XHas2 activity is required during somitogenesis and precursor cell migration in Xenopus development

Michela Ori¹, Martina Nardini¹, Paola Casini¹, Roberto Perris²,³ and Irma Nardi¹,*

In vertebrates, hyaluronan biosynthesis is regulated by three transmembrane catalytic enzymes denoted Has1, Has2 and Has3. We have previously cloned the Xenopus orthologues of the corresponding genes and defined their spatiotemporal distribution during development. During mammalian embryogenesis, Has2 activity is known to be crucial, as its abrogation in mice leads to early embryonic lethality. Here, we show that, in Xenopus, morpholino-mediated loss-of-function of XHas2 alters somitogenesis by causing a disruption of the metameric somitic pattern and leads to a defective myogenesis. In the absence of XHas2, early myoblasts underwent apoptosis, failing to complete their muscle differentiation programme. XHas2 activity is also required for migration of hypaxial muscle cells and trunk neural crest cells (NCC). To approach the mechanism whereby loss of HA, following XHas2 knockdown, could influence somitogenesis and precursor cell migration, we cloned the orthologue of the primary HA signalling receptor CD44 and addressed its function through an analogous knockdown approach. Loss of XCD44 did not disturb somitogenesis, but strongly impaired hypaxial muscle precursor cell migration and the subsequent formation of the ventral body wall musculature. In contrast to XHas2, loss of function of XCD44 did not seem to be essential for trunk NCC migration, suggesting that the HA dependence of NCC movement was rather associated with an altered macromolecular composition of the ECM structuring the cells’ migratory pathways. The presented results, extend our knowledge on Has2 function and, for the first time, demonstrate a developmental role for CD44 in vertebrates. On the whole, these data underlie and confirm the emerging importance of cell-ECM interactions and modulation during embryonic development.

KEY WORDS: Has2, CD44, Hyaluronan, Somitogenesis, Myogenesis, Cell migration, Neural crest, ECM, Xenopus

INTRODUCTION

Hyaluronan (HA) is a key glycosaminoglycan (GAG) of the embryonic ECM because of its recognized importance in the correct assembly of the interstitial matrices and its putative ability to influence cell behaviour through binding to signal transducing receptors, such as CD44 and RHAMM (Lesley et al., 2000; Turley et al., 2002; Toole, 2004). Additional cellular regulatory functions of the GAG have been proposed to take place intracellularly (Lee and Spicer, 2000), but little is known about their significance. Early studies in the chick embryo strongly suggested that HA is central in creating migration- permissive microenvironments for the moving precursor cells, such as those of the peripheral nervous system, muscle and cartilage/bone (Perris et al., 1991; Perris and Perissinotto, 2000). Furthermore, the observed HA synthesis and secretion by the migrating precursor cells themselves suggest that pericellular accumulation of the GAG could favour the motile behaviour of the cells and potentially contribute to their correct homing by mediating important interactions with other ECM components (Perris, 1997; Perissinotto et al., 2000), or by triggering CD44-mediated signalling cascades (Ponta et al., 2003).

The vertebrate HA biosynthesis is governed by three catalytic enzymes that reside at the plasma membrane and are designated Has1, Has2 and Has3. The catalytic efficiency of these three enzymes seems to differ and the same applies to the composition of the HA product that they generate (Itano et al., 1999; Spicer and McDonald, 1998). In fact, HA polymers generated by Has1 and Has2 are of a similar size, reaching molecular weights of up to $2 \times 10^6$ Da, whereas Has3 polymerizes shorter chains in the range of $2.5 \times 10^5$ Dalton. The precise biological significance of these diverse catalytic properties of the Has molecules is still not fully understood, nor it is known how the expression and activity of these enzymes may be regulated at the molecular and cellular level. Moreover, the three synthases are expressed in different temporal patterns during mouse development (Tien and Spicer, 2005) and in particular Has2 has been identified as a major source of HA during initial organogenesis. Mice with a homozygous deletion of the Has2 gene manifest severe cardiac and vascular abnormalities leading to death at midgestation (E9.5-10), underpinning a pivotal role of Has2 during mammalian embryogenesis (Camenisch et al., 2000). The technical limitations in carrying out detailed analyses of the Has2 gene function by transgenic approaches in rodents have incited analogous investigations in more accessible embryos, such as that of the fish and frog. Recently, downregulation of the Has2 gene in zebrafish has been found to perturb the mesodermal cell movements responsible for the gastrulation process (Bakkers et al., 2004).

