Impaired Mammary Gland Development and Function in Mice Lacking LAR Receptor-like Tyrosine Phosphatase Activity


The LAR receptor-like protein tyrosine phosphatase is composed of two intracellular tyrosine phosphatase domains and a cell adhesion molecule-like extracellular region containing three immunoglobulin-like domains in combination with eight fibronectin type-III-like repeats. This architecture suggests that LAR may function in cellular signalling by the regulation of tyrosine phosphorylation through cell–cell or cell–matrix interactions. We used gene targeting in mouse embryonic stem cells to generate mice lacking sequences encoding both LAR phosphatase domains. Northern blot analysis of various tissues revealed the presence of a truncated LAR mRNA lacking the cytoplasmic tyrosine phosphatase domains and indicated that this LAR mutation is not accompanied by obvious changes in the expression levels of one of the LAR-like receptor tyrosine phosphatases PTP6 or PTPα. LAR−/− mice develop and grow normally and display no appreciable histological tissue abnormalities. However, upon breeding we observed an abnormal neonatal death rate for pups from LAR−/− females. Mammary glands of LAR−/− females were incapable of delivering milk due to an impaired terminal differentiation of alveoli at late pregnancy. As a result, the glands failed to switch to a lactational state and showed a rapid involution postpartum. In wild-type mice, LAR expression is regulated during pregnancy reaching maximum levels around Day 16 of gestation. Taken together, these findings suggest an important role for LAR-mediated signalling in mammary gland development and function. © 1997 Academic Press

INTRODUCTION

Protein tyrosine phosphorylation, a key event in signal transduction, is a posttranslational modification controlled by the agonistic or antagonistic action of protein tyrosine kinases (PTKs) and protein tyrosine phosphatases (PTPases). Mourey and Dixon, 1994; Sun and Tonks, 1994). The PTPases comprise a diverse family of receptor-like and cytoplasmic-type enzymes including multiple isoforms resulting from alternative splicing and posttranslational modifications (for review see Saito, 1993).

Receptor-like PTPases (RPTPases) contain one or two homologous PTPase domains, a transmembrane segment, and diverse combinations of domains with possible ligand-binding properties in the extracellular part. For example, the closely related RPTPases RPTPμ and RPTPκ mediate cell–cell interactions in a homophilic, but not heterophilic manner (Brady-Kalnay et al., 1993; Gebbink et al., 1993; Sap et al., 1994; Zondag et al., 1995). In RPTPβ the extracellular moiety binds to a nonrelated cell-surface protein, the neuronal recognition molecule contactin (Peles et al., 1995). It has not been clarified if and how such interactions modulate tyrosine phosphatase activity and whether RPTPases play
a role early in signal transduction or later in adaptation or response cessation (Ninfa and Dixon, 1994).

Although LAR was among the first RPTPases to be identified (Streuli et al., 1988) and has been studied extensively at the cellular level, its physiological function remains elusive. LAR is composed of two cytoplasmic phosphatase domains in tandem, a transmembrane segment, and an extracellular part which shares homology to immunoglobulin (Ig)-like and fibronectin type III (Fn-III) domains, commonly found in cell adhesion molecules (Edelman and Crossin, 1991). This architecture suggests a physiological function for LAR in cellular signalling by tyrosine dephosphorylation as a response to cell–cell or cell–matrix interactions. Recently, an intracellular LAR-interacting protein (LIP.1) has been identified, which binds to the second PTPase domain and colocalizes with LAR to the ends of foci adhesions most proximal to the cell nucleus, suggesting a role for LAR in disassembly of focal adhesions (Serra-Pages et al., 1995).

LAR has a broad tissue distribution and is expressed on the cell surface as a complex of two noncovalently associated subunits of 150 and 85 kDa, resulting from cleavage of the pro-protein (Streuli et al., 1992; Yu et al., 1992). The N-linked glycosylated 150-kDa fragment is shed during growth. Whether this shedding, which is PMA-inducible (Serra-Pages et al., 1994), has an effect on the intracellular phosphatase activity remains to be established. The 85-kDa fragment contains a short ectodomain, the transmembrane segment, and the two PTPase domains of ~280 amino acid residues each. Two closely related family members do exist that show a similar intracellular processing and cell surface expression, namely the LAR-like RPTPases PTP6 and PTP@ (Pulido et al., 1995a; Yan et al., 1995).

