Expression and regulation of the Msx1 natural antisense transcript during development

Amélie E. Coudert, Laurence Pibouin, Brigitte Vi-Fane, Bethan L. Thomas¹, Mary Macdougall², Anuradha Choudhury¹, Benoit Robert³, Paul T. Sharpe¹, Ariane Berdal and Frédéric Lezot*

Laboratoire de Biologie Oro-Faciale et Pathologie, INSERM U 0714, Centre de recherches biomédicales des Cordeliers, 15-21, rue de l’Ecole de Médecine, 75270 Paris Cedex 6, France, ¹Department of Craniofacial Development, Dental Institute, King’s College London, Floor 28 Guy’s Tower, Guy’s Hospital, London SE1 9RT, UK, ²Department of Pediatric Dentistry, Dental School, University of Texas Health Science Center at San Antonio, San Antonio, TX, USA and ³Unité de Génétique Moléculaire de la Morphogenèse, Institut Pasteur, CNRS URA 2578, 25, rue du Dr Roux, 75724 Paris Cedex 15, France

ABSTRACT

Bidirectional transcription, leading to the expression of an antisense (AS) RNA partially complementary to the protein coding sense (S) RNA, is an emerging subject in mammals and has been associated with various processes such as RNA interference, imprinting and transcription inhibition. Homeobox genes do not escape this bidirectional transcription, raising the possibility that such AS transcription occurs during embryonic development and may be involved in the complexity of regulation of homeobox gene expression. According to the importance of the Msx1 homeobox gene function in craniofacial development, especially in tooth development, the expression and regulation of its recently identified AS transcripts were investigated in vivo in mouse from E9.5 embryo to newborn, and compared with the S transcript and the encoded protein expression pattern and regulation. The spatial and temporal expression patterns of S, AS transcripts and protein are consistent with a role of AS RNA in the regulation of Msx1 expression in timely controlled developmental sites. Epithelial–mesenchymal interactions were shown to control the spatial organization of S and also AS RNA expression during early patterning of incisors and molars in the odontogenic mesenchyme. To conclude, this study clearly identifies the Msx1 AS RNA involvement during tooth development and evidences a new degree of complexity in craniofacial developmental biology: the implication of endogenous AS RNAs.

INTRODUCTION

Until very recently, the significance of natural antisense (AS) transcripts was underestimated. AS transcripts in prokaryotes have been known for at least two decades (1,2) while a limited number of cases have been reported in eukaryotes. Recent data have established their importance in eukaryotes (3–5). Indeed, these transcripts are involved in gene expression regulation (5) as exemplified by RNA interference, presently applied in numerous knockdown strategies (6). Natural AS transcripts are grouped into two classes: cis AS transcripts which are transcribed with the sense (S) transcripts from a unique gene locus, and trans AS transcripts which are transcribed from a different locus. Rare data are available on the physiological impact of AS RNAs during development. For example, in Caenorhabditis elegans let-44 controls the timing of post-embryonic cell division and fate [for review see (7)]. In mouse, miR196a negatively regulates Hoxb8 and restricts Hox homeogene expression pattern (8). Interestingly, these two AS RNAs belong to the specific subclass of small RNAs also named microRNA (21–23 nt).

Recent studies have highlighted another subclass of AS RNAs: the long cis AS (containing >100 bp). In silico studies based on expressed sequence tag database have predicted that they may constitute ~15% of the mouse genome (9) and >20% of the human genome (4). Long cis AS transcripts have been shown to exert regulatory functions on protein expression at various levels such as epigenetic imprinting, RNA maturation, edition and translation inhibition (5,10). However, the functional data on AS transcripts have been essentially generated in vitro. Very few long AS transcripts have been analyzed in the specific context of mammalian development. Some expression patterns have been reported: for instance, Hoxa1 AS and...
S transcripts show complementary expression territories in developing limbs (11).

The mouse Msx1 locus has been shown previously to undergo a bidirectional convergent and overlapping transcription (12). Msx1 AS transcript belongs to the long cis-AS subclass (2184 nt. in mouse), and was proposed to control protein expression. This assertion was based on (i) in vitro evidence of protein down-regulation by the AS transcript, and (ii) in vivo expression patterns in newborn mouse osteoblasts (12). Indeed, in the mandibular bone Msx1 AS transcript evidenced a complementary expression pattern to the Msx1 S transcript. More specifically, the Msx1 AS transcript is expressed in the latest stage of osteoblast maturation (osteocytes) whereas Msx1 S transcript is expressed in preosteoblasts and osteoblasts (12). According to these observations, it was hypothesized that Msx1 AS transcript expression is instrumental in the regulation of osteoblastic cell differentiation. It would control the progressive reduction of Msx1 homeoprotein expression and therefore induce the interdependent cell cycle exit and differentiation (12). This assertion is supported by several in vitro and in vivo data on Msx1 homeoprotein. In vitro, Msx1 overexpression blocks myoblasts differentiation (13), induces myotubes dedifferentiation into myoblasts and promotes transdifferentiation into osteoblasts (14). Consistently, in vivo, Msx1 expression is reversely correlated with cell differentiation progression (15,16).