We and others have recently cloned the three known Has genes in Xenopus laevis and established their spatiotemporal distribution during early phases of development (Koprunner et al., 2000; Viggeti et al., 2003; Nardini et al., 2004). XHas1, XHas2 and XHas3 mRNAs are found to exhibit distinct and non-overlapping spatial expression patterns that differ significantly from those observed in zebrafish and which suggest an evolutionary divergence in the control of Has genes expression between tetrapods and teleosts. In particular, XHas2 is mainly found in mesoderm-derived structures, such as developing myotomes and heart anlage, and it is expressed by premigratory trunk neural crest cells (NCC). Interestingly, expression of XHas2 overlaps that of MyoD in cells committed to a muscle fate (Nardini et al., *Author for correspondence (e-mail: inardi@dfb.unipi.it)
2004). These findings have prompted us to investigate the possible role of XHas2 in somitogenesis, myogenic differentiation and trunk NCC migration, which, thus far, have not been possible to elucidate in Has2-null mice. To this end, we have also cloned the Xenopus orthologue of CD44, known to be the principal cell surface receptor of HA (Wheatley et al., 1993; Ponta et al., 2003) for which the precise role during vertebrate development still remains to be elucidated.

MATERIALS AND METHODS
Embryo manipulations and whole mount in situ hybridization
Xenopus laevis embryos obtained by hormone induced laying, were in vitro fertilized, dejellied, washed and incubated in 0.1×MMR. Embryos were staged according to Nieuwkoop and Faber (Nieuwkoop and Faber, 1967), fixed and stained for β-galactosidase (200-300 pg injected per embryo) as previously described (Sive et al., 2000) using alternatively a red or light-blue substrate for detection. Whole-mount in situ hybridization was performed on embryos fixed in MEFRA according to standard procedures (Harland, 1991). Linearized plasmid from MyoD (HindIII/T7), XCardiac Actin (PstII/SphI), Xp27 (BamHI/T7), XHas3 (BglII/SphI), XGreason (SalI/T3) were used to generate digoxigenin-11-UTP-labelled (Roche) antisense RNA probes from the polymerases indicated. BM purple (Roche) was used as substrate.

CD44 cloning and tissue distribution
The EST clone IMAGE:7008877 (NCBI GenBank Accession Number BC074228) was found to correspond to the Xenopus orthologue of CD44 receptor. The EST clone was completely sequenced and the full cDNA sequence (NCBI GenBank Accession Number DQ143881) aligned with the vertebrate CD44 orthologues using the CLUSTALW (http://www.ebi.ac.uk/CLUSTALW) software. The XCD44 cDNA sequence was found to correspond to the standard form of CD44. The coding region of XCD44 was subcloned into the pGEM-T vector (Promega) and used for preparing RNA probe for in situ hybridization from the linearized plasmid (NolI/T7). RT-PCR analyses were performed on total RNA from Xenopus embryos isolated at different developmental stages, ranging from blastula to late tailbud. The corresponding cDNAs were prepared using ImProm-II Reverse Transcriptase (Promega). Amplification of the ornithine decarboxylase gene (ODC) has been used as internal control. The following primers were used: XODC, 5′-AATGGATTTCA-GACCCA-3′ (forward) and 5′-CCAAGGTAAATGTCAGC-3′ (reverse), 25 cycles; XCD44, 5′-CACGGCGTACAGTTACGAGC-3′ (forward) and 5′-TACAGGTCTCCTGATCT-3′ (reverse), 30 cycles.

Animal cap experiments
Embryos were injected in one blastomere at the two-cell stage with 100 pg activin cDNA construct kindly provided by Jim Smith (University of Cambridge, UK), using the SP6 Cap Scribe kit (Roche). Activin-injected embryos were fixed in 4% paraformaldehyde, paraffin wax embedded and sectioned. The obtained slides were counterstained with Hoechst to allow the simultaneous visualization of normal and apoptotic nuclei.

Immunohistochemistry, BrdU incorporation and TUNEL staining
Whole-mount antibody staining was performed following standard procedures for indirect immunohistochemistry using an anti-muscle ATPase monoclonal antibody 12/101 (Developmental Studies Hybridoma Bank) at 1:10 dilution and HRP-conjugated secondary antibodies and DAB for detection. Immunostaining with the anti-phosphorylated H3 antibody was performed as described by Saka and Smith (Saka and Smith, 2001). BrdU incorporation and detection was performed essentially as previously described (Vernon and Philpott, 2003) and nuclei were counterstained with Hoechst. TUNEL staining for the identification of apoptotic cells was performed as described by Hensey and Gautier (Hensey and Gautier, 1998). After whole-mount TUNEL, XHas2-Mo injected neurula embryos were paraffin wax embedded and sectioned. The obtained slides were counterstained with Hoechst to allow the simultaneous visualization of normal and apoptotic nuclei.