In vitro site-directed mutagenesis studies suggested that the first, membrane-proximal phosphatase domain of LAR exhibits catalytic activity, whereas the second, membrane-distal phosphatase domain may have only a regulatory function in modulating the substrate specificity of the first domain (Pot et al., 1991; Streuli et al., 1990). However, the extracellular ligand(s) and downstream substrate(s) of LAR have not been identified. Therefore, we set out to study the consequences of the loss of LAR PTPase function in vivo by means of gene targeting using homologous recombination in mouse embryonic stem (ES) cells. Characterization of the resulting LAR-deficient mice points to a role for LAR PTPase activity in mammary gland development during pregnancy.

MATERIALS AND METHODS

Generation of LAR-Deficient Mice

The isolation and characterization of mouse 129 genomic LAR sequences were described previously (Schaapveld et al., 1995). A 7.5-kb BamH1–EcoR1 fragment just upstream of the exon encoding the cytoplasmic phosphatase domains was subcloned into pBluescript KS+ (Stratagene). From this, the 5′ segment was subcloned as a 3.2-kb Pstl–SacI fragment into a modified pOEM3 vector having a XhoI-linker inserted in the SmaI-site, resulting in pLARS′. From the 4.5-kb BamH1 clone just 448 bp downstream the stop-codon of LAR, the 5′ 2.3-kb BamH1–BglII fragment was subcloned into the BamH1-site of pLARS′, generating pLARS′-3′. Finally, a neomycin phosphotransferase expression cassette (Neo) (van Deursen et al., 1991) was inserted into the SalI-site of pLARS′-3′. Prior to electroporation, the targeting construct (pLARNeo) was linearized using the unique XhoI-site from the introduced linker.

E14 ES cells were cultured on irradiated SNL-H9 feeder cells as described (van Deursen and Wieringa, 1992). Exponentially growing ES cells were collected and mixed with 20 μg of linearized pLARNeo, electroplated at 250 V/500 μF (Gene Pulser, Bio-Rad), and plated at 5 x 10^6 per 9-cm dish onto irradiated feeder cells. Selection was applied 24 hr later using 300 μg/ml G418 (Gibco/BRL). After 9–11 days of selection, G418-resistant ES clones were picked and expanded.

Genomic DNA from individual ES cell clones was extracted and analyzed by Southern blot analysis as described (Steeghs et al., 1995). Initial screening was performed using a 3′-flanking probe (a Sau3A fragment derived from a 2.5-kb BamH1 fragment just downstream of the 4.5-kb BamH1 clone mentioned above). Positive clones were also analyzed with a 5′-flanking probe (a 1.0-kb BamH1–Xba1 fragment representing the 5′ end of the 7.5-kb BamH1–EcoR1 fragment mentioned above), a 0.8-kb PstI fragment from the Neo cassette, and a 1.8-kb BamH1 mouse LAR cDNA fragment comprising all exons encoding both cytoplasmic phosphatase domains (Schaapveld et al., 1995) to check for proper homologous recombination.

Three correctly targeted ES cell clones that also displayed the correct number of 40 chromosomes (CA1, CA7, and BC2) were used for injection into C57BL/6 recipient blastocysts and implanted into the uterine horns of pseudopregnant (C57BL/6 x CBA/CaF1)F1 foster mothers (Bradley, 1987). Resulting male chimeras were mated with C57BL/6 females to check for germline transmission. DNA obtained from tail biopsies of agouti offspring and subsequent generations was screened for the presence of the mutant LAR allele by Southern blot analysis and/or polymerase chain reaction (PCR, Hoffmann–La Roche).

