was 3.9 ± 0.4 μg/ml breast milk, while that using the Trizol method was 4.5 ± 0.4 μg/ml breast milk ($P=NS$). RNA isolated
using Trizol method had significantly less RNA degradation when compared with the RNeasy method (data not shown). Therefore, all subsequent RNA isolations were done by the Trizol method.

Identification of select gene transcripts in MFG by real-time RT-PCR

\(\alpha\)-LA, a milk protein gene, was only detected in the MFG RNA but not in the RNA isolated from T cells. PCK1 was not detectable, while PCK2 was detected in both MFG and T-cell RNA, albeit in low amounts. CSF1 (marker of macrophage contamination) expression was not detected in the MFG RNA. R18S was expressed in high amounts in both MFG and T-cell RNA, thus we proceeded to validate this as a reference gene (see below).

Microarray analysis

Based on the fluorescence intensity data, milk protein-related genes such as CSNs, \(\alpha\)-LA, and XDH were highly expressed. IGF1-R was expressed but at a much lower level than the milk protein-related genes, while GHR and IGF1 were not detectable (Fig. 1). RT-PCR confirmed the array results: GHR and IGF1 were not detectable (\(C_t\) of 40) in up to 2 \(\mu\)g MFG RNA, while IGF1-R was consistently expressed at low levels when using 1–4 \(\mu\)g RNA (Table 1).

Evaluation of candidate reference genes for quantitative real-time RT-PCR

Ribosomal 18S

R18S expression in MFG RNA varied greater than fivefold over the time course of the samples analyzed (data not shown) and was deemed unsuitable as a reference gene.

Human endogenous control array

Among the candidate genes in the array, R18S was found to be the most highly expressed but varied considerably across time, confirming our initial real-time PCR results using R18S primers (see above). The expression of other endogenous reference genes varied by as much as 16-fold from the baseline, but followed the same expression pattern. As a result, they were deemed unsuitable as reference genes for the quantitation of \(\alpha\)-LA (Fig. 2).

Mouse \(\beta\)-actin

Using the external standard, fold change of Mm \(\beta\)-actin expression was 1.6 when compared with the baseline (Fig. 3). The intra-assay variability was determined using ten replicates of 10 ng MFG RNA + 10 ng Mm lung RNA. The average \(C_t\) for Mm \(\beta\)-actin was 25.10 ± 0.04 (mean ± S.E.M.) and the coefficient of variation was 0.2% (data not shown). The slope for the plot of the log input (0.1–100 ng) RNA versus \(\Delta C_t\) \((C_{t_{\alpha\text{-}LA}} - C_{t_{\text{Mm}\beta\text{-actin}}})\) was 0.11, demonstrating comparable amplification efficiencies over the assessed range.

Table 1

<table>
<thead>
<tr>
<th>Gene</th>
<th>10 ng</th>
<th>100 ng</th>
<th>1000 ng</th>
<th>2000 ng</th>
<th>4000 ng</th>
</tr>
</thead>
<tbody>
<tr>
<td>(\alpha)-LA</td>
<td>32.7 ± 1.4</td>
<td>29.4 ± 1.6</td>
<td>NT</td>
<td>NT</td>
<td>NT</td>
</tr>
<tr>
<td>IGF1-R</td>
<td>40</td>
<td>40</td>
<td>36.5 ± 0.7</td>
<td>35.5 ± 0.3</td>
<td>34.3 ± 0.2</td>
</tr>
<tr>
<td>IGF1</td>
<td>40</td>
<td>40</td>
<td>40</td>
<td>40</td>
<td>NT</td>
</tr>
<tr>
<td>GHR</td>
<td>40</td>
<td>40</td>
<td>40</td>
<td>40</td>
<td>NT</td>
</tr>
</tbody>
</table>

Real-time PCR cycle thresholds (\(C_t\)) for detection of \(\alpha\)-lactalbumin (\(\alpha\)-LA), growth hormone receptor (GHR), insulin-like growth factor (IGF1), and insulin-like growth factor receptor (IGF1-R) in varying concentrations of MFG RNA. A \(C_t\) of 40 means no detection. The PCR results for these genes support the microarray data (Fig. 1B). \(n=4\). NT, not tested.
(Suslov & Steindler 2005). Thus, the Mm β-actin was suitable as a reference gene for ΔΔCt quantitation.