RESULTS
XHas2 transcription is controlled by activin signalling during gastrulation
During Xenopus development, XHas2 expression is first detected at gastrula stage in the inverting mesoderm and is subsequently seen in the paraxial mesoderm (Nardini et al., 2004). We find here that XHas2 transcription is ectopically induced in activin mRNA-injected embryos in the ventrolateral region of the injected side demarcated by the co-injected β-gal (100%, n=50; Fig. IA,A′). This finding indicates that XHas2 is a downstream target of activin signalling and, hence, may be among the genes activated through mesoderm induction. In order to further investigate this, we compared the temporal expression profile of the XBrachyury gene, known to be a direct target of activin signalling, with that of XHas2 in animal caps. The results reported in Fig. 1B show that XHas2 transcription is activated within 1 hour of activin treatment presenting a time response behaviour similar to XBrachyury. This observation suggests that XHas2 may be a direct target of activin signalling.

mRNA and morpholino injections
The complete coding sequence of XHas2 was obtained by RT-PCR using the primers described above, on the basis of the sequence reported in NCBI GenBank (Accession Number AF168465). The PCR products were cloned into pGEM-T vector (Promega) and subsequently subcloned into the Xhol/SstI sites of the CS2 vector. The full-length clone was completely sequenced and was found to be identical to the reported sequence for XHas2 (Koprunner et al., 2000). Capped mRNAs were synthesized in vitro from nuc-β-gal (NotI/Sp6) (Chitinis et al., 1995) and from XHas2-Cs2+ (Asp718/Sp6), using the SP6 Cap Scribe kit (Roche). Sequences of the two non-overlapping XHas2 antisense morpholino oligos were: XHas2-Mo1 (5′ non-translated region of the gene), 5′-GATTATCTGGTCTGTTGTGCACACC-3′; XHas2-Mo2 (coding region from the start codon), 5′-TCATATACACCCGTATATAGCT-3′. Sequences of the two non-overlapping XCD44 antisense morpholino oligos were: XCD44-Mo1 (5′ non-translated region of the gene), 5′-TGCATATACACCCGTATATAGCT-3′; XCD44-Mo2 (coding region from the start codon), 5′-TAA-ACATCCACAGTTGGGTC-3′. A control morpholino was synthesized as a random sequence of the same length (Gene Tools, Philomath, OR). Embryos were routinely co-injected with morpholino oligos and β-gal mRNA into one blastomere at the two-cell stage in 0.1×MMR supplemented with 4% Ficoll. Rescuing experiments were performed by injecting the optimal effective dose of XHas2-Mo1 (15 ng/embryo) in conjunction with XHas2 mRNA (800-1000 pg/embryo) and β-gal mRNA.

Hyaluronan detection on tissue sections
Hyaluronan detection has been carried out using a Neurocan-GFP fusion protein kindly provided by Professor Uwe Rauch. Wild-type and XHas2-Mo injected embryos were fixed in 4% paraformaldehyde, paraformin wax embedded, processed for hyaluronan detection with the Neurocan-GFP probe essentially as described by Zhang et al. (Zhang et al., 2004), and counterstained with Hoechst.

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**Fig. 1. XHas2 is transcriptionally activated by activin.**

(A,A') Ectopic XHas2 mRNA expression in activin-injected embryos detected by whole-mount in situ hybridization. The site of injection is visualized by the Red-gal staining (red arrow). A, dorsal view; A’, lateral view. (B) Comparison of the expression profile of XBrachyury and XHas2 in animal caps following activin treatment. XODC was used as positive control. RT- indicates representative samples of RNA from activin-treated animal caps, processed without reverse transcriptase and subsequently used as a negative control for XHas2, XBrachyury and XODC amplification.

**XHas2 knockdown alters somitogenesis**

In order to address the function of the XHas2 knockdown during early phases of development, we used two different non-overlapping antisense morpholino oligos, XHas2-Mo1 and XHas2-Mo2. These were designed such as to be complementary to the XHas2 mRNA sequence in a region surrounding the translational start codon. XHas2 was targeted by injecting the morpholino oligo in one blastomere of Xenopus embryos at the two- or four-cell stages. The optimal morpholino concentration was established by independent pilot experiments and was determined to be in the range of 10-20 ng/embryo. At higher doses, the survival rate of the embryos decreased from 90-95% to 5-10% of the total number of injected embryos, whereas at lower doses we did not observe overt developmental defects. If not otherwise stated, all the experiments were performed by injecting both the morpholino oligonucleotides (indicated as XHas2-Mo) and β-gal mRNA in order to be able to select properly manipulated embryos on the basis of Salmon-gal or X-gal staining.