Genotyping

A PCR reaction using four primers was designed to discriminate between wild-type (LAR+/+), heterozygous (LAR+/−), and homozygous mutant (LAR−/−) mice. The wild-type allele was detected as a 152 bp amplicon using the primers LAR5s (5′-GAG CTG CGT CAC TTT CA-3′, sense), located 129 bp upstream of the codon for the conserved cysteine residue in the first phosphatase domain, and LAR2as (5′-GAC TAC GTT TTC TCT ACC-3′, antisense), a genomic primer located 410 bp downstream of the same cysteine codon. The mutant allele was detected as a 394 bp amplicon using the primers Neo3′ (5′-CTA TCG CCT TCT TCA CGA-3′, sense), located 25 bp upstream of the stop-codon in the Neo cassette, and LAR2as (5′-GAC TAC GTT TTC TCT ACC-3′, antisense), located 532 bp downstream of the stop-codon of LAR. The PCR cycle profile consisted of 94°C for 1 min, 59°C for 1 min, and 72°C for 2 min, for 35 cycles, and was performed in a programmable thermocycler (Perkin–Elmer–Cetus). Each 50-μl reaction contained 10 mM Tris–HCl (pH 8.3), 50 mM KCl, 2.5 mM MgCl2, 0.01% BSA, 0.01% gelatin, 0.05% NP-40, 0.05% Tween-20, 1 mM dNTPs, 100 ng genomic DNA, 100 ng of each primer, and 1 U Taq polymerase. One-fifth of the reaction products was separated on 2% agarose gels and visualized by ethidium bromide staining.
Breeding of Mice

Mice were kept at the Central Animal Facility of the University of Nijmegen in a standard room with a day/night rhythm of 06:00-18:00 hr at a temperature of 21°C and a humidity of 50-60%. Males were housed together with four females in a macronol type I cage and fed ad libitum. Upon pregnancy, females were separated to give birth to their pups. The first, second, and third litter of each female was counted and pups were observed every day. Experiments were performed on F2 mice with a 129x C57BL/6 hybrid genetic background. Breeding results were statistically analyzed using MANOVA (SPSS) and Student’s t test.

RNA Analysis

Poly(A)+ RNA from kidney, brain, heart, liver, and lung (pooled from four 3-months-old male LAR+/+, LAR+/-, and LAR-/- mice, respectively) was isolated as described previously (Hendriks et al., 1995). For Northern blot analysis, 3 μg of each sample was fractionated on a 1% (w/v) agarose/2.2 M formaldehyde gel, transferred to a Hybond-N+ membrane (Amersham), and linked by UV-radiation (UV Stratalinker 1800, Stratagene). Blots were subsequently probed with the 1.8-kb BamHI mouse LAR cDNA fragment described above, a 162-bp EcoRI fragment from mouse LAR cDNA#9 upstream of the deleted region (Schaapveld et al., 1995), a 1.1-kb XhoI fragment from the Neo cassette, and mouse cDNA probes (Schaapveld et al., 1995) spanning the phosphatase domains of the LAR-like RTPases PTP6 (pos. 2486–3815, Mizuno et al., 1993) and PTPs (pos. 4518–3’ UTR, Ogata et al., 1994), respectively. A rat 1.3-kb PdI glyceraldehyde-3-phosphate dehydrogenase (GAPDH) cDNA probe (Fort et al., 1985) was used to enable comparison of RNA loading. Hybridization signals on autoradiograms were analyzed on a GS-670 imaging densitometer (Bio-Rad). Hybridized probes were stripped for 10 min in boiling 0.1x SSC/0.1% SDS. Removal of probes was checked by exposing filters overnight between hybridizations.

For analysis of LAR expression during mammary gland postnatal development, the first inguinal glands of 3-4 wild-type mice were collected (pregnancy staged by detection of vaginal plug) and RNA isolated. For hybridization, oligonucleotide probes specific for WDNM1, WAP, β-casein, and α-lactalbumin were used.

Histological Analysis

Various tissues from 7-, 14-, and 21-weeks-old mice (male and females) were dissected, fixed in buffered formaldehyde, dehydrated, and embedded in paraffin. Sections of 6-μm thickness were stained with haematoxylin-eosin according to standard histological procedures. Brains were analyzed using parasagittal and coronal sections stained with cresyl violet.

RESULTS

Targeted Deletion of the LAR Phosphatase Domain Gene Sequences

To study LAR function in an organismal context we used gene targeting by homologous recombination in ES cells to produce LAR+/- mice. A replacement-type targeting vector was constructed in which a positive selection marker, a 1.1-kb neomycin phosphotransferase expression cassette (Neo), is flanked by 3.2 and 2.3-kb of endogenous LAR genomic segments (Schaapveld et al., 1995) which provide the necessary homology for targeted integration. Upon correct homologous recombination, a 4.5-kb genomic segment containing all exons encoding the phosphatase domains of LAR is replaced by the Neo cassette in the same transcriptional orientation (Fig. 1A). This event results in a shorter BamHI fragment (12.9 to 8.3 kb) and EcoRV fragment (20.5 to 12.0 kb) spanning the 5’ and 3’ regions of homology, respectively. This targeting construct was introduced into E14 ES cells by electroporation and 365 C418-resistant clones were screened for homologous recombination. Southern blot analysis using 5’- and 3’-diagnostic probes derived from genomic DNA flanking the targeting vector region revealed a targeting frequency of about 1 in 50 clones. Three cell lines
**LAR Tyrosine Phosphatase-deficient Mice**