During embryonic development, Msx1 is instrumental in various systems, notably in the craniofacial complex where it acts as a transcriptional repressor (17–21). Msx1 expression is observed early in development in neural crest cells and their derivatives, including first branchial arch ectomesenchymal cells devoted to tooth formation (17,22,23). In mice, the first evidence of tooth morphogenesis occurs at embryonic day 11.5 (E11.5) as a thickening of the dental epithelium, called the dental lamina (24). However, before this morphological event and as early as E10.5, the respective incisor and molar fields are already determined. Oral epithelium induces a site-specific combination of homeobox genes expressions in the subjacent dental mesenchyme, and these combinations are organized as an ‘odontogenic homeobox code’ (25–27). Msx1 has been shown to be a key element within this code, specifying the incisor presumptive region at E10.5 (25,28). After E11.5, tooth morphogenesis is already initiated and the dental lamina epithelium progressively invades the subjacent mesenchyme and forms the dental bud (E12.5–E13.5). Thereafter, dental development progresses through the cap (E14.5) and bell stages (E16.5), characterized by tooth-specific morphogenesis and cell differentiation. Tooth morphogenesis is orchestrated by successive organization centers, called primary and secondary enamel knots (29). This overall process of tooth morphogenesis is driven by sequential and reciprocal interactions between dental epithelium and mesenchyme [for review see (30,31)]. Msx1 plays a central role in these epithelial–mesenchymal interactions as evidenced by molar tooth development arrest at the bud stage in mice lacking Msx1 (23,32,33).

Finally, during tooth development, Msx1 is important for two major processes, firstly, the dental field determination and secondly, the tooth morphogenesis. Msx1 is, therefore, an exemplary model to analyze cell–cell communication leading early determination and subsequent morphogenesis in mammals. Based on this conclusion and on the recent discovery of the endogenous AS transcript of Msx1 (12), the present study aimed to delineate the timing and impact of this AS transcript in these established developmental cascades; firstly, to determine whether Msx1 AS transcript is expressed prior to the late terminal differentiation stages (12), and secondly, whether Msx1 AS transcript is instrumental in epithelial–mesenchymal interactions leading to the two distinct steps of odontogenesis, namely, tooth field determination (E10.5) and tooth morphogenesis (E11.5–E16.5). Using different approaches we have proposed a novel role for Msx1 AS in tooth development.

MATERIALS AND METHODS

Embryo collection
Timed matings were set up such that noon of the day on which vaginal plugs were detected was considered as embryonic day 0.5 (E0.5). Wild-type mouse embryos used for in situ hybridization and explants cultures were collected from matings of CD-1 mice (ElevageDépré, Saint Doulchard). Msx1/nLacZ heterozygous embryos and Dlx2/LacZ transgenic embryos were collected from CD-1 females crossed with Msx1/nLacZ heterozygous males (23) and Dlx2/LacZ transgenic males (34), respectively. Pregnant mice were sacrificed by cervical dislocation and the embryos collected from E9.5 to E18.5. Newborns, 1- and 2-day-old mice were sacrificed by head cutting.

Msx1/nLacZ and Dlx2/LacZ embryos whole mount β-galactosidase staining
β-galactosidase activity was evidenced by standard histochemical methods as described previously (35). Briefly, the embryos were harvested, fixed for 30 min in a 1× phosphate-buffered saline (PBS) containing 4% paraformaldehyde (PFA), washed in 1× PBS and finally stained overnight at 32°C in a PBS 1× solution containing 5 mM potassium ferricyanide, 5 mM potassium ferrocyanide, 2 mM magnesium chloride, 0.1% Nonidet P-40 and 400 μg/ml of X-Gal substrate (all products from Sigma, Saint Quentin Fallavier). The embryos were then fixed overnight in the same fixative solution and rinsed in PBS 1× before being either photographed, wax embedded and sectioned, or used for whole mount in situ hybridization.

In situ hybridization experiments
In situ hybridization experiments were performed for both Msx1 transcripts and for Dlx2 and Barx1 S transcripts. Four probes were designed to detect Msx1 transcripts as presented in Figure 2. Two probes, E2A and E2B, are localized in Msx1 exon 2 and are complementary for the AS and S transcripts, respectively (Figure 2). These probes were generated as described previously (12) from a SphI/SphI Msx1 exon 2 960 bp DNA fragment cloned in a bluescript plasmid (18). The E1 probe, complementary to the S transcript, was obtained by EcoRI digestion and T7 transcription of a bluescript plasmid containing the XbaI/EcoRI 368 bp fragment of Msx1 exon 1 (Figure 2). This fragment was obtained by PCR amplification. The I probe, complementary to the
AS transcript, was obtained by EcoRI digestion and T7 transcription of a bluescript plasmid containing the Smal/Smal 935 bp fragment of Msx1 intron (Figure 2). The Dlx2 probe was generated as described previously from a bluescript derivative (named E61) (35). The Barx1 probe was generated, using EcoRI digestion and T7 transcription, from a bluescript vector containing a 951 bp Barx1 DNA fragment (kindly gifted by J.-F. Brunet).

