INTRODUCTION

Foetal development in the mouse mammary gland can first be detected at embryonic day 10-11 (E10-11) as a line of epithelial thickening between the limb buds on both sides of the animal. The underlying fibroblastic mesenchyme then induces the epithelium to thicken and invaginate (E12-E14; Kratochwil, 1969; Sakakura et al., 1976; Sakakura, 1991). By E17-E18, the mammary epithelium has branched into a deeper adipocytic mesenchyme that (after birth) is referred to as the stromal fat pad. Three distinct periods of postnatal mammary gland development are driven by combinations of systemic hormones including oestrogen, progesterone and prolactin (Daniel and Silberstein, 1987). Ductal growth, which is dependent on the presence of oestrogen (Haslam, 1987; Lubahn et al., 1993; Korach, 1994), occurs from 6 to 8 weeks of age when epithelial 'end buds' ramify from the nipple throughout the fatty mesenchyme. Pregnancy initiates the second phase of development in which lobular-alveolar structures develop from the existing ductal system in a process that is driven by pregnancy-induced hormones and oestrogen (Nandi, 1958). The lobular system grows and differentiates to form alveoli in which milk protein synthesis takes place during lactation. Following weaning of the young, the mammary gland undergoes extensive remodelling, leading to the selective loss of the alveolar structures, in a process involving large scale apoptosis (Strange et al., 1992).

Although the major systemic hormones that drive mammary development have been characterised and the importance of epithelial-mesenchymal interactions has been demonstrated (Nandi, 1958; Sakakura et al., 1991; Cunha et al., 1992), the molecular mechanisms by which these processes function at the local level are poorly understood. Molecules that have been implicated include growth factors such as members of the EGF, Wnt, FGF, TGFβ, tachykinin families (Snedeker et al., 1991; Gavin et al., 1992; Büehler et al., 1993; Coleman and Daniel, 1990; Daniel and Robinson, 1992; Coleman-Krnacik and Rosen, 1994; Weber-Hall et al., 1994; Weil et al., 1995) as well as extracellular matrix components (Jones et al., 1993; Thesleff et al., 1995a,b). Recent data from null mutant mice have also shown that the High Mobility Group (HMG)-box transcription factor, Lymphoid Enhancer Factor 1 (LEF-1) and cyclin D1 are necessary for foetal and pregnancy stages of mammary development respectively (Van Genderen et al., 1996).
taken. Ovariectomy was performed on 6-week old animals 2 weeks
epithelial contamination, only tissue distal to the lymph node was
not extended far from the nipple (data not shown). To ensure no
from their mothers (day 0). Fat pad mRNA was prepared from glands
Days involution were measured from the day the pups were removed
embryonic day (E), where E0.5 is the morning a plug was observed.
The age of embryos are stated as
were between 6 and 8 weeks of age. Pregnancies were measured from
the morning a vaginal plug was observed (day 0.5 post coitus (p.c.)),
performed as described by Davidson et al. (1988).

**MATERIALS AND METHODS**

**Animals and tissues**

In all experiments, the fourth abdominal mammary gland was taken
from female Parks mice (MRC; outbred). Following lymph node
removal, the tissue was snap frozen in liquid nitrogen and stored at
−80°C until use. At least 6 mice (3 each for 17.5 day pregnant and
lactating) were used per experimental point. Mice used for mating
were between 6 and 8 weeks of age. Pregnancies were measured from
the morning a vaginal plug was observed (day 0.5 post coitus (p.c.)),
following overnight matings. The age of embryos are stated as
embryonic day (E), where E0.5 is the morning a plug was observed.
Days lactation were measured from the day pups were born (day 0). Days
involution were measured from the day the pups were removed
from their mothers (day 0). Fat pad mRNA was prepared from glands
taken from 5-week old animals at which time epithelial growth had
not extended far from the nipple (data not shown). To ensure no
epithelial contamination, only tissue distal to the lymph node was
taken. Ovariectomy was performed on 6-week old animals 2 weeks
prior to killing and gland removal. Unless otherwise stated, poly(A)+
mRNA was prepared from glands of 8-week old virgin mice that had
been ovariectomised at 6 weeks of age. Visual confirmation of the
ovariectomy was made at the time of gland removal. Embryos for the
Bmp in situ hybridisation were from C57 mice.