Effect of breast pumping on prolactin (PRL) and α-LA mRNA expression

Protocol A The PRL concentration following breastfeeding at 0400 h was 246 ± 23 μg/l, gradually fell to a nadir at 0800 h (61 ± 7 μg/l), and then peaked acutely to 248 ± 43 μg/l by 14 min after the start of intense pumping. This peak was essentially identical to that observed following the 0400 h breastfeeding, suggesting that similar stimulation of the breast occurred under both study conditions. α-LA mRNA in MFG increased 3.5 ± 0.9-fold after 6 h (P < 0.03), and then returned toward baseline by 8 h (Fig. 4).

Protocol B The PRL concentration after the 0400 h breastfeeding (234 ± 33 μg/l) declined to 69 ± 14 μg/l by 0800 h. During the short pulses of q30 min pumping from 0800 to 1200 h, PRL concentration gradually increased to 205 ± 28 μg/l by 1200 h. Intense breast pumping at noon resulted in a further increase of PRL to 329 ± 23 μg/l by 12 min, and then declined continuously until the end of the study. Alternatively, we calculated the PRL area under a curve (AUC) from 0400 to 1600 h, 1799 ± 246 μg/l/12 h (protocol A) versus 1588 ± 201 μg/l/12 h (protocol B), P = 0.21, suggesting similar breast stimulation for both protocols. The milk yield during breastfeeding at 0400 h (127 ± 14 ml) was significantly higher than that during the 2-min pumping at 0800 h (24 ± 4 ml), P = 0.0003, suggesting...
that the breasts were incompletely emptied during the 2-min pumping. During the intense pumping from 1200 to 1214 h, total milk yield was only 22 ± 7 ml. None of the subjects had enough milk to complete the intense pumping collection, and by min 6 of collection, four subjects pumped <1 ml milk per 2-min collection. The α-LA mRNA expression varied between 0.5 and 1.5 times the baseline, but the fold change differences were not significant (Fig. 4).

**Discussion**

The development of a non-invasive technique for obtaining tissue samples from lactating women would make possible the exploration of molecular mechanisms regulating human lactation. Fat secretion occurs through an apocrine mechanism and brings with it mammary epithelial cell cytoplasmic material, including ribosomes, mitochondria, and other organelles (Huston & Patton 1990, Lindquist et al. 1994, Thompson et al. 1998). As much as 38% of the lipid droplets in human breast milk contain cytoplasmic crescents (Huston & Patton 1990). From this cytosol within the MFG, we have been able to consistently isolate ~4 μg total RNA per milliliter of breast milk. Initial efforts at RNA isolation using the RNeasy kit were hampered by RNA degradation, but the quality was substantially improved using the Trizol method, suggesting that degradation by ribonucleases had not occurred in the mammary lacteal prior to milk collection.

DNA and RNA of epithelial cells isolated from human milk have been shown to represent gene expression in the mammary gland (Lindquist et al. 1994, Thompson et al. 1998, Boutinaud & Jammes 2002). However, breast milk contains a significant number of leukocytes, and 4–44% of cells in milk from women 4 weeks post partum are non-epithelial. Thus, additional procedures are needed to isolate mammary epithelial cells prior to RNA isolation (Brooker 1980, Obermeier et al. 2000, Boutinaud & Jammes 2002). Since we discarded the pellet that results from centrifugation of the whole milk, we eliminated these other cellular elements. This was confirmed by the absence of CSF1 gene expression (marker for contaminating macrophage RNA).