Knockdown of XHas2 by injection of XHas2-Mo in one of the blastomeres of two-cell stage embryos did not affect gastrulation movements, but resulted in embryos bent towards the injected side by early tailbud stages (Fig. 2A-B'). Thus, we further investigated whether the manifested phenotype of XHas2-Mo-injected embryos could depend upon altered morphogenesis of the somites. XHas2-Mo-injected embryos were processed for in situ hybridization with a cardiac actin (CA) probe, or immunostained with the 12/101 antibody, a marker of terminal muscle differentiation. Myotome alterations were observed in 75% (n>100) of the embryos injected with 15-20 ng of XHas2-Mo (Fig. 2). The effect was reproducible, but relative penetrance of the phenotype differed between embryos that were therefore arbitrarily grouped into two main phenotype classes: those exhibiting mild and those exhibiting severe developmental abnormalities. In mild phenotypes, the somite tissue of the injected side was less abundant and had lost its canonical pattern, i.e. it did not have the chevron-like shape typical of somites at this developmental stage (tailbud stages). In these embryos, somite segmentation did not seem to be overtly affected (Fig. 2A'). By contrast, in severe class phenotypes, the segmental organization of the somites appeared disrupted in the injected side: individual somites had failed to segregate and no intersomitic boundaries were discernible (Fig. 2B-D'). During Xenopus somitogenesis, segmentation is accomplished by rotation of a block of cells by 90° and myotomal cells become dorsoventrally aligned. Tissue sections from injected embryos that were double stained with the 12/101 antibody and the nuclear dye Hoechst showed a failure of the somitic cells to rotate and align, causing most cells to remain in a disorganized mass (Fig. 2C',D'). Moreover, the extension and

**Fig. 2. Myotome alterations in XHas2-Mo injected embryos.** All embryos are at stage 28-30 and are visualized by the expression of CA (A,A') and by 12/101 immunoreactivity (B, B', C, D). Red-gal staining identifies the injected side of the embryos. (A) Bending of the embryos was observed in the injected side. (A') Example of a mild class phenotype embryo; the myotome arrangement is altered in the injected side of the embryo (arrow). (B) Lateral view of the control side of a representative case of a severe class phenotype at stage 26 (arrowheads indicate the somites). (B') Injected side of the embryo in B showing a complete disruption of somites segmentation, as indicated by the arrowheads and a strong reduction in the 12/101-positive cells (compare double-headed arrows in B and B'). Red spots on the head and trunk region (Red-gal staining) identify the site of injection. (C-D') Two representative cases of severe class phenotype embryos, longitudinally sectioned and stained with Hoechst to visualize the nuclei (C', D'). (C, D) The pattern of the 12/101 positive myocytes is altered within the somites in the injected side (arrows).
intensity of staining for the muscle-specific marker 12/101 was decreased in the injected side, suggesting that terminal muscle differentiation was inhibited (Fig. 2B’-C,D).

Specificity of the observed XHas2-Mo phenotypes was asserted by the following experiments. First, the two non-overlapping morpholino oligos were found to yield analogous developmental abnormalities when injected separately (not shown). Second, a morpholino oligonucleotide of the same length as the above ones, but with a random sequence, did not have any effect. This was ascertained by the normal expression pattern of CA in embryos selected for the presence of Red-gal staining in the somites (n=150; Fig. 3A). Third, the observed phenotypic abnormalities could effectively be rescued by co-injection of XHas2-Mo1 (complementary to the non-translated 5’-UTR region) and 800/1000 pg of XHas2 mRNA. In fact, at tailbud stage, 76% of these embryos (n=80) developed normally (Fig. 3B-D).

In order to identify the developmental time-window within which XHas2-generated HA was essential for somitogenesis, we analyzed the expression of early muscle-specific markers, such as XMyoD and CA at mid-neural plate stage, corresponding to the stage at which characteristic muscle-specific genes are first detected. In situ hybridization for XMyoD and CA in XHas2-Mo-injected embryos demonstrated that loss of XHas2 function had no effect on XMyoD expression (n=175; Fig. 4A), whereas it severely affected the expression of CA in 70% of the embryos (n=111; Fig. 4B,B’). These findings suggest that HA synthesized through XHas2 may not be required for myogenic specification, but is of relevance for the differentiation of presomitic mesodermal cells into muscle cells, probably by acting as a vital constituent of their surrounding ECM.