Whole mount digoxigenin-labeled hybridizations were carried out as described previously (35). Briefly, after proteinase K and triethanolamine/acetic anhydride pretreatments, samples were fixed in 4% PFA before overnight hybridization at 65°C with probe at 1 μg/ml. After post-hybridization washes, digoxigenin immunodetection was realized with an antidigoxigenin antibody coupled to alkaline phosphatase (AP) (Roche Diagnostics, Meylan) diluted at 1/2000. The AP enzymatic activity was finally revealed using NBT/BCIP solution (Roche) according to the manufacturer’s instructions.

Radioactive (35S-UTP) in situ hybridizations were performed on 7 μm paraffin frontal sections as described previously (36). Sample sections floated onto polylysine (Sigma) coated slides were pretreated with proteinase K and triethanolamine/acetic anhydride pretreatments, samples were fixed in 4% PFA before overnight hybridization at 65°C with probe at 1 μg/ml. After post-hybridization washes, digoxigenin immunodetection was realized with an antidigoxigenin antibody coupled to alkaline phosphatase (AP) (Roche Diagnostics, Meylan) diluted at 1/2000. The AP enzymatic activity was finally revealed using NBT/BCIP solution (Roche) according to the manufacturer’s instructions.

Cell culture and transfection assays
MD10H1 cell line was obtained by large T antigen immortalization of E18 mouse embryo first molar mesenchyme (39). These cells were used for transfection assays in triplicate using Exgen transfection system according to the manufacturer’s protocol (Euromedex, Mundolsheim). Briefly, MD10H1 cells were plated out in α-MEM supplemented with 10% of FCS (GibcoBRL) at 5 × 10^4 cells/cm². After 24 h, cells were transfected with 0.5 μg of either Dlx2 or Barx1 expression vectors (provided by S. Harris and P. T. Sharpe, respectively) or with 0.5 μg of Msx1 AS expression vectors. The latter one was generated by PCR amplification from a DNA template with the following primers (5' TCA CAT GGT GGT TCC TCA AGC TGT CCA CTA CGC AA-3'); the amplified fragment corresponds to the entire AS transcript. Control transfection experiments were performed using empty expression plasmids. After 24 h, the medium was removed, the cells rinsed with 1× PBS and used for RNA analysis.

RNA analysis
RNA from the transfected cells, from the heads dissected from E9.5 to E18.5 embryos and from newborn to 2-day-old mice were extracted using TriReagent (Euromedex) as described previously (40) and used for RT–PCR. RT was carried out on 1 μg of total RNA with Superscript II using oligo(dT) primer according to the manufacturer’s protocol (Invitrogen). The PCR was performed in 20 μl with 2 μl of the RT reaction and 10 pmol of the following primers for 30 cycles: Msx1 S (forward primer: 5'-TCA AGC TGC CAG AAG AT-3'); reverse primer: 5'-TCA GGT GGT ACA TGC TGT AG-3'); Msx1 AS (forward primer: 5'-TGA TGT CCA CCT GCC CTT TC-3'); reverse primer: 5'-GGG CCC AAA GGA TTA TTG TT-3'); Dlx2 (forward primer: 5'-TCC TAC CAG TAC CAA GCC A-3'); reverse primer: 5'-AAG CAC AAG GTG GAG AAC C-3'); Barx1 (forward primer: 5'-CCA TGC CCG GCC CGG CAG CAG CAT C-3'); reverse primer: 5'-GAA TTC AGT CCT GCG AAT TTC GG-3'); and GAPDH (forward primer: 5'-TTC CAG TAT GAT TCC ACT CA-3'); reverse primer: 5'-CTG TAG CCA TAT TCA TTG TG-3'). In all analysis, RNA without RT served as control.
RESULTS

First evidence of Msx1 AS transcript expression during development

The first evidence for endogenous Msx1 AS transcripts was shown previously in postnatal mice (12). In order to determine if Msx1 AS was expressed during embryonic development and in early postnatal life, semi-quantitative RT–PCR was performed on RNA from E9.5 to E18.5 embryos and from day 0 to day 2 newborn mice. These experiments showed that both Msx1 transcripts were detected as early as E9.5 and throughout development until postnatal day 2, suggesting a potential role in embryogenesis (Figure 1).

Msx1 S and AS transcripts and protein expression from E9.5 to E11.5

Expression of both S and AS Msx1 transcripts was analyzed during early embryonic development by whole mount in situ hybridization. The protein expression was analyzed at these same stages using Msx1/LacZ heterozygous embryos, in which the LacZ knock in enabled protein expression followed indirectly (23).