**RNA isolation**

Total RNA was isolated by homogenisation of tissues in a guani-
dinium isothiocyanate solution followed by extraction with acidified
phenol and ethanol precipitation (van de Vijver et al., 1989). Poly(A)+
RNA was isolated from total RNA samples using the PolyA+ Tract
Kit (Promega) according to the manufacturer’s protocol. Total RNA
from cultured cells was isolated according to the method of Boehm
(Boehm et al., 1988).

**Northern analysis**

Poly(A)+ RNA (0.5 μg or 2 μg) or total RNA (12 μg) was fraction-
ated in 1% agarose gels as previously described (Weber-Hall et al.,
1994), transferred to ZetaProbe membrane (Biorad), and hybridised
with specific cDNA probes. Random oligonucleotide DNA probes
were generated as previously described (Ravidin, 1993) while
[32P]UTP-labelled RNA probes were synthesized as described by
Melton et al. (1984). Control rat GAPDH (pRGAPDH-13) probes
were as described previously (Weber-Hall et al., 1994), the 36B4
cDNA was donated by P. Darbre (Reading UK), the β-casein cDNA
was donated by J. Rosen (Houston, TX) and the β2 cDNA was
described by Skilton et al. (1989; Md2 fragment). Murine Bmp-2 and
Bmp-4 cDNA clones were kindly donated by Dr Mike Jones (Jones
et al., 1991). Msx-1, Msx-2 and human Msx2 probes were provided
by P. Sharpe (Hodgkinson et al., 1993; Jowett et al., 1993). DNA
probes were hybridised as described previously (Weber-Hall et al.,
1994), while for RNA probes, membranes were hybridised under
more stringent conditions (60°C formamide, 5x SSC, 5x Denhardts
solution, 100 μg/ml ss salmon sperm DNA at 65°C) and were washed
in 0.1x SSC, 0.1% SDS at 65°C.

**Cell culture**

MCF-7 cells (McGrath subline) were maintained in DMEM minus
phenol red (Gibco BRL), 5% foetal calf serum, 6 ng/ml insulin, 10-8
M oestradiol, penicillin/streptomycin and passaged weekly. Prior to
analysis, cells were plated for 24 hours in phenol red-free DMEM,
5% charcoal dextran stripped foetal calf serum (Darbre et al.,
1983), 6 ng/ml insulin and antibiotics, media was subsequently replaced
with or without the components described.

**In situ hybridisation**

For the postnatal in situ hybridisation, 7 μm frozen sections of fourth
abdominal mammary gland were fixed for 5 minutes in 4% paraformaldehyde in PBS, then hybridised, washed and developed
as described by Weber-Hall et al. (1994) with the following exceptions.
The hybridisation buffer contained 70% formamide and yeast RNA
at 10 μg/ml instead of random oligonucleotides. Hybridisation was
with [35P]UTP-labelled RNA probes that were prepared as described
above and the posthybridisation washes included an RNase A
digestion at 50 μg/ml, 45 minutes at 37°C. The sense control probe
was generated from a 500 bp cDNA coding for the mouse BRCA2
gene (A. Ashworth, ICR, London). Whole-mount in situ hybridisa-
tion was performed as described by Wilkinson (1992) with the following
alterations: embryos were incubated only once in RNase
following hybridisation and were washed for only 30 minutes
in TBST (140 mM NaCl, 2.7 mM KCl, 25 mM Tris-HCl, pH 7.5, 0.1%
Tween) following incubation with antisera. 35S radioactive in situ
hybridisation (Bmp-2 probe to embryonic fetal mammary glands) was
performed as described by Davidson et al. (1988).

