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Gene expression profiling of mouse mammary gland: transition from pregnancy to lactation*

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Gene expression analysis comparing pregnant and lactating mouse mammary gland was performed with Mouse Panorama Apoptosis cDNA macroarray containing 243 genes. Transition from pregnancy to lactation led to repression of 15 and induction of 24 genes, while 12 genes were found to change their expression more then twice. Expression of 16 genes was shown, not described so far in the mammary gland of mouse. Simultaneous analysis of 243 genes made it possible to begin arranging them into the gene regulation network of the mammary gland.

KEY WORDS: mouse / mammary gland / gene expression / cDNA macroarray

Unlike most mammalian organs, which develop primarily during embryonic and foetal stages, development of the mammary gland occurs also in the postpubertal period. There are six defined stages involved in development of the mammary gland including: foetal, prepubertal, pubertal, pregnancy, lactation and involution. These stages can be characterized further as a series of highly orchestrated transitions, or switches, in which critical developmental decisions are made concerning cell differentiation, pattern formation and cell function. Each of these stages involves a complex interaction of hormones, growth factors, and signal transduction pathways, leading to expression of

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developmentally regulated genes [Cunha and Hom 1996, Medina 1996, Visvader and Lindeman 2003].

Near midpregnancy, the alveolar epithelium acquires the capacity to produce milk proteins (the stage I transition of lactogenesis) but secretory function is inhibited. At parturition, inhibition of secretory function is released and these cells begin to secrete large volumes of milk (the stage II transition of lactogenesis). Milk protein gene expression has been investigated by numerous authors [Marti *et al*. 1999, Rosen *et al.* 1999, Rijnkels 2002]. There is, however, no comprehensive analysis of other genes expression during transition from pregnancy to lactation.

Microarray analysis has had a major impact on our understanding of the transcriptional basis of complex biological systems. The few microarray studies of normal mouse mammary gland have either focused on early stages in the developmental cycle [Master *et al.* 2002, Visvader and Lindeman 2003] or have used the mammary data to illustrate methods of data analysis [Lemkin *et al*. 2000, Phang *et al.* 2003]. One of our long-term goals is to elucidate genes and pathways associated with lactation. To begin, we compared gene expression profiles of lactating mouse mammary tissue *versus* pregnant on Panorama macroarray. In the present study we applied a macroarray approach to study the transcriptional expression of 243 mouse genes in a mammary gland during transition from pregnancy to lactation.

Material and methods

Animals and tissues

Mammary glands of MIIZ mice on day 16 of pregnancy and day 1 of lactation were used. Mammary gland samples were excised immediately after cervical dislocation. Mammary tissues were cleared from most adjacent muscles, fat and connective tissues, frozen at -25^{o}C and stored at -75^{o}C until use.

RNA extraction

Total RNA from frozen tissues was extracted with TRI Reagent (SIGMA-ALDRICH, Inc.) according to the manufacturer protocol. Briefly, up to 100 mg of frozen tissue was homogenized in 1 ml of TRI Reagent. Next, 0.2 ml of chloroform was added, shacked vigorously and incubated 15 min. at room temperature. The mixture obtained was centrifuged at 12 000 g for 15 min. at 4°C. Aqueous phase was collected, and transferred into fresh tube. Isopropanol (0.5 ml per ml of TRI Reagent) was added and the mixture was incubated for 10 min. at room temperature. It was then precipitated and RNA pellet washed with 75% ethanol. In order to quantify the amount of total RNA extracted, the optical density was determined with DU-68 Spectrophotometer (BECKMAN, Inc.). RNA integrity was electrophoretically verified on agarose gel stained with 0.5 μg/ml ethidium bromide.