DISPLAYING CORRECT HOMOLOGOUS RECOMBINATION AND A NORMAL KARYOTYPE WERE INJECTED INTO BLASTOCYSTS. CHIMERAIC MICE DERIVED FROM ALL THREE CELL LINES WERE MATED WITH C57BL/6 FEMALES AND SHOWN TO TRANSMIT THE ES CELL GENOME. O弗SPRING CARRYING THE DESIRED MUTATION WERE THEN SIBLING MATED AND USED TO PRODUCE HETEROZYGOUS AND HOMOZYGOUS MUTANT MICE IN A MIXED 129× C57BL/6 BACKGROUND.

To verify the presence of the correct replacement mutation in our lines, offspring born from F1 heterozygote crosses were genotyped by Southern blot (Fig. 1B) or PCR analysis of genomic DNA isolated from tail biopsies. The 5' - and 3'-flanking probes revealed the correct targeting of the LAR locus (Fig. 1B, panels A and B). A LAR cDNA probe encompassing both phosphatase domains (Schaapveld et al., 1995) failed to detect the wild-type 12.0-kb BamHI fragment in DNA isolated from homozygous mutant mice, as anticipated (Fig. 1B, panel C). Using the neomycin-resistance gene as a probe, only the 12.0-kb EcoRV fragment and no additional integrations of the targeting construct were detected (Fig. 1B, panel D).

The mutant LAR allele was identified in 145 heterozygous (LAR+/−, 49.7%) and 68 homozygous (LAR−/−, 23.3%) mice out of a total of 292 mice tested. Thus, the mutant allele segregated essentially according to Mendelian laws, indicating that the removal of the LAR PTPase domains is not lethal.

**The Mutant LAR Allele Produces a Truncated mRNA**

To investigate the consequences of LAR gene targeting at the RNA level, poly(A)+ RNA was isolated from several tissues and analyzed by Northern blot analysis (Fig. 2). Using the mouse LAR cDNA encompassing both LAR PTPase domains as a probe, no wild-type LAR mRNA was detected in LAR−/− mice (Fig. 2A). The faint signals present in the LAR−/− brain isolate are due to cross-hybridization to the highly homologous RPTPα PTPα (Schaapveld et al., 1995, see also below). Total absence of LAR mRNA containing the PTPase domains was confirmed by RT-PCR using...
mouse LAR-specific primers and poly(A)+ RNA isolated from various tissues (data not shown). In mRNA isolated from wild-type brain, an additional mRNA isoform of ~6.5 kb is seen along with the ubiquitously expressed messenger of ~8 kb.

The mutant LAR allele is expected to give rise to shorter transcripts that contain the sequences encoding the LAR extracellular region and ending at the poly(A) addition site present in the Neo cassette. Indeed both an EcoRI mouse LAR cDNA fragment located just upstream of the deleted region and the neomycin-resistance gene probe detect a ~5.5-kb mRNA (Figs. 2B and 2C). In brain a ~4-kb transcript is also found in LAR+/− and LAR−/− mice that likely encodes a shorter LAR isoform lacking extracellular region sequences (O’Grady et al., 1994; Zhang and Longo, 1995). The truncated transcript(s) in the LAR−/− mice, if translated at all, encode(s) a mutated LAR molecule that lacks PTPase activity.

**Histological Analysis of LAR Mutant Mice**

Mice lacking the LAR PTPase domains had normal weight, behaved normally and appeared healthy upon veterinary inspection. We then performed an extensive histological survey to look for possible consequences of the absence of functional LAR at the tissue and cellular level. A wide variety of tissues, including brain, kidney, adrenal, liver, lung, heart, stomach, colon, ileum, duodenum, testis, uterus, pancreas, muscle, spleen, thymus, and mammary gland were isolated from 6-, 14-, and 21-week-old male and female mice, sectioned, and stained with haematoxylin-eosin. In addition, serial parasagittal and coronal sections of brain were stained with cresyl violet. This analysis revealed no significant differences between LAR+/−, LAR+−/−, and LAR−/− mice (data not shown).