**Generation and analysis of transgenic mice**

The transgenic mice carrying the bacterial lacZ gene driven by the
Msx-1 promoter will be described in more detail (Hill, manuscript in
preparation). Briefly, the lacZ gene from pCH110(rf) was subcloned to produce a fusion with a 4.9 kb NcoI genomic restriction fragment of the Msx-1 5' upstream region. This DNA fragment extends into the coding region of Msx-1 carrying the predicted start codon and the open reading frame encoding the first 41 amino acids (Monaghan et al., 1991). This is in frame with the coding region for β-galactosidase which will produce a fusion protein. This construct was used to make mice transgenic (Hogan et al., 1986) and nine independent mouse lines were established.

Male mice carrying the transgene were mated with Swiss wild-type females and the embryos were harvested at day 13.5 of development. Embryonic β-galactosidase expression was detected by the method of Beddington et al. (1989). The expression of β-galactosidase in the developing mammary glands was detected in the majority of the transgenic lines.

The Msx-2-lacZ mice carrying the -5.2+3lacZ transgene were generated as described previously (Liu et al., 1994). The embryos were stained as described previously (Sanes et al., 1986), dehydrated and paraffin embedded for sectioning.

The generation of the Msx-1 null mice have been previously described (Satokata and Maas, 1994). Sections of glands were taken from 6 newborn Msx-1 mutants and 6 wild type at day P0.

RESULTS

**Msx-1 and Msx-2 are developmentally regulated in the postnatal mammary gland**

In this study we have correlated Msx mRNA levels with temporal changes in mammary gland morphology (Fig. 1A,B). Msx-1 and Msx-2 are both expressed in the glands of virgin females during ductal development and in the glands of early pregnant females during the proliferative phase of lobular development. Expression of both genes is down-regulated
(Msx-2 prior to Msx-1) during late pregnancy and lactation, corresponding with a reduction of the proliferative index and the expression of terminal differentiation markers such as β-casein (Fig. 1B, [Zwierzchowski et al., 1984]). During the period of lobulo-alveolar apoptosis that characterises involution, both genes were partially reinduced.

Msx-1 but not Msx-2 was expressed in isolated stroma (fat pads) taken from epithelial-free regions of glands prior to the ductal outgrowth (5 weeks old). These data show that expression of Msx-1 occurs in the stroma at this stage, while expression of Msx-2 is either present within the epithelium or requires the presence of the epithelium. To resolve these alternatives, expression of Msx-1 and Msx-2 was localised by in
situ hybridisation. In glands from 7 week virgin and 4.5 day pregnant mice, Msx-1 and Msx-2 expression was found in ductal epithelial cells (Fig. 2E-H). Northern analysis confirmed that Msx-1 was expressed in purified mammary epithelial cells (data not shown). Taken together, these data strongly argue that Msx-2 is expressed in the epithelium while Msx-1 is expressed in the epithelium and stroma. However, given the limitations of the resolving power of radioactive in situ hybridisation, it is not possible to exclude additional Msx-2 expression in stromal fibroblasts that are immediately adjacent to the epithelium.