cDNA macroarray

Synthesis of labelled cDNA. For cDNA synthesis equal amounts of RNA extracted from five 16-days pregnant or 1-day lactating mice were pooled. To confirm the validity of the assay, cDNA synthesis was performed in duplicate. The cDNA labelling reactions were performed in two steps according to the manufacturer's protocol. In the first step Mouse Apoptosis Labelling Primers were annealed to RNA template. Then, the reverse transcriptase was added to initiate cDNA synthesis reaction (Panorama Mouse Apoptosis cDNA Labelling and Hybridisation Kit). To 2 µg of total RNA added were 4 µl Mouse Apoptosis cDNA labelling primers, and water to 14.5 µl final volume. RNA was denatured at 90°C 2 min. and Mouse Apoptosis cDNA primers were annealed to RNA template for 20 min. at 42°C. After annealing, reverse transcriptase buffer, dATP, dGTP and dTTP to final concentration of 333 mM, 20 U ribonuclease inhibitor, 50 U reverse transcriptase, and 40 µCi[α-^{32}P]dCTP were added. Reaction mixture was incubated at 42°C for 3 h. The unincorporated radiolabelled nucleotide was removed from labelled cDNA by purification over Sephadex G-25 gel-filtration column according to manufacturer instructions.

Hybridization and analysis of array. Nylon array (Panorama Mouse Apoptosis Gene Arrays, Sigma-Genosys, The Woodlands, TX) was rinsed in 50 ml 2×SSPE at room temperature for 5 min, and pre-hybridized in 5 ml of hybridization solution for 1 h at 65°C. Labelled probes were denatured at 90°C for 10 min and added to 3 ml of hybridization solution. Probes were hybridized to a nylon array at 65°C overnight. After hybridization, the nylon membranes were washed three times for 2-3 min at room temperature with 50 ml 0.5×SSPE + 1% sodium dodecyl sulphate (SDS), and twice with 50 ml 0.5×SSPE + 1% SDS at 65°C for 20 min. On the next step, membranes were washed once with 50 ml 0.1×SSPE + 1% SDS at 65°C for 20 min., and then exposed to Phosphorscreen (KODAK, Japan) for 24 hours. The screens were scanned by Bio-Rad FX Scanner at a maximum resolution of 25 µm. Results from three independent hybridizations were obtained for each probe. Images were analysed by Quantity One (BioRad) software. Each image was overlaid with grids so that signal intensities of individual spots could be assessed. Local background for each membrane was calculated on the basis of 10 positions with no DNA spotted area. Expression levels of individual genes are represented in arbitrary units after subtracting background. Intensity-based global normalization was then performed.

Results and discussion

Macroarrayas provide a powerful tool for analysing complex biological systems because they can extract patterns of gene expression from a significant proportion of the total genomic content of an organism. In this study we simultaneously analysed 243 transcripts to determine basic expression patterns in adult mammary gland during the transition from pregnancy to lactation. Autoradiographs of arrays hybridized with [^{32}P-cDNA] from 16 day of pregnancy and 1 day of lactation are presented in Photo