**Expression of LAR-like RPTPases**

The LAR-like RPTPases, PTPδ (Mizuno et al., 1993), and PTPα (Ogata et al., 1994; Wagner et al., 1994), are ~90% identical to LAR at the amino acid level for both PTPase domains (Schaapveld et al., 1995), exhibit similar in vitro PTPase activity, and all three interact with the LAR-interacting protein, LIP1, suggesting similar functions in various tissues (Pulido et al., 1995b). To determine whether PTPδ and/or PTPα could compensate for LAR function in the LAR−/− mice, we performed Northern blot analysis using mouse cDNA probes encompassing the cytoplasmic regions of PTPδ and PTPα (Schaapveld et al., 1995). Signal quantitation by densitometry revealed no significant difference in mRNA levels of PTPδ or PTPα in LAR−/− mice compared with LAR+/− and LAR+−/− mice (Figs. 2D and 2E), and the expression distribution of the tissue-specific alternative mRNA isoforms was consistent with data published elsewhere (Mizuno et al., 1993; Ogata et al., 1994; Wagner et al., 1994). This finding cannot rule out any redundancy at the enzymatic level and ultimately crosses between LAR−/−, PTPδ−/−, and PTPα−/− mice will be needed to reveal a potential overlap in function between these RPTPase subfamily members.

**Increased Neonatal Mortality for Pups from LAR−/− Females**

Unexpectedly upon interbreeding LAR−/− males and females normal-sized litters were obtained, but many of the pups died within 1–3 days after birth. To substantiate this finding, an extensive breeding program was performed in which four possible intercrosses were examined (Fig. 3). We observed an increased neonatal death rate for pups from LAR−/− mothers (>50%) compared to pups from LAR+/−.
FIG. 3. Increased neonatal mortality for pups of LAR<sup>-/-</sup> female mice. Upon breeding, LAR<sup>-/-</sup> females show normal fertility and give birth to normal-sized litters. However, >50% of the pups die within 1-3 days after birth compared to only <10% in the case of LAR<sup>+/+</sup> females. The ratio death/born (%) are indicated reflecting the lack of complete penetrance of the phenotype. Comparable results were found for second and third litters (data not shown). Diagram represents the sum of results with mice derived from the CA1 and BC2 ES cell clones.

At autopsy, pups born from LAR<sup>-/-</sup> females which died at Days 1-3 postpartum appeared smaller compared with pups of the same age born from wild-type mice. As indicated by the absence of a white colored belly, no milk was found in their stomachs. Because milk ingestion failed despite multiple attempts to suckle the mothers’ nipple, we attribute the neonatal death to a defect in the lactating capacity of the LAR<sup>-/-</sup> mothers rather than to a behavioral abnormality of neonates. To validate this observation, 1-day-old LAR<sup>-/-</sup> pups from LAR<sup>-/-</sup> parents without white bellies were swapped to lactating wild-type mothers. These pups survived demonstrating that their suckling capacity was normal. In contrast, 1-day-old healthy looking LAR<sup>+/+</sup> pups from wild-type parents were accepted by LAR<sup>-/-</sup> mothers and did suckle their nipples, but dehydrated and died within 5 days (data not shown).

To investigate a possible milk production defect in LAR<sup>-/-</sup> mothers in more detail, the quantity of the milk produced by these mice was analyzed. In contrast to lactating LAR<sup>+/+</sup>, LAR<sup>-/-</sup>, or LAR<sup>-/-</sup> mothers from which normal amounts of milk (20-50 µl) could be readily obtained already at postpartum, we never obtained more than 2-3 µl milk from LAR<sup>-/-</sup> mothers whose pups died within 1-3 days. Neither the injection of higher doses of oxytocin (2-5 IU) nor the intensive massaging of the mammary glands helped to increase milk production (data not shown), suggesting that the lactational defect in LAR<sup>-/-</sup> mice may be due to a general lack of milk protein synthesis or impaired milk secretion.