**Developmental regulation of Bmp-2 and Bmp-4 in the postnatal mammary gland**

As Bmp-2 and Bmp-4 have been shown to be coordinately regulated with Msx genes during tooth development, we examined their expression patterns during postnatal mammary gland development. Both Bmp-2 and Bmp-4, like Msx-1 and Msx-2 were expressed in the postnatal mammary gland at the earliest stage examined (Fig. 3A,B). While Bmp-4 was down-regulated during late pregnancy and was not reinduced during involution, Bmp-2 transcripts were not significantly regulated during development by comparison with the GAPDH. Levels of the GAPDH control mRNA reproducibly fell during lactation, possibly as a result of a dilution by milk protein mRNAs (Fig. 1B; Weber-Hall 1994; Gavin and McMahon, 1992; Bühler et al., 1993). Both Bmp-2 and Bmp-4 were expressed in the stromal fat pad in the absence of epithelium. Comparisons of Bmp and Msx expression profiles showed that the Bmp-2 timecourse was most similar to Msx-1 while the Bmp-4 timecourse was most similar to Msx-2 (Figs 1A,B, 3A,B). In situ hybridisation analyses showed that both Bmp-2 and Bmp-4 were expressed in the epithelial component (Fig. 2B-D). Taken together with the northern analyses, these data strongly argue that Bmp-2 and Bmp-4 are expressed in both the epithelial and stromal compartments.

**Msx-2 is regulated by oestrogen**

As the development of the mammary gland is under the tight control of ovarian hormones, we investigated the regulation of Msx and Bmp transcripts following ovariectomy. Ovariectomy during ductal development causes end buds to regress to blunt-ended ducts, although the ductal system itself is not lost (Nandi, 1958; Daniel and Silberstein, 1987). The effect of ovariectomy (at 6 weeks of age) on Bmp and Msx gene expression during ductal development was examined by northern analysis (Figs 1A,B, 3A,C). Both 6- and 8-week old unoperated mice were used as controls. Previous studies have shown that ovariectomy does not cause gross changes in content of mammary epithelium in this strain of mice (Weber-Hall, 1995). Following ovariectomy, levels of Msx-2 expression were greatly reduced, while levels of Msx-1, Bmp-2 and Bmp-4 transcripts were unaltered, suggesting that Msx-2 may be regulated by ovarian hormones. The regulation of Msx-2 by ovarian hormones was confirmed by Northern analysis of mRNA derived from both 6- and 12-week old animals (Fig. 4A).

To determine the basis for the ovarian dependence of Msx-2 expression, we used the oestrogen-responsive, breast cancer cell line MCF-7, to study the regulation of the human Msx-2 homologue, MSX-2. As oestrogen has been shown to be the only ovarian steroid that is required for ductal epithelial development, we focused on the effects of 17β-oestradiol. To show specificity, we also studied the effects of the steroid vitamin D3 which has been shown to regulate MSX-2 levels in osteoblasts (Hodgkinson et al., 1993). 24 hours after 17β-oestradiol addition, quantitation with a phosphomager showed that levels of Msx-2 transcripts were induced 3-fold (1.7 kb transcript) and 2-fold (2.9 kb transcript) relative to controls (Fig. 4B; 36B4 and β-actin). The levels of MSX-2 transcript induction by 17β-oestradiol were comparable to the observed 4-fold induction of pS2, a gene previously demonstrated to be 17β-oestradiol-dependent (Chalbos et al., 1993). The increased levels of MSX-2 in the MCF-7 cells were not a secondary consequence of oestrogen-dependent changes in cell proliferation as no significant increases in cell numbers were observed within the time period of hormone treatment (24 hours). No changes in transcript levels were observed in the presence of vitamin D3 (1,25(OH)2D3), suggesting that the induction of MSX-2 expression by this steroid may be specific to osteoblasts. In addition, no changes in transcript levels were seen in the presence of progesterone or prolactin (unpublished data). Expression of Bmp-2 and Bmp-4 were not oestrogen-dependent in the MCF-7 cells, while expression of MSX-1 was not detected (Phippard, 1995).