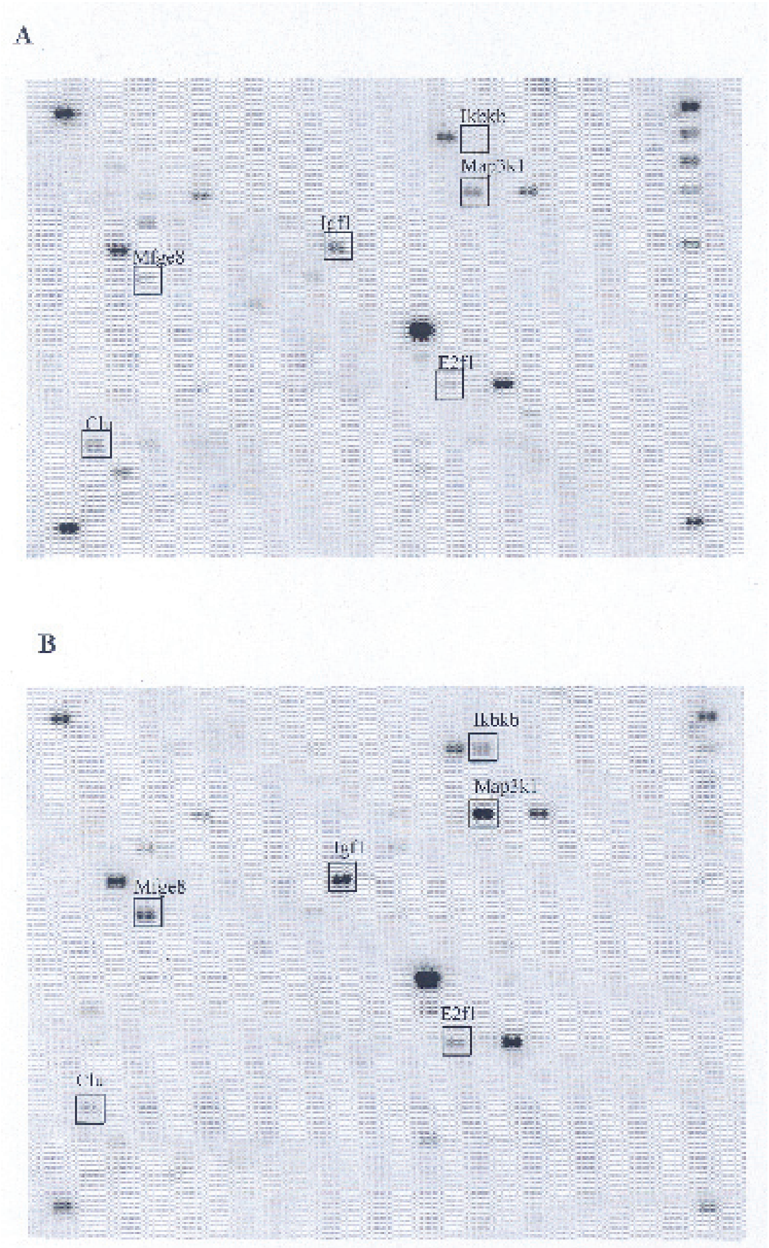
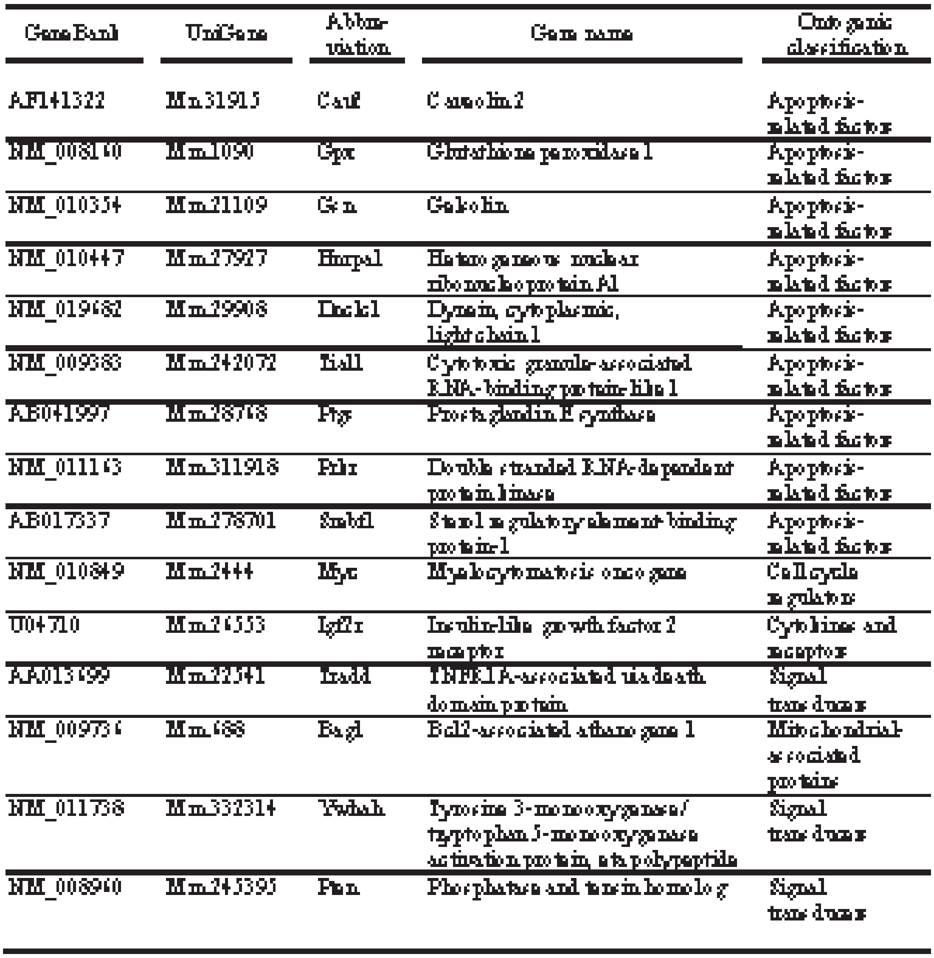