**Regulation of LAR Expression during Pregnancy**

To determine whether LAR has a role in mammary gland development and function, we examined LAR mRNA expression in mammary glands isolated from female mice at various stages during postnatal development. LAR expression is already present in mammary glands of virgin females as determined by RT-PCR (data not shown). Northern blot analysis of total RNA isolated from glands of wild-type females at various stages during pregnancy (P9-18) and at parturition (L1) revealed that LAR expression during pregnancy is developmentally regulated (Fig. 4). LAR expression is evident at day 9 of gestation, increases five-fold during mid-pregnancy and reaches maximum levels at Day 16. Since GAPDH expression might vary during pregnancy, as was found during lactation (Bohler et al., 1993), the variations in the amount of RNA loaded was also assessed by hybridizing the blot with a 28S rRNA cDNA probe. The obtained LAR expression profile is consistent with a role for LAR during mammary gland development at late pregnancy. The expression pattern of the LAR-like RPTPases was also in-
The regulation of LAR expression during postnatal development of wild-type mammary gland. Total RNA isolated from mouse mammary gland at various stages during pregnancy (P) and at parturition (L, lactating) was analyzed by Northern blotting. The blot was subsequently hybridized with cDNA probes for mouse LAR, PTPδ, PTPγ, rat GAPDH, and 28S RNA (28S). The numbers indicate the stage of gestation (in days) at which the mammary glands were dissected.

Investigated. PTPδ transcripts are undetectable, but PTPγ is expressed, although at very low levels, during mammary gland development (Fig. 4). Compared to LAR, a 20-fold longer exposure time was needed for PTPγ signals to become visible.

**Impaired Terminal Differentiation of Mammary Alveoli in Nonlactating LAR<sup>−/−</sup> Females**

To examine whether the lactational defect found in LAR<sup>−/−</sup> female mice could result from an impaired mammary gland development, we histologically analyzed mammary glands from virgin, late pregnant, postpartum, lactating, and involuting female mice. We termed LAR<sup>−/−</sup> females "nonlactating" if they consistently showed for two or three successive litters that their pups would die within 1-3 days after birth. LAR<sup>−/−</sup> females which were indistinguishable from wild-type mice regarding the percentage of surviving pups per litter were considered as "lactating" LAR<sup>−/−</sup> mice. We observed no significant difference in the number of ducts per unit volume of fat pad in glands of virgin LAR<sup>+/+</sup>, LAR<sup>−/−</sup>, and lactating LAR<sup>−/−</sup> females (data not shown). Extensive alveolar development was observed during lactation in LAR<sup>+/+</sup>, LAR<sup>−/−</sup>, and LAR<sup>−/−</sup> females which could lactate (Fig. 5B; and data not shown). The lumina were extended and contained secretion. In contrast, less extended alveoli with filled lumina were found in the exceptional case of a nonlactating LAR<sup>−/−</sup> female which pups survived until Day 7 postpartum (Fig. 5A). The alveolar development in LAR<sup>−/−</sup> females without the ability to lactate appears incomplete, and the epithelial cells in the alveoli do not have the secretory phenotype and apparently milk production and/or secretion coupled with the formation of an extended lumen was abrogated in nonlactating mice.

The development of mammary glands from nonlactating LAR<sup>−/−</sup> females up to late pregnancy (Days 18-20) parallels that of wild-type glands, as determined by whole mount analysis (data not shown). Thus, ductal outgrowth and

**FIG. 4** Regulation of LAR expression during postnatal development of wild-type mammary gland. Total RNA isolated from mouse mammary gland at various stages during pregnancy (P) and at parturition (L, lactating) was analyzed by Northern blotting. The blot was subsequently hybridized with cDNA probes for mouse LAR, PTPδ, PTPγ, rat GAPDH, and 28S RNA (28S). The numbers indicate the stage of gestation (in days) at which the mammary glands were dissected.