The Msx1 AS transcript was described previously as a 2.1 kb long transcript which contains sequence overlapping the entire exon 2 and 1012 bp of the intron of Msx1 gene (Figure 2). Both the S and AS Msx1 transcripts are complementary in exon 2 sequence. A set of four probes (E1, I, E2A and E2B) was used for in situ hybridization experiments. The S transcript probe (E1) was nested in the Msx1 exon 1 since this sequence is specific to the S transcript (Figure 2). The AS transcript probe (I) was nested in Msx1 intron since this sequence is specific to the AS transcript (Figure 2). With the original Msx1 vector (18) containing part of exon 2 sequence, two probes were generated. E2A probe was complementary for the AS transcript whereas E2B probe was complementary for the S transcript (Figure 2). For all experiments the four probes were used. In all experiments, with the exception of E13.5–E16.5, detected expression using both S probes produced the same pattern of expression, as also seen with both the AS probes.

At E9.5, the Msx1 AS transcript was not detected in mandibular and maxillary regions (Figure 3B and E) but appeared to be expressed in brain. In contrast, the S transcript (Figure 3A and D) and protein (Figure 3C and F) were detected in the

Figure 1. Msx1 S and AS transcripts detection from E9.5 to 2 days post natal. The two Msx1 transcripts were detected by semi-quantitative RT–PCR during this entire period.

Figure 2. Schematic representation of the two Msx1 transcripts and position of the four probes used in situ for hybridizations. Msx1 S and AS transcripts organization in regard of the Msx1 gene structure (accession number S73812) is schematically presented. The Msx1 S (top) and AS (bottom) transcripts are shown. The S transcript correspond to exons 1 and 2 sequences. The AS transcript sequence is complementary to the exon 2 and a major part of the intron. Positions of probes used for hybridization are given. Green and red arrows, respectively, represent S and AS promoter.

Figure 3. Msx1 S and AS transcripts and Msx1 protein expression from E9.5 to E11.5 in mouse embryos. Both Msx1 transcripts are detected by whole mount in situ hybridization on wild-type mice embryos. Msx1 protein expression is revealed by the β-galactosidase activity using Msx1-nLacZ heterozygous mouse embryos. (A–F) At E9.5, the Msx1 AS transcript is not detected in the first branchial arch in contrast to the S transcript and the protein. (G–L) At E10.5, both S and AS Msx1 transcripts are detected in complementary regions of the mandible. The Msx1 S transcript and the protein are detected in the distal part of the mandible and the Msx1 AS transcript in the proximal parts. (M–R) At E11.5, both Msx1 transcripts are detected in progressively overlapping areas in mandible outlining two reverse gradients, proximal-distal for the Msx1 AS transcript and distal-proximal for the Msx1 S transcript and the protein. The bar scale represent 800 μm for whole embryos, and 500 μm for the mandible.
distal parts of the mandible primordium. In the facial region, *Msx1* AS transcript expression was first detected at E10.5 (Figure 3H and K). At this stage, both *Msx1* transcripts exhibited an interesting opposite pattern in the mandibular arch. *Msx1* AS transcript was detected in the proximal part of mandible (Figure 3H and K) whereas *Msx1* S transcript (Figure 3G and J) and protein (Figure 3I and L) were still detected in the distal part of mandible. *Msx1* AS transcript was detected in other anatomical sites such as the future brain and limb buds (Figure 3H). At E11.5, in the facial region, the territories of both *Msx1* transcripts and protein appeared to be enlarged and overlapping, corresponding to almost all the oral part of mandible (Figure 3M–R). Two opposite gradients of *Msx1* S and AS transcript expression patterns were observed. *Msx1* S transcript expression level appeared higher in the distal region (Figure 3P) and reversely the *Msx1* AS transcript was expressed more significantly in the proximal regions (Figure 3Q). Protein expression also appeared to be expressed at a higher level in the distal region (Figure 3R). *Msx1* AS transcript was still detected in the forming brain and in the limb buds at this stage (Figure 3N).

**Comparative expression of *Dlx2*, *Barx1*, *Msx1* S and AS transcripts at E10.5 in presumptive molar and incisor fields**

The expression of *Dlx2*, *Barx1* and both *Msx1* transcripts were comparatively analyzed in the presumptive incisor and molar fields of E10.5 embryo mandible by whole mount *in situ* hybridization. The *Msx1* AS transcript was detected in the proximal regions of the E10.5 mandibular arch (Figure 4A) whereas the *Msx1* S transcript was detected in the distal part of the mandible (Figure 4C) adjacent to the *Dlx2* epithelial expression (blue in Figure 4C and D). The mesenchymal expression of *Dlx2* (Figure 4F) and *Barx1* (Figure 4D) was evidenced in the proximal area, as was the *Msx1* AS expression. However, the *Barx1* mesenchymal expression pattern appeared more restricted than that of the *Dlx2* and *Msx1* AS. In the epithelium, the *Msx1* AS transcript was not detected in the distal region of *Dlx2* epithelial expression (Figure 4B and blue LacZ staining in Figure 4C and D).