We next asked whether the downregulation of p27 could be related to an altered proliferation, or to augmented apoptosis rate, in the presomitic mesoderm depleted of HA. To this end, we performed BrdU incorporation assays, immunohistochemistry with an anti-PH3 antibody and TUNEL assays to determine the relative levels of proliferating and apoptotic cells. We found that the amount of proliferating cells in the injected side of the neurula stage embryos was not significantly altered (n=80, Fig. 4E,F), whereas at the same stage, programmed cell death was greatly increased (70%, n=84, Fig. 4G,G’). Assessment of the relative percentage of apoptotic cells in paraxial mesoderm sections at neurula stage revealed that 30-40% of the presomitic cells were apoptotic in the injected side of the XHas2-Mo embryos (data not shown). In accordance, at early tailbud (stage 22), a clear reduction in the size of the forming somites was evident (Fig. 4D). When we carefully examined XHas2-Mo injected embryos at tailbud stages by TUNEL assay, we did not find any significant increase in the apoptotic rate in muscle cells, neither at stage 24 (n=52, Fig. 4H,H’) nor at stage 30 embryos (n=45; Fig. 4I,I’). In these embryos, a high level of apoptosis was normally found in the telencephalon with no differences between the injected
and the uninjected side of the embryo (Fig. 4I'). It may therefore be concluded that XHas2 activity plays a crucial role in preventing cells from apoptosis during a limited developmental time window that seems to concur with the early steps of myogenic differentiation.

Characterization and mRNA expression profile of XCD44

In order to shed light on the molecular mechanisms underling the HA/XHas2 function during early embryogenesis, we cloned the Xenopus orthologue of the main hyaluronan receptor, CD44, and determined its expression pattern during development. Starting from an in silico screening using the human cDNA sequence of CD44 we identified an EST clone (IMAGE ID: 4175501, partial sequence reported in GenBank: Accession Number BG657011) containing the putative Xenopus CD44 orthologue. From the complete sequencing of this clone and a comparative analysis of the sequence with that of the known vertebrate CD44 cDNAs, we were able to confirm that the identified clone corresponded to the standard form of the Xenopus hyaluronan receptor CD44 (XCD44). The deduced amino acid sequence of XCD44 encompasses a characteristic link protein domain (residues 30-119), known to be responsible for hyaluronan binding, a consensus ERM (ezrin/radixin/moesin) protein-binding motif (residues 365-374) and a C-terminal putative binding site (KIVV) for class II PDZ proteins, similar to that found in the mammalian CD44 orthologues (Thorne et al., 2004).

The transcriptional profile of XCD44 determined by RT-PCR analysis and whole-mount in situ hybridization showed that XCD44 was first transcribed at early neurula stage (stage 13) and persisted until tadpole stage 45 (Fig. 5A). At late neurula stage, the XCD44 transcript was detected in the presomitic mesoderm where it showed a segmental pattern that preceded the subsequent mesoderm segmentation and somite formation (Fig. 5B). By stage 24, XCD44 was strongly expressed in the somites (Fig. 5C) and in the cement gland, and at lower levels in the migrating cranial NCC (Fig. 5C). In tailbud embryos (stage 32), XCD44 was transcribed in the somites, in the otic vesicle and in the branchial arches (Fig. 5D), whereas later on, it was found to be downregulated in the somitic tissue, except for the dorsal somite tips, and de novo expressed in the central nervous system, notochord and migrating hypaxial muscle cell precursors (Fig. 5E). Overall, the spatiotemporal gene expression pattern of XCD44 largely overlapped that of XHas2, suggesting that the receptor could, at least in part, mediate the hyaluronan function during these stages of development.

XCD44 activity is not necessary for the early muscle differentiation and somitogenesis

Two non-overlapping morpholino oligos, XCD44-Mo1 and XCD44-Mo2, complementary to the 5'-end region of XCD44, were injected into one blastomere of Xenopus embryos at the two- or four-cell stages (15-20 ng/embryo). The downregulation experiments were performed by co-injecting a mixture of the two morpholino oligos (XCD44-Mo) that was found to yield a stronger effect and was consistently used throughout the study. β-Gal mRNA was injected with the XCD44-Mo in order to select properly manipulated embryos on the basis of the Salmon-gal or the X-gal staining. Morphological analysis of the injected embryos