Photo 1. DNA array hybridization of 16 day pregnant (A) and 1 day lactating mice (B). Hybridizations were performed using radioactive ^{32}P-labelled probes prepared from pregnant and lactating mice mammary gland of five animals each. Selected genes changing expression during transition from pregnancy to lactation are indicated.

1-A and 1-B. Gene expression signals were quantified by Quantity One software (Bio-Rad). Analysis of these data show that during transition from pregnancy to lactation 15 genes were repressed (Tab. 1), 24 genes induced (Tab. 2), and expression of 12 genes changed more than twice (Tab. 3). Macroarray analysis confirmed the previously described expression of several genes in the mammary gland: IGF1 and IGF2 receptor [Boutinaud *et al*. 2004], PTEN [Moorehead *et al*. 2003], and transforming growth factor beta [Ewan *et al.* 2002].

Moreover, the analysis found 16 genes expression of which has not yet been de-

Table 1. Genes repressed in lactation

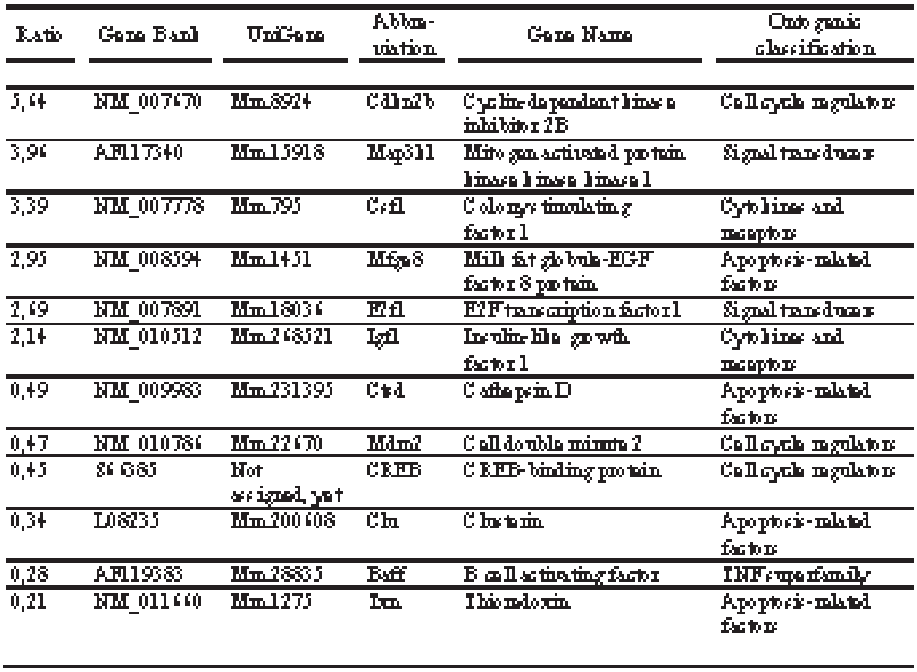


GeneBank	UniGene	Abbreviation	Gene name	Ontogenic classification
AF141322	Mm.31915	Cav2	Caveolin 2	Apoptosis-related factor
NM_008160	Mm.1090	Gpx	Glutathione peroxidase 1	Apoptosis-related factor
NM_010354	Mm.21109	Gsn	Gelsolin	Apoptosis-related factor
NM_010447	Mm.27927	Hnrpa1	Heterogeneous nuclear ribonucleoprotein A1	Apoptosis-related factor
NM_019682	Mm.29908	Dncl1	Dynein, cytoplasmic, light chain 1	Apoptosis-related factor
NM_009383	Mm.242072	Tial1	Cytotoxic granule-associated RNA-binding protein-like 1	Apoptosis-related factor
AB041997	Mm.28768	Ptgs	Prostaglandin E synthase	Apoptosis-related factor
NM_011163	Mm.311918	Prkr	Double stranded RNA-dependent protein kinase	Apoptosis-related factor
AB017337	Mm.278701	Srebf1	Sterol regulatory element binding protein 1	Apoptosis-related factor
NM_010849	Mm.2444	Myc	Myelocytomatosis oncogene	Cell cycle regulators
U04710	Mm.26553	Igf2r	Insulin-like growth factor 2 receptor	Cytokines and receptors
AA013699	Mm.22541	Tradd	TNFR1A-associated via death domain protein	Signal transducers
NM_009736	Mm.688	Bag1	Bcl2-associated athanogene 1	Mitochondrial-associated proteins
NM_011738	Mm.332314	Ywhah	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eta polypeptide	Signal transducers