**FGF8 regulates *Msx1* AS transcript expression in mandible explant culture**

In order to determine whether *Msx1* AS transcript expression would be integrated in the epithelial signaling pathways that establish the morphogenetic fields in E10.5 mandible, epithelial induction of *Msx1* AS transcript mesenchymal expression was evaluated in mandibular explants cultures. Interestingly, 12 h after the removal of mandibular arch, a loss of *Msx1* AS transcript expression was observed in the mandibular explant (Figure 4E). To test the potential induction of *Msx1* AS transcript expression by epithelium signals, BMP4 and FGF8 soaked beads were applied to the mandibular mesenchyme explants. After 12 h of culture, *Msx1* AS transcript expression was detected around the FGF8 beads (Figure 4F), as was *Msx1* S transcript (Figure 4G), whereas BMP4 or BSA beads had no effect (Figure 4H and I). In contrast to the AS transcript, the *Msx1* S transcript expression was increased by BMP4 soaked beads (Figure 4J). To explore a potential inhibitory effect of BMP4 on *Msx1* AS transcript expression was observed in the mandibular explant beads (Figure 4J). To explore a potential inhibitory effect of BMP4 on *Msx1* AS transcript expression, BMP4 soaked beads (H and I) in contrast to the AS transcript, the *Msx1* S transcript expression was increased around the BMP4 soaked beads (J). No inhibitory effect on *Msx1* AS transcript expression was observed when BMP4 soaked beads are put in presence of epithelium (K). L The *Msx1* AS transcription activation by *Dlx2*. MD10H cells were transfected with either an empty vector, a *Dlx2* expression vector, or an *Msx1* AS expression vector. RNA extracted from these cells was reverse-transcribed and cDNA analyzed by PCR. *Dlx2* overexpression appears to be able to induce a moderate increase of the *Msx1* AS transcript synthesis whereas *Msx1* S AS transcript overexpression had no effect on either *Dlx2* or *Barx1* expressions. M Schematic representation of the regulation of both *Msx1* transcripts by epithelial BMP4 and FGF8 signaling. In proximal regions of the E10.5 mandible, FGF8 activate *Msx1* AS transcript expression directly or/and potentially through *Dlx2* activation. The AS transcript is suspected to inhibit *Msx1* homeoprotein expression in these proximal regions through a mechanism that remains to be elucidated. In the distal region, BMP4 activates *Msx1* S transcript and protein expression and inhibits *Dlx2* expression. No direct effect of BMP4 on *Msx1* AS transcript expression was evidenced.
BMP4 on the Msx1 AS transcript expression, mandibular explants were cultured for 12 h with BMP4 soaked beads in the presence of epithelium (Figure 4K). No significant change was observed in the Msx1 AS transcript expression (Figure 4K).

Impact of Dlx2 and Barx1 overexpression on Msx1 AS transcript expression in dental cells

As Dlx2 and Barx1 are coexpressed with Msx1 AS transcript in the proximal parts of E10.5 mouse embryo mandible, a potential regulation between these genes was analyzed in vitro in undifferentiated mesenchymal MD10-H1 cells. In order to examine whether the Msx1 AS transcript could be under the control of Dlx2 and Barx1 in the mesenchyme, the expression level of this transcript was analyzed after Dlx2 or Barx1 overexpression. The semi-quantitative RT–PCR results showed a small but reproducible increase in Msx1 AS transcript steady state levels which was observed 24 h after the transfection with a Dlx2 vector (Figure 4L). Quantitative analyses of Msx1 AS transcript expression increase after Dlx2 overexpression were realized using two techniques: real-time PCR (Roche) and classical PCR fragments quantification on BET gel using Optimate 5.21 (Visiomic). Both techniques showed a moderate stimulation to 1.2 times that of Msx1 AS transcript steady state expression. The impact of Dlx2 on Msx1 AS transcript expression in these experiments is probably underestimated according to the low transfection efficiency obtained for MD10-H1 cells (only 35%). Barx1 transcript expression level was not affected by Dlx2 overexpression (Figure 4L), nor Dlx2 expression affected by Barx1 overexpression (data not shown). The controlled overexpression of Msx1 AS transcript showed no effect on either Dlx2 or Barx1 expression levels (Figure 4L).

Msx1 S, AS transcripts and protein expression during tooth morphogenesis

All in situ hybridization experiments were carried out with the panel of four different probes (Figure 2). From E9.5 to E12.5, similar results were obtained with the two probes for Msx1 AS transcript. The two probes for Msx1 S transcript also gave identical results. At E11.5, both Msx1 transcripts and the protein were detected in similar regions of the dental mesenchyme surrounding the dental lamina (Figure 5A–C). At E12.5, both Msx1 transcripts and the protein were still detected in the same anatomical sites, more precisely in the mesenchyme surrounding the growing tooth buds (Figure 5D–F). At E13.5, the probes revealed different expression patterns. The Msx1 S transcript was detected in the dental mesenchyme (Figure 5G and H) with both probes (E1 and E2B) and unexpectedly in the dental epithelium with the E1 probe (Figure 5G). The Msx1 AS transcript was detected, with both AS probes, in the dental epithelium (Figure 5I and J), and also, at a low level, in the dental mesenchyme. At this stage, the protein was expressed only in the dental mesenchyme (Figure 5K). At E16.5, the Msx1 S transcript was detected by the two probes in the dental mesenchyme (Figure 5L and M). At this stage, as observed previously at E13.5, an epithelial expression of Msx1 S transcript was revealed only by the E1 probe (Figure 5L). The Msx1 AS transcript was detected at E16.5 only in the dental epithelium with whatever probes used (Figure 5N and O). No protein expression was detectable at this stage (Figure 5P). In newborns, before the first sign of odontoblast differentiation, the S and AS transcripts were detected with E1 (Figure 5Q) and I (Figure 5T) probes, respectively, whereas the exon two probes (Figure 5R and S) gave no signal.