**FIG. 5** Histological analysis of mammary tissue from postpartum nonlactating LAR<sup>−/−</sup> (A) and LAR<sup>+/−</sup> (B). The former litters of the LAR<sup>−/−</sup> female died within the first 3 days after birth, but this time the litter was nursed very poorly and the last pups died at Day 7. For the ~50% of females that show the nonlactating phenotype, this was the only exception for which we could monitor a lactational state. The fat pad of the LAR<sup>−/−</sup> mice is not completely filled and the alveoli are overall smaller than those in hemizygous and wild-type mice (not shown). The epithelial cells in the LAR<sup>−/−</sup> mice do not have a secretory appearance as witnessed by their cuboidal appearance and flattened apical side (arrow in A). In contrast, milk is visible in the hemizygous mice, both as proteinaceous luminal content and as intracellular secretory products (arrow in B). Bar, 200 μm.
branching is not overtly impaired. The formation of the lobuloalveolar structures was examined in more detail by histological analysis using haematoxylin-eosin (Figs. 6A and 6B) or oil-red O staining (data not shown) of mammary glands at late pregnancy. Only minor differences in lumen size and alveoli cluster formation were observed between wild-type and nonlactating LAR−/− glands. However, clear differences in the morphology of secretory epithelial cells and luminal contents were evident. While intraluminal secretions were visible in glands from wild-type mice (Fig. 6A), the LAR−/− epithelial cells contained large secretory vesicles and lipid droplets indicating an impaired secretion (Fig. 6B).

At parturition, enlarged alveoli with extended lumina were clearly visible in wild-type glands (Fig. 6C). In contrast, the number and size of alveoli in nonlactating LAR−/− were reduced, and local interstitial fibrosis and congestion of secretion could be observed (Fig. 6D). Whole mount analysis of mammary glands isolated from nonlactating LAR−/− mothers at parturition showed an advanced state of involution (Figs. 7C–F). Although there is unavoidable variation in the moment of tissue collection, the involution state is at least comparable with that of glands isolated from wild-type mice 2 days after removal of their pups (Fig. 7A) and in some cases already resembles complete involution as observed for wild-type mice at 2 weeks following weaning of the pups which had been nursed for three weeks (Fig. 7B).

To test whether altered expression of milk protein genes...
In partition (A), and in a similar manner, data from 2 weeks after means of rape were analyzed. In Fig. 3, are shown the 550 LAR-F-2 models of partition (C). In comparison, a numerically large group of data were analyzed. In partition (B), a model of partition (D) was observed. The results were analyzed with partition (E). Rapid evolution partition in LAR-F-2 remains whole mouse meaning glands were dissected. Each method with carriage.
could explain the failure of nonlactating LAR−/− females to
switch to the lactational state. RNA was isolated and
probed for WDNM1, WAP, β-casein, and α-lactalbumin
transcript levels by Northern blot analysis. No differences
were apparent between nonlactating LAR−/− and wild-type
mice (data not shown). Also, immunohistochemical
staining for WAP expression did not point to altered milk
protein synthesis (data not shown). Moreover, the protein
and triglycerides content of the few microliters that inci-
dentally could be obtained from nonlactating mice is com-
parable to that of wild-type and lactating LAR−/− mice (data
not shown).

Pups did recognize, attach, and bite the nipple of their
mothers, but in about half of the LAR−/− females alveolar
development which is characteristic for late pregnancy was
not attained and milk secretion was not initiated. Moreover,
the transition to involution and apoptosis of alveolar epithe-
lum occurred more readily in these mice, even before milk
secretion started. These findings suggest an impaired de-
velopment of mammary alveoli in LAR−/− females at late preg-
nancy: the failure of the alveoli to acquire secretory activity
is paralleled by a rapid involution at parturition.

DISCUSSION

To address the biological role of LAR PTPase activity in
growth and development we generated mice lacking expres-
sion of the LAR PTPase cytoplasmic region. The LAR−/−
mice are viable, grow, and behave normally. Furthermore,
histological analysis of a wide variety of tissues at different
ages did not reveal structural abnormalities, consistent with
a previous report on the generation of LAR-deficient mice
using a gene trap-based method capturing the N-terminal
signal sequence and generating a β-galactosidase fusion pro-
tein (Skarnes et al., 1995). However, our current detailed
analysis reveals that LAR has a function during mammary
gland differentiation. We observed an increased neonatal
mortality for pups from LAR−/− mothers, independent of
the litter size and the genotype of the male or the offspring.
The pups suckled the nipples of their mother, but failed to
ingest milk, became dehydrated and died. Swapping experi-
ments demonstrated that the increased neonatal death was
due to a lactational defect of the LAR−/− mothers rather
than to an abnormal behavior of neonatal pups. Due to ge-
etic background heterogeneity this phenotype displayed a
50% penetrance in the F2 hybrid 129×C57BL/6 mice that
were used in this study, which might explain why it was
not detected by Skarnes et al. (1995). Interestingly, also in
Drosophila the inactivation of CAM-like RPTPases resulted
in phenotypes with a limited penetrance (Desai et al., 1996;
Krueger et al., 1996). To map potential modifier loci, it will
be necessary to cross the LAR allele into different genetic
backgrounds. Regarding ductal outgrowth and branching in
wild-type mammary glands, we did not observe significant
background differences between mouse strain 129, C57BL/6,
the F2 hybrid 129×C57BL/6, and F4 mice on C57BL/6
background, although the ductal system at the virgin state
in 129 mice is less developed.