NM_008960	Mm.245395	Pten	Phosphatase and tensin homolog	Signal transducers

Table 1. Genes induced in lactation

Gene Bank	UniGene	Abbreviation	Gene Name	Oncogenic classification
NM_007702	Mm.449	Cidea	DNA fragmentation factor, alpha subunit-like effector A	Apoptosis-related factors
[illegible]	[illegible]	[illegible]	[illegible]	Apoptosis-related factors
NM_008771	[illegible]	P2rx1	Purinergic receptor P2X, ligand-gated ion channel 1	Apoptosis-related factors
NM_008798	[illegible]	Pdcd1	Programmed cell death 1	Apoptosis-related factors
NM_008799	[illegible]	Pdcd2	Programmed cell death 2	Apoptosis-related factors
[illegible]	[illegible]	Casp1	Caspase 1	Caspases and their regulators
NM_009689	Mm.8552	BIRC5	BIRC5 Baculoviral IAP repeat-containing gene	Caspases and their regulators
NM_009687	[illegible]	Apex1	Apurinic/apyrimidinic endonuclease	Cell cycle regulators
[illegible]	[illegible]	Sp1	Transcription factor Sp1	Cell cycle regulators
[illegible]	Mm.4189	Ccna1	Cyclin A1	Cell cycle regulators
[illegible]	[illegible]	[illegible]	[illegible]	Cytokines and receptors
NM_008086	Mm.22701	Gas1	Growth arrest specific 1	Cytokines and receptors
NM_010557	[illegible]	Il4ra	Interleukin 4 receptor, alpha	Cytokines and receptors
NM_008348	[illegible]	Il10ra	Interleukin 10 receptor, alpha	Cytokines and receptors
NM_007779	Mm.22574	Csf1r	Colony stimulating factor 1 receptor	Cytokines and receptors
NM_011577	Mm.248380	Tgfb1	Transforming growth factor, beta 1	Cytokines and receptors
[illegible]	Mm.2904	Tyro3	TYRO3 protein tyrosine kinase 3	Cytokines and receptors
NM_008580	[illegible]	Map3k5	Mitogen activated protein kinase kinase kinase 5	Signal transduction
NM_010943	Mm.1059	Nsmaf	Neutral sphingomyelinase activation associated factor	Signal transduction
AF088910	[illegible]	Ikbkb	Inhibitor of kappaB kinase beta	Signal transduction
NM_008655	[illegible]	Gadd45b	Growth arrest and DNA-damage-inducible 45 beta	Signal transduction
S56660	Not assigned yet	Rarb	Retinoic acid nuclear receptor isoform beta 2	Signal transduction
NM_011529	[illegible]	Tank	TRAF family member-associated NF-kappa B activator	Signal transduction
NM_009352	[illegible]	Terf1	Telomeric repeat binding factor 1	Telomerase-related proteins

Table 3. Changes of gene transcription activity during transition from pregnancy to lactation