Msx1 S, AS transcripts and protein expression during early limb bud development

Msx1 transcripts and protein expression were comparatively analyzed during anterior limb bud development, from E9.5 to E14.5, by whole mount in situ hybridization and β-galactosidase staining (Figure 6). At E9.5, Msx1 S transcript and protein were detected in the entire limb bud whereas Msx1 AS transcript was absent (Figure 6A–C). At E10.5, similarly to the observed pattern in the mandible, both Msx1 transcripts were detected with complementary expression patterns. Msx1 S transcript and protein were detected in the area bordering the apical ectodermal ridge whereas the Msx1 AS transcript was detected in a more proximal region, but immediately adjacent to the Msx1 S transcript positive region (Figure 3G–I and Figure 6D–F). At E11.5, the Msx1 AS transcript was still located in an area adjacent to the Msx1 S transcript region (Figure 3M and N and Figure 6G and H). At E14.5, the Msx1 AS transcript was detected in the proximal part of the interdigital regions (Figure 6I), whereas the protein was expressed with a proximal-distal gradient in the same interdigital areas and also in tip of digits (Figure 6K).

DISCUSSION

The Msh-like homeobox genes, orthologous to the Muscle Segment Homeobox gene of Drosophila melanogaster, constitute an ancient family described in numerous species ranging from coelenterates to mammals (20). Inside this family, a variable number of members have been reported for different species, corresponding to evolutionary duplications (20). These genes exhibit a simple genomic structure with two exons separated by a single intron (41). The Msx1 gene appears to be the most conserved gene within the Msh family of mammals and avians (20). Interestingly, a bidirectional overlapping and convergent transcription was identified for this Msx1 gene in mouse and human and might also be conserved in at least three other species: rat, bovine and chicken. Such a possibility was suggested by the existence of a conserved identical 60 bp sequence containing a TATA box and such a possibility was suggested by the existence of a conserved 60 bp sequence containing a TATA box (Figure 6). At E9.5, Msx1 AS transcript was detected in the proximal part of the interdigital areas and also in tip of digits (Figure 6K).
Evidence for Msx1 AS transcript expression during embryonic development

The Msx1 AS transcript was originally identified in newborn and young adult mice (12), in association with skeletal growth. Msx1 AS transcript was proposed to be instrumental postnatally in terminal differentiation, by inhibiting Msx1 protein expression (12,45). Indeed, Msx1 homeoprotein expressing cells were considered as undifferentiated cells, based on in vitro observations that Msx1 (i) inhibits master gene expression such as MyoD (46) and Runx2 (12), (ii) modulates the expression of cell cycle determinants such as cyclin D1 (47) and p19(INK4d) (48), (iii) induces dedifferentiation of myotubes (14), and (iv) is specifically present in progenitor cell niches in adults (49). Interestingly, the initial analysis of Msx1 AS transcript expression during antenatal mouse development (Figure 1) revealed that, similar to the S transcript, the Msx1 AS transcript was already expressed at E9.5 before the initial steps of skeleton morphogenesis and cell differentiation, and continuously up to birth. These data suggest that the Msx1 bidirectional convergent and overlapping transcription may not only be linked to the control of cell terminal differentiation but also implicated in more complex processes during development, such as dental and skeletal morphogenesis.
Msx1 AS transcript and tooth initiation