The demonstration of high α-LA expression in the MFG RNA lends further support that the MFG RNA was representative of the mammary epithelial cell. α-LA is a whey protein found only in mammary epithelial cells and forms the non-catalytic subunit of the enzyme lactose synthetase. α-LA modifies the specificity of the active enzymatic subunit galactosyl transferase, central to the synthesis of lactose. Lactose, in turn, is thought to be the primary osmotic agent in milk. In mice, it has been shown that the absence of α-LA results in failure of lactation, while lactation was restored with the expression of human α-LA gene (Stinnakre et al. 1994, Stacey et al. 1995). A 170 bp fragment, the size predicted for the human α-LA PCR product, was obtained from MFG RNA (data not shown). This RT-PCR product was not detected in RNA from a T-cell culture line, indicating that the α-LA transcripts were specific to mammary epithelial cells. R18S, as expected, was highly expressed in all RNA samples, PCK1 expression was absent, and PCK2 was detected at low levels. Our results are reminiscent of those observed in guinea pigs where PCK2 (mitochondrial PCK) is the more active isoenzyme during lactation (Jones et al. 1989).

In addition, we evaluated the MFG transcriptome by microarray analysis. α-LA, CSNs, and XDH (Fig. 1) genes that are expressed by the mammary epithelial cell (Naylor et al. 2005) were highly expressed. The mechanism by which hGH acts on the lactating mammary gland is controversial. Others have been unable to demonstrate specific binding of GH to mammary epithelial cells (Akers & Keys 1984, McFadden et al. 1990), and IGF1 mRNA was shown to be expressed by the mammary stroma and not by the mammary epithelial cell (Naylor et al. 2005). 2005) were highly expressed. The mechanism by which α-LA results in failure of lactation, while lactation was restored with the expression of human α-LA gene (Stinnakre et al. 1994, Stacey et al. 1995). A 170 bp fragment, the size predicted for the human α-LA PCR product, was obtained from MFG RNA (data not shown). This RT-PCR product was not detected in RNA from a T-cell culture line, indicating that the α-LA transcripts were specific to mammary epithelial cells. R18S, as expected, was highly expressed in all RNA samples, PCK1 expression was absent, and PCK2 was detected at low levels. Our results are reminiscent of those observed in guinea pigs where PCK2 (mitochondrial PCK) is the more active isoenzyme during lactation (Jones et al. 1989).

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epithelium (Berry et al. 2001). Kleinberg proposed that GH induces IGF1 from the stroma, which then acts through specific epithelial cell receptors (Kleinberg et al. 1990). In the single subject studied with the microarray, GHR and IGF1 were not detectable, while IGF1R mRNA was expressed (Fig. 1). RT-PCR on these genes confirmed the array results (Table 1). Thus, our data are consistent with Kleinberg’s proposal and we believe that the RNA isolated from MFG is solely produced by mammary epithelial cells and reflects the cytoplasmic environment of these cells.

The comparative C\textsubscript{t} (\(\Delta\Delta C\textsubscript{t}\)) method for relative quantitation (Livak & Schmittgen 2001, Pfaffl 2001) has been used for gene expression studies (Schmittgen & Zakrjasek 2000). While eliminating the need for standard curves, a validated internal control gene is a pre-requisite for its use (Wong & Medrano 2005). However, endogenous genes thought to be stable (e.g. GAPDH, \(\beta\)-actin) have been shown to vary and not be appropriate for normalization purposes (Schmittgen & Zakrjasek 2000, Hamalainen et al. 2001, Dheda et al. 2004).

*Figure 4* Comparison of PRL levels and \(\alpha\)-LA mRNA expression for protocols (A) and (B). Protocol A: intense breast pumping at 0800 h (time 0). PRL levels peaked after 0400 h (time -4) breastfeeding at 246±23 \(\mu\)g/l, declined to 61±7 \(\mu\)g/l at 0800 h and then increased acutely to 248±43 \(\mu\)g/l by 14 min after the start of intense pumping, and \(\alpha\)-LA mRNA increased 3-5-fold \((P<0.03)\) 6 h from 0800 h. Protocol B: intense breast pumping at 1200 h, PRL increased after 0400 h to 234±33 \(\mu\)g/l (time -4) breastfeeding, declined to 69±14 \(\mu\)g/l at 0800 h, gradually increased to 205±28 \(\mu\)g/l by 1200 h (start of intense pumping), then increased further to 329±23 \(\mu\)g/l by 12 min after the start of intense pumping, while \(\alpha\)-LA did not change significantly from 0800 h. \(\alpha\)-LA mRNA expressed as a fold change from 0800 h (time 0). *\(P<0.05\), significantly different from time 0.
Despite utilizing a constant amount of total MFG RNA for each QRT-PCR, R18S, a commonly used endogenous reference gene, varied greater than fivefold from the baseline. Normally used housekeeping genes can vary as much as 34-fold (Dheda et al. 2004). Even with the low-density human endogenous control array containing probes for 16 commonly used reference genes, we did not identify a suitable control gene. Interestingly, in our study, the expression pattern of the above 16 genes was similar at each time point (Fig. 2). From these results, one might surmise that the expression of these genes may have a time-dependent expression, or that the breast pumping stimulus induced an upregulation of these genes. If this were the case, then other non-milk-related genes may be necessary for milk synthesis.