Ratio	Gene Bank	UniGene	Abbreviation	Gene Name	Ontogenic classification
5,64	NM_007670	Mm.8924	Cdkn2b	Cyclin-dependent kinase inhibitor 2B	Cell cycle regulators
3,96	AF117340	Mm.15918	Map3k1	Mitogen activated protein kinase kinase kinase 1	Signal transducers
3,39	NM_007778	Mm.795	Csf1	Colony stimulating factor 1	Cytokines and receptors
2,95	NM_008594	Mm.1451	Mfge8	Milk fat globule-EGF factor 8 protein	Apoptosis-related factors
2,69	NM_007891	Mm.18036	E2f1	E2F transcription factor 1	Signal transducers
2,14	NM_010512	Mm.268521	Igf1	Insulin-like growth factor 1	Cytokines and receptors
0,49	NM_009983	Mm.231395	Ctsd	Cathepsin D	Apoptosis-related factors
0,47	NM_010786	Mm.22670	Mdm2	Cell double minute 2	Cell cycle regulators
0,45	S66385	Not assigned, yet	CREB	CREB-binding protein	Cell cycle regulators
0,34	L08235	Mm.200608	Clu	Clusterin	Apoptosis-related factors
0,28	AF119383	Mm.28835	Baff	B cell activating factor	TNF superfamily
0,21	NM_011660	Mm.1275	Txn	Thioredoxin	Apoptosis-related factors

scribed in the mammary gland:

- heterogeneous nuclear riboprotein A1;
- light chain 1 of dynein;
- Tial1, cytototoxic granule-associated RNA-binding protein 1;
- double stranded RNA-dependent protein kinase;
- TNFR1a-associated via death domain protein;
- Bcl2-associated athanogene 1;
- ε chain of tyrosine3-monooxygenase/tryptofan5-monooxygenase activation protein;
- cell deadh-inducing DNA fragmentation factor, alpha subunit;
- programmed cell death 1;
- programmed cell death 2;
- caspase 2;
- baculovirus IAP repeat containing protein;
- apurinic/apyrimidining nuclease;
- interleukin Il4 receptor alpha;
- TYRO3 protein kinase;
- neutral sphyngomyelinase activation associated factor.

Probes present on the Panorama Array cover eight ontologic categories as defined by the Gene Ontology Consortium http://www.geneontology.org [Khatri *et al.* 2002] – Table 4. As it was expected, the biggest category (66 genes) is apoptosis-related factors. The 29 genes (44%) of this group were found to be expressed in the mammary gland at pregnancy and (or) lactation. More than half of them (16 from 29) undergo qualitative or quantitative expression changes during transition from pregnancy to lactation. The second big ontologic category is cell cycle regulators (52 genes). In the mammary gland expressed were 32% of genes of these group. Transition to lactation was associated with induction of 7 genes from the cytokines and receptors group, and 6 genes from signal transduction group. Probes on the Panorama Array representing genes belonging to remaining four ontogenic classes: mitochondrial associated, caspases and regulators, telomerase-related and tumor necrosis factors (41 genes) were rarely expressed in the mammary gland during pregnancy and (or) lactation (9 genes).

Several genes expressed in the mammary gland can be organized in a putative network (Fig. 1). During transition from pregnancy to lactation we showed induction of TGF-β gene expression (Tab. 2). TGF-β rapidly inhibits c-*myc* expression in a wide variety of cell types [Yue and Mulder 2001], and in the mammary gland too (Tab. 1). TGF-β also downregulates expression of cyclin A and E2F genes in the mammary gland cell line NMuMG [Xie *et al*. 2003], and phosphatase and tensin homolog (PTEN) [Li and Sun 1997, Clarkson *et al.* 2004]. PTEN is a major tumor suppressor that acts by hydrolyzing membrane phosphatidylinositol (PtdIns)-3-phosphates. IGF2 and thioredoxin also regulate expression of PTEN. IGF2 injection into mouse mammary gland significantly increased PTEN expression [Moorehead *et al*. 2003]. Expression of PTEN is downregulated by thioredoxin. Thioredoxin binds in a redox-dependent manner to PTEN to inhibit its PtdIns-3-phosphatase activity [Meuillet *et al*. 2004]