Msx1 (S transcript) has been proposed to be an important factor in the odontogenic homeobox code proposed to define the different tooth fields at E10.5 in mouse prior to the morphological appearance of tooth formation (25–27). This homeobox code is based on combinations of homeobox gene expression patterning territories in the first branchial arch neural crest derived mesenchyme (37,53–56). In this homeobox code, Msx1 may define the incisor region (28) whereas Barxl in combination with Dlx2 specifies molar region (27,57,58). This assertion is exemplified in Msx1 knock out mice which exhibit no initiation of incisor development in contrast to molars where development is blocked later at the bud stages (32). To understand further the means of spatially restricting the expression of the Msx1 homeoprotein, the role of Msx1 AS transcript in the control of protein expression was considered. Our data showed that at E9.5 Msx1 AS transcript was not expressed in the mandibular arch in contrast to the S transcript, whereas at E10.5 Msx1 AS transcript was detected and presented an expression pattern complementary to the S transcript and protein. Such a result suggests that Msx1 AS transcript could participate to Msx1 homeoprotein expression restriction within the distal region of the mandible. At this stage, some homeobox containing gene expression patterns in the mesenchyme are driven by epithelial signaling (28,31,33,34,37,54,59,60). Two major signaling molecules implicated are growth factors BMP4 and FGF8. They are secreted by the distal and proximal parts of the mandibular oral epithelium, respectively. Effects of these diffusible growth factors on Msx1, Barxl and Dlx2 expression have been established by application of protein soaked beads in mandibular explant cultures. These experiments show that mesenchymal expression of Barxl and Dlx2 is induced by FGF8 while inhibited by BMP4 (34,53,61). In contrast, Msx1 S transcript appears to be induced around both FGF8 and BMP4 soaked beads (28,33,37,53) raising the question of Msx1 S transcript expression control (inhibition) in the mandible proximal parts in vivo. Interestingly, at E10.5, Msx1 AS transcript showed an expression pattern in the mesenchyme of the mandible similar to those of Barxl and Dlx2 (Figure 4A, B and D) and in opposition to Msx1 S transcript and homeoprotein expression pattern (Figure 4C). The presently reported expression of Msx1 AS transcript lead to propose a hypothesis: the AS RNA would inhibit S RNA and protein expression in the proximal parts of the mandible by a mechanism that still remains to be elucidated but that could occur at transcriptional level according to the absence of S transcript detection. The present soak-beads experiments provided evidence that the mesenchymal expression of Msx1 AS transcript at E10.5 is indeed responsive to FGF8 and not BMP4 (Figure 4F, I and K). Interestingly, the Msx1 AS transcript activation by FGF8 at E10.5 appears to be correlated to an absence of Msx1 S transcript response to this growth factor, while beads experiments suggest that Msx1 S transcript should be activated (Figure 4G).

In vitro overexpression experiments in mesenchymal MD10-H1 dental cells (39) show that Msx1 AS transcript expression may be regulated by Dlx2 but not by Barxl (Figure 4L), suggesting that Dlx2 could act as an intermediary in the pathway between FGF8 and Msx1 AS. A schematic representation of FGF8 and BMP4 differential regulation of both Msx1

![Figure 6. Msx1 S and AS transcripts detection and Msx1 protein expression from E9.5 to E14.5 in mouse anterior limb bud. Both transcripts of Msx1 were detected by whole mount in situ hybridization in wild-type mouse embryos. Msx1 protein expression was detected by the β-galactosidase activity in Msx1-lacZ heterozygote mouse embryos. The Msx1 AS transcript was detected in limb bud at E10.5 and E11.5 but not at E9.5 (B, E and H). Its detections territories edged the Msx1 S transcript and protein detection territories (A, C, D, F, G and I). At E14.5, Msx1 AS transcript and protein show complementary expression pattern (J and K). The bar scale represent 200 µm.](https://academic.oup.com/nar/article-abstract/33/16/5208/2401135)
transcripts mesenchymal expression in the E10.5 mandible is presented in Figure 4M.

Finally, Msx1 AS transcript appeared to be inserted inside the homeobox code at E10.5 through its joint expression in the proximal region with Barx1 and Dlx2. At this developmental stage, the obtained data suggest that Msx1 AS transcript would spatially limit Msx1 S transcript and protein expression areas. The exclusive Msx1 AS transcript expression might result in the complete inhibition of Msx1 S transcript expression by a mechanism that remains to be elucidated.

**Msx1 AS transcript and tooth morphogenesis**

During tooth morphogenesis, Msx1 (S transcript) was shown to be expressed in the mesenchyme with a progressive restriction, from E11.5 to E12.5, to the dental mesenchyme surrounding both incisor and molar buds (22,62,63) (Figure 5). The importance of epithelial signaling, in particular BMP4 expression, in such a restriction has been shown and corresponds to a crucial step in the tooth morphogenesis process (31,33). Moreover, the importance of Msx1 homeoprotein expression in dental mesenchyme is evidenced by the observation of molar development arrest at the bud stage (E13.5) in Msx1 null mutant mice (32). Recombination experiments between wild-type and Msx1 null mutant dental tissues showed that Msx1 mesenchymal expression is transiently necessary at the early bud stage (33) mainly to induce BMP4 expression in the dental mesenchyme as validated by BMP4 complementation experiment using transgenic animals (64,65). Indeed, the important function of Msx1 homeoprotein in tooth morphogenesis is its implication in epithelial–mesenchymal interactions and the question of the AS transcript part in this function control is raised from this point of view. Our results showed that Msx1 AS transcript was continuously expressed during tooth morphogenesis with a stage-specific pattern. At the dental lamina stage (E11.5), the AS transcript was detected jointly with the S transcript in the mesenchyme and by E12.5, its expression was progressively restricted to the mesenchyme area surrounding the epithelial invagination, as reported previously for the S transcript. At the following stages (cap and bell stages), the Msx1 S and AS transcripts expression patterns diverge showing a complementary in the mesenchyme. The S transcript was expressed in the dental cells which will differentiate into odontoblasts and pulp cells whereas the AS transcript was expressed in cells which will give rise to the follicular sac and alveolar bone. However, the function associated to such a distribution of the two transcripts remains unclear. Concerning Msx1 S and AS transcript expression in dental epithelium (detected only with certain probes), the situation is even more complex and discussed below. Indeed, according to our data whatever be the stage of tooth morphogenesis Msx1 homeoprotein expression was restricted to the mesenchyme. Finally, our result establishes that during tooth morphogenesis, Msx1 AS transcript showed a dynamic expression pattern relative to the S transcript and the protein suggesting its implication in the protein localization and expression level.