![Fig. 5. In situ hybridisation of Msx-1 and Msx-2 to E13.5 embryonic mammary glands. Sequential sections of E13.5 foetal mammary gland. A and D show bright-field images; B, C, E and F are dark-field images following hybridisation to riboprobes for Msx-1 antisense, Msx-1 sense, Msx-2 antisense and Msx-2 sense probes respectively. Exposure times were 8 weeks. Magnification 100x.](image-url)
Msx-1 and Msx-2 are expressed in the foetal mammary epithelium

As both Msx-1 and Msx-2 were expressed at the earliest stages of postnatal development examined, we examined whether they were also expressed in the foetal gland (Figs 5, 6). These studies focused on the E13.5 foetal gland because the mammary bud is relatively easy to detect at this stage and is analogous in structure to the bud stage of tooth development in which both Msx and Bmp expression have been detected (Thesleff et al., 1995). The epithelium of the mammary bud at E13.5 expressed Msx-1 and Msx-2 as shown by in situ hybridisation (Fig. 5A-F). Msx-1 was not expressed in the fetal mesenchyme, but we were not able to exclude expression of Msx-2 in the mesenchyme as relatively high levels of background were observed with the Msx-2 sense RNA control.

To confirm the location of Msx-1 and Msx-2 expression, the control regions of the Msx-1 (4.9 kb of 5′ flanking sequence) and Msx-2 genes (5.2 kb of 5′ flanking sequence, the intron, both exons and 3 kb of 3′ flanking sequence) were fused to the lacZ marker gene and stably introduced into lines of transgenic mice (R. E. Hill, unpublished data; Liu et al., 1994). The lines of transgenic mice characterised have previously been shown to express β-galactosidase in areas of the embryo that correspond to those expressing endogenous Msx transcripts. At E13.5, β-galactosidase expression driven by both the Msx-1 and Msx-2 promoters was detected in the foetal epithelium (Fig. 6A,B), confirming the in situ hybridisation results and showing that the Msx-1 and Msx-2 promoters were sufficient to direct expression to the appropriate sites. No lacZ expression was detected in the mesenchyme immediately adjacent to the epithelial bud, but some expression driven by the Msx-2 promoter was detected in underlying tissues that may be related to the appearance of the fat pad (Fig. 6B; Sakakura, 1991).

Msx-1 is not required for early mammary development

Although Msx-1 expression was detected throughout mammary development (Figs 1A, 5B) it was not clear whether it was necessary for development. To investigate potential function(s) for Msx-1 in mammary development, we examined mammary glands from six control and mutant Msx-1/Msx-1 null mice. The mice were studied at day 0 (new born) since the mice die shortly after birth from respiratory problems (Satokata and Maas, 1994). Glands from all the homozygous null mice had a rudimentary ductal network and were found to be indistinguishable from normal or heterozygous littermates, showing that Msx-1 function is not essential for normal mammary gland development up to this stage (data not shown).

Bmp-2 and Bmp-4 are expressed in the foetal mammary gland

As both Bmp-2 and Bmp-4 were expressed at the earliest stages
of postnatal development examined (Fig. 3A,B), we examined whether they were also expressed in the foetal gland. In situ analyses localised Bmp-2 expression to the epithelial bud of the E13.5 gland (Fig. 7B,C). By contrast, Bmp-4 was expressed in the mesenchyme surrounding the epithelium, appearing as a ring structure as determined by whole-mount in situ hybridisation (Fig. 7A). Subsequent sectioning of the whole mounts confirmed that Bmp-4 expression was localised in the mesenchyme underlying the mammary knob (data not shown).

**DISCUSSION**

Our findings show that mRNAs from the Msx-1 and Msx-2 homeodomain-containing genes and the Bmp-2 and Bmp-4 signalling ligands are expressed during both foetal and postnatal mammary gland development. As coordinate expression of these genes has been implicated in the regulation of organogenesis in other systems, this suggests that they may play similar roles in mammary gland development (Davidson, 1995; Thesleff et al., 1995b).