Table 4. Ontogenic classification of genes expressed in the mouse mammary gland

Category	Number of genes in array	Percent of genes expressed in the mammary gland	Number of genes			
			repressed	induced	changing expression	not changing expression
Apoptosis-related factors	66	44	9	5	2	11
Cell cycle regulators	28	32	1	3	3	3
Cytokines and receptors	52	32	1	7	2	7
Signal transducers	43	35	2	6	2	5
Mitochondrial-associated proteins	14	35	1	0	0	1
Caspases and their regulators	21	10	2	0	0	0
Telomerase-related proteins	3	75	1	0	1	0
TNF superfamily	3	100	0	0	1	2

Downregulation of *c-myc* expression can be a cause of induction of caveolin 2 gene during lactation (Tab. 2). It was previously reported that c-myc down-regulate

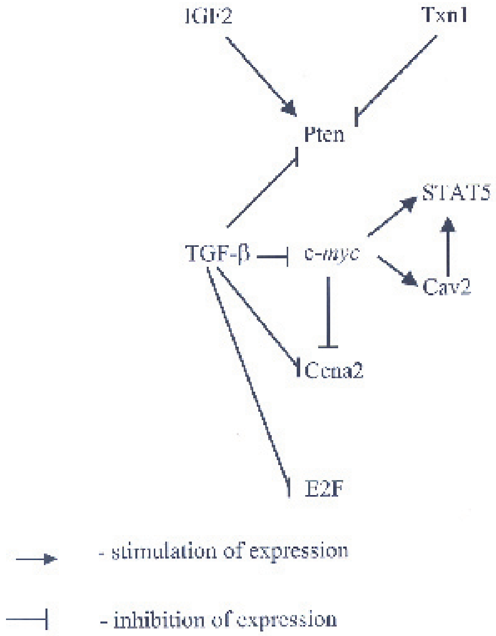


Fig 1. Hypothetical gene network of genes expressed in the mouse mammary gland.

expression of caveolin 1 and activates STAT5 [Blakely *et al*. 2005], E2F1 and cyclin A2 gene expression [Liao *et al.* 2000]. Caveolins are principal structural proteins of caveolae, sphingolipid and cholesterol-rich invaginations of the plasma membrane involved in vesicular trafficking and signal transduction. During caveolae-dependent signalling, caveolin acts as a scaffold protein to sequester and organize multi-molecular signalling complexes involved in diverse cellular activities. Park *et al*. [2001] showed that caveolin-1 expression is significantly downregulated during late pregnancy and lactation. In the presence of lactogenic hormones, recombinant expression of caveolin-1 in HC11 cells dramatically suppresses the induction of the promoter activity and the synthesis of β-casein. Cav-1 null mice show accelerated development of the lobuloalveolar compartment, premature milk production, and hyperphosphorilation of STAT5a at its Jak-2 phosphorylation site (pY694). In addition, the Ras-p42/44 MAPK cascade is hyper-activated [Park *et al*. 2002].

Macroarray analysis of mice mammary gland during transition from pregnancy to lactation allowed finding expression of several new genes and making of genetic network. Future research should more precisely estimate expression profile of genes which expression was found in the mammary gland. Growing number of gene expression profiling should make possible expand the gene regulatory network in the mammary gland.

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Profilowanie ekspresji genów w gruczole mlekowym myszy podczas przejścia od ciąży do laktacji

Streszczenie

Porównano ekspresję 243 genów w gruczole mlekowym myszy stosując makromacierz Mouse Panorama Apoptosis. Stwierdzono, że podczas przejścia od ciąży do laktacji następuje indukcja 24 genów, represja 16 i ponad dwukrotna zmiana ekspresji 12 genów. Analiza pozwoliła znaleźć 16 nowych genów, których ekspresja zachodzi w gruczole mlekowym myszy. Równoczesna analiza ekspresji 243 genów umożliwiła rozpoczęcie budowania sieci regulacji genów w gruczole mlekowym.