We then added an external standard (foreign RNA) to MFG RNA prior to RT-PCR. Others have added cloned artificial RNA molecules or an in vitro transcribed RNA (cRNA) without homology to the total RNA as external standards (Huggett et al. 2005, Gilsbach et al. 2006). However, these procedures are more costly and time-consuming. In our studies, Mm β-actin primers did not cross-react with human DNA/RNA sequences (data not shown), minimizing the potential of cross-contamination with the human samples. The amplification efficiencies for Mm β-actin and α-LA were comparable, and a constant amount of Mm RNA spiked into MFG RNA resulted in a small change in Mm β-actin expression (Fig. 3). Although ideally unchanged, the variability may have been due to methodological errors or the presence of inhibitors in the sample. The ΔΔCt method of relative quantitation could then be used to quantitate α-LA expression.

In cell culture studies, the expression of α-LA gene has been shown to be hormonally regulated. Addition of PRL, in particular, results in an increase in α-LA mRNA expression in the following 4–6 h (Nagamatsu & Oka 1983, Golden & Rillema 1995). The suckling stimulus evokes a neuroendocrine reflex resulting in PRL secretion (Freeman et al. 2000). Simultaneous electric breast pumping elicits a similar PRL response as normal breastfeeding (Zinaman et al. 1992). Our two protocols provided similar stimuli (number and length of each pumping episode during the study period) and the similar values obtained for PRL AUC support this.

With the 0800 h intense pumping, an almost 4-fold increase in plasma PRL occurred by 14 min after the start of pumping and α-LA mRNA expression increased significantly 3.5-fold 6 h later, in keeping with the results from in vitro studies (Fig. 4). In protocol B, we did not observe a sharp PRL increase during the q30 min pumping; instead, it gradually increased from 0800 to 1200 h, such that with intense pumping from 1200 to 1214 h, the PRL increased by only 50% from the start of intense pumping when compared with the fourfold increase in protocol A. There was no significant change in α-LA mRNA expression when compared with the baseline sample in protocol B.

Incomplete emptying of the breast at each 2-min pumping in protocol B or a lack of a clear stimulus (large PRL increase) may have hindered further milk synthesis resulting in the low milk yield at 1200 h. Alternatively, milk collection during the q30 min pumping from 0800 to 1200 h, which yielded 132 ± 23 ml, may have emptied the breasts just before intense pumping since the total collected volume was similar to the 0400 h breastfeeding (127 ± 14 ml). Despite a higher peak PRL concentration in protocol B, this was reached gradually rather than acutely as in protocol A. It is possible that the magnitude of PRL change regulates the change in α-LA mRNA expression. On the other hand, breast fullness, the time of day PRL peaks, and the influence of other hormonal factors may have also contributed to the difference in α-LA mRNA expression profiles.

This is the first report to show that high-quality RNA can be isolated from MFG and that mRNA transcripts can be identified and quantitated accurately and reproducibly in human milk. We demonstrated that a fourfold increase in PRL concentration was associated with a significant increase in α-LA mRNA expression 6 h following intense pumping at 0800 h; but not when the intense pumping was at noon, preceded by short pulses of breast pumping q30 min. Because of the complexity of milk synthesis, we believe that this research methodology will have great value in unraveling the molecular regulation of milk production and will enable us to further explore the hormonal regulation of gene expression in the lactating mammary gland. The exact mechanism by which PRL regulates α-LA mRNA expression and that of other milk genes requires further investigation.

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