In the foetal mammary gland at E13.5, Msx-1, Msx-2 and Bmp-2 were expressed in the foetal epithelium (Figs 5, 6), whilst Bmp-4 was expressed in the mesenchyme. At E13.5, the mammary bud has a similar morphology to bud stages in other organs in which epithelium invaginates into underlying mesenchyme (Thesleff et al., 1995b). One of the best studied systems in which the Msx and BMP gene products have been implicated as regulators is tooth development. At the structurally analogous bud stage of tooth development (E12-13), Bmp-4 and Msx-1 are expressed in the mesenchyme. Bmp-2 is expressed in the epithelium and Msx-2 is expressed predominantly in the epithelium (Vainio et al., 1993; Thesleff et al., 1995b). This analysis suggests that there are significant differences between tooth and mammary gland development, however, a simple 'snapshot' of tooth development at the bud stage conceals a complex series of temporal and spatial expression patterns in which 'compartment switching' of Msx and Bmp expression precedes and follows the bud stage (MacKenzie et al., 1991a,b; Vainio et al., 1993). As Msx-1 expression domains have been shown to undergo stage-specific expansions and restrictions in the developing limb bud (reviewed by Reginelli et al., 1995; Wang and Sassoon, 1995), it is reasonable to expect that detailed temporal studies of mammary development could reveal complex patterns of Msx expression while the use of soluble BMP factors may help elucidate regulatory BMP/Msx interactions. Interestingly, analysis of foetal glands from Msx-2-lacZ transgenic mice suggest that Msx-2 is expressed in both the mesenchyme and epithelium at a day earlier than the data shown here (E12, unpublished data), suggesting that Msx expression patterns are dynamic. Following more extensive analyses, the differences between foetal mammary and tooth expression of Msx and Bmp genes may resolve into patterns that are consistent with conserved function or may be accounted for by tissue-specific processes.

While the importance of Msx-1 expression for normal tooth development was recently demonstrated by the analysis of transgenic mice that lack a functional Msx-1 gene (Satokata and Maas, 1994), no abnormal phenotype was detected in mammary glands from the same strain of mice in these studies (data not shown). The lack of a mutant/abnormal phenotype could be a result of functional redundancy in which the function of Msx-1 is compensated for by a related gene or because Msx-1 is non-functional in the foetal mammary gland. Given that both Msx-1 and Msx-2 are expressed in the E13.5 mammary epithelium, Msx-2 could functionally compensate for loss of Msx-1 expression at this stage. Support for this hypothesis has come from recent observations in Msx-2 mutant and Msx-1/Msx-2 double mutant mice in which defects in mammary development have been observed at E13 (R. Maas, unpublished data). In contrast to the mammary gland, during the bud stage of tooth development, Msx-1 and Msx-2 are predominantly expressed in different compartments (Vainio et al., 1993; Thesleff et al., 1995), perhaps explaining why a tooth phenotype was observed in the Msx-1 mutant mice (Satokata and Maas, 1994). Although Msx-1 may be redundant to Msx-2 during foetal development, a unique function for Msx-1 cannot be excluded during postnatal mammary development as Msx-1 is expressed in the absence of Msx-2 during late pregnancy (compare Figs 1A and 2A). Analysis of postnatal functions are not possible since Msx-1/Msx-1 null mice die at birth. In a recent paper, Bmp-4 mutant mice have also been described (Winnier et al., 1995), however neither the tooth nor the mammary phenotype of these animals could be judged because the animals die from multiple developmental defects between E6.5 and E9.5.