Development of the mammary gland progresses gradually
during puberty and pregnancy and acquires full function
during lactation (for review see Daniel and Silberstein,
1987). In several natural mouse mutants, as well as transgen-
ic and knock-out mice this process is affected (Gal-
lanah et al., 1996; Jhappan et al., 1992, 1993; Kordon et
al., 1995; Li et al., 1994, 1996a,b; Robinson et al., 1996; Slicinski
et al., 1995). For example, in transgenic mice expressing
TGFα under the control of the mouse WAP gene promoter
mammary development and differentiation proceeds during
pregnancy, but the secretory cells do not establish and/or
maintain a functional state characterized by milk secretion
(Robinson et al., 1996; Sandgren et al., 1995). A similar
phenotype was observed in mice which contain a nonfunc-
tional mCSF1 (Pollard and Hennighausen, 1994) or inhibit
β gene (Vassalli et al., 1994). The high amounts of intracel-
lar fat droplets at late pregnancy is also seen in "milchlos"-
transgenic mice (Robinson et al., 1995). In nonlactating
LAR−/− mice a normal epithelial cell proliferation up to late
pregnancy is observed, but histological sections of glands
at late pregnancy showed a more intracellular storage of
secretion products in comparison with the intraluminal se-
cretion in wild-type glands. At parturition, mammary
glands showed a regression of alveolar structures as is seen
normally at a progressed stage of involution following wean-
ing of the pups. Taken together, these observations suggest
that LAR function is evoked relatively late in mammary
gland development and that most likely the LAR−/− pheno-
type is a combination of a loss of alveolar cells around partu-
rition and the inability of the remaining alveoli to undergo
secretory differentiation.

Complex molecular interactions are involved in the regu-
lation of lactation (Rillema, 1994). The initiation of lacta-
tion following parturition involves many endocrine changes,
of which the reduced influence of sex steroid hor-
mones appears to be the most important (for review see
Daniel and Silberstein, 1987; Rillema, 1994). Hormonal in-
fluences at the level of some milk protein gene promoters
are mediated by the mammary gland-specific transcription
factor MGF/Stat5 (Wakao et al., 1994). Regulation of milk
protein expression via regulation of Stat5 activity also re-
quires the basement membrane (Sypson et al., 1994; Tal-
houk et al., 1992), which provides signals via interaction
with epithelial cells through cell surface receptors (Streuli
et al., 1995). Mice lacking Stat5a show reduced mammary
lobuloalveolar outgrowth and fail to lactate due to an im-
paired terminal differentiation (Liu et al., 1997). The pheno-
type becomes apparent during midpregnancy and is re-
flected by a marked reduction in WAP transcript levels.
LAR deficient mice show signs of abnormal mammary
gland development at a later stage, shortly before parturi-
tion, and no reduction in WAP levels could be observed. It
remains to be investigated whether or not LAR and STAT5a
signalling pathways are intertwined at some stage of mam-
mmary gland development.
LAR is expressed in brain and therefore could perhaps play a role in the regulation of the appropriate hormone balance needed for proper mammary gland development and function. However, at the moment it is not known if LAR is specifically localized to regions in the brain that are involved in the hormonal regulation of lactation and further studies will be required to address this issue. LAR is predominantly expressed in epithelial cells and localized at regions of association of these cells and the basement membrane (Streuli et al., 1992). Consistent with this is the recent finding of colocalization of LAR and its interacting protein LIP1 at focal adhesions and its proposed role in disassembly of focal adhesions (Serra-Pages et al., 1995). In view of the developmental regulation of LAR expression in the mammary gland during pregnancy and the phenotypic consequences of the ablation of LAR PTPase activity, these data point to an important role for LAR in cell–matrix interactions that are crucial for mammary gland development and function.

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