In conclusion, regarding Msx1 transcripts and relative protein expression during tooth morphogenesis, five distinct situations were identified depending on the developmental stages, areas and tissues: no expression (at E11.5–E12.5 in the epithelium), exclusive expression of S transcript (at E14.5 and E16.5 in dental mesenchyme), exclusive expression of AS transcript (at E16.5 in epithelial regions such as stellate reticulum and stratum intermedium), coexpression of S and AS (i) with all probes (E11.5–E12.5) or (ii) with certain probes (at E13.5, E16.5 and D0). The differences observed with the set of probes used could be explained by the complementarities of S and AS exons 2 sequences. Indeed, the exclusive results obtained with S and AS specific probes suggest that at E13.5, E16.5 and D0 the overlapping sequence from both transcripts are not accessible to exon two probes. So, we hypothesized that S and AS transcripts could physically interfere and impair riboprobe hybridization in this area. Functionally, the five situations should be considered through the narrow window of AS RNA knowledge. Several transcriptional and post-transcriptional events are candidates for the inhibition of Msx1 homeoprotein. These events have been recently reviewed and classified in four categories (5). Transcriptional interference and S gene silencing ends with exclusive expression of AS RNA. Posttranscriptional mechanisms (RNA masking and degradation) are those which involve S–AS coexpression and finely tuned ratios of S/AS transcripts or modifications in RNAs overlapping sequences. According to coexpression or distinct expression patterns of both Msx1 transcripts, the bidirectional convergent and overlapping transcription system would function differently. In the case of distinct expression pattern of S and AS transcripts, transcriptional interference or gene silencing could be implied, whereas, in the case of coexpression, RNA masking and degradation could be involved (5,66,67). Hence two types of ratio threshold could be defined. A macrothresholding when only one kind of Msx1 transcript is expressed (E9.5–E10.5) and a microthresholding (E13.5–E16.5–D0) when the two transcripts are coexpressed. Further complementary studies at the cellular level would be necessary to clearly establish the presumably distinct mechanisms.

**Natural antisense transcripts: a growing list**

The Msx1 AS transcript is not an isolated case of large natural AS RNA. Bidirectional convergent and overlapping transcription is an emerging field opening a previously unsuspected level of complexity in protein expression regulation (5). AS transcripts have been associated with different processes during development including parental imprinting (68), developmental clock control (7) and transcriptional regulation (5). The precise molecular modalities of such a control are not clarified. However, in vitro experiments have established the importance of the relative ratio of the two transcripts. This has been shown previously for Msx1 by in vivo observations of the two transcripts distribution during osteoblast differentiation process (12).

Interestingly, Msx1 is not the only gene implicated in maxillofacial and limb development showing a bidirectional convergent and overlapping transcription. Thus, homeobox containing genes belonging to the Dlx gene family have also AS transcripts. This is the case for Dlx1 (69) and Dlx6 (67) genes. AS transcripts were also described for other divergent homeobox genes as Otx2 (70) and members of the Hox clusters such as HoxA11 (11) and HoxD3 (71), raising the question of the general importance of bidirectional convergent
and overlapping transcription during development. In vitro studies have established that (i) Msx and Dlx homeoproteins can form heterodimers through their homeodomains and consequently inhibit each other’s transcriptional activity (21) (F. Lezot, unpublished data) and (ii) that Dlx5 (12) and Dlx2 (this study) homeoproteins can differentially modulated Msx1 AS transcript expression, and thus Msx1 homeoprotein expression. These in vitro observations strongly suggest that understanding AS transcript integration in developmental signaling pathways will be a difficult, but necessary challenge for the next decade. Interestingly, 9 out of 248 genes shown to be involved in tooth development (indexed on http://bite-it.helsinki.fi) have so far been shown to have AS transcripts. Moreover, computer analysis of available human and mouse genome sequences have shown that 15 and 20% of the mouse and human genes can have AS transcript, respectively (4,9). Finally it appears that the importance of AS transcripts is largely underestimated concerning development and more precisely during tooth development. ‘Making sense with antisense’ may be operative for the understanding of morphogenetic gradients in developmental biology.

ACKNOWLEDGEMENTS

We thank Drs Isabelle Miletich, Agamemnon Grigoriadis and Stephanie Ricaud for discussions and critical reading of the manuscript. This work was supported by grants of INSERM U714 laboratory, ‘ATC Viellissement 2002 INSERM’ grant to F.L. and ‘GIS Maladie Rare INSERM’ grant no. A0217715S0 to A.B. A.E.C. was a recipient of fellowship from MENRT (Ministère de la Recherche). Funding to pay the Open Access publication charges for this article was provided by INSERM U714.

Conflict of interest statement. None declared.

REFERENCES