In the postnatal gland, Msx-1, Bmp-2 and Bmp-4 are expressed in the stromal fat pad while Msx-2 is expressed in the epithelium (Fig. 1A, B ‘fat pad’, Fig. 2). The transition from foetal to postnatal development must involve the expansion of Msx-1 and Bmp-2 expression into the mesenchymally derived fat pad from the epithelium (Figs 5B, 7B,C). Thus, the postnatal functions of Msx and BMP molecules may be significantly different from those in foetal development. Studies in other systems have implicated Msx-1 and Msx-2 in the control of a diverse range of regulatory processes including the spatial definition of developing fields of cells (MacKenzie et al., 1991a,b, 1992; Jowett et al., 1993), cellular adhesiveness, epithelial morphology, cellular proliferation, apoptosis and an anti-differentiative/regenerative role (Reginelli et al., 1995; Thesleff et al., 1995). In addition to analogous functions for Msx and BMP proteins during foetal mammary and tooth development, some of these proposed roles may have particular relevance during postnatal mammary development since the gland retains a high proliferative and differentiative potential throughout adult life. Studies of limb regeneration and F3 myoblast differentiation have suggested that Msx-1 (and possibly Msx-2) prevent terminal differentiation and maintain proliferation of undifferentiated cells (Song et al., 1992; Noveen et al., 1995). The continued expression of Msx-1 and Msx-2 in the mammary gland after birth (Fig. 1) may be related to the necessity to maintain a state of developmental competence in which the mammary epithelium can respond rapidly to changes in systemic hormones. During early pregnancy, the slight increase in expression of Msx-1 and Msx-2 may be related to an increase in cellular proliferation at that time and may prevent the lactational differentiation of lobular cells until the onset of lactation (Fig. 1A,B; Zwierzchowski et al., 1984). Alternatively, constant Msx expression in ductal but not lobular cells may prevent inappropriate lactational differentiation of the ducts. To distinguish between these possibilities,
a detailed analysis of the distribution of Msx expression throughout postnatal development will be required. Msx-1, Msx-2 and Bmp-4 expression have been correlated with apoptosis of avian cranial neural crest cells and exogenous BMP-4 has been shown to induce both Msx-2 expression and apoptosis in isolated hindbrain rhombomeres (Graham et al., 1994). As Msx-1 expression precedes apoptosis at other locations including the limb bud, it is reasonable to suggest that the reinduction of Msx-1 expression in the involuting gland may be involved in the control of the major apoptotic phase of mammary development. In this context, it will be particularly interesting to determine if Msx-1 is expressed in the alveolar cells prior to apoptosis or in the ductal cells which are selectively retained.

In principle, members of the TGFβ, FGF, EGF, HGF/Scatter and Wnt families of secreted ligands could function in inductive interactions in the mammary gland as members from each family have been shown to be developmentally regulated during mammary gland morphogenesis (Snedeker et al., 1991; Gavin and McMahon, 1992; Robinson et al., 1992; Buhler et al., 1993; Coleman-Krnacik and Rosen, 1994; Niranjani et al., 1995). An important additional question is how the control of epithelial-mesenchymal interactions is integrated with the regulation of mammary development by hormones such as oestrogen, progesterone and prolactin. The observation that Msx-2 is regulated by ovarian hormones in vivo (Fig. 1B) and that MSX-2 expression is directly regulated by 17β-estradiol in vitro, raises the possibility that hormonal regulation may be mediated through existing epithelial-mesenchymal regulatory systems. During mammary gland evolution, key developmental control genes may have acquired hormone responsive control regions, thus imposing hormonal control on the entire network of epithelial-mesenchymal interactions. This may be a mechanism common to other genes in addition to Msx-2 since expression of putative mammary control genes such as Wnt-4 and Hoxc6 were also affected by ovariectomy (Weber-Hall et al., 1994; Bradbury et al., 1995; Friedman et al., 1995). The mechanism by which Msx-2 is regulated is not clear at present. In principle, oestrogen induction could be mediated by alterations in transcript stability or induction of transcription. Surveys of 800 bp of the murine Msx-2 promoter, failed to detect canonical oestrogen-responsive elements (unpublished data), although this does not rule out further upstream elements or more indirect mechanisms of oestrogen regulation. An additional point of interest concerns the time at which the mammary epithelium becomes responsive to oestrogen and the time at which Msx-2 expression becomes estrogen responsive. Studies in mutant mice that lack the oestrogen-receptor suggest that mammary development can proceed normally until postnatal stages of development when end bud development fails to take place (Lubahn et al., 1993; Korach et al., 1994). Future studies may be able to determine if Msx-2 expression also becomes oestrogen responsive only at the onset of postnatal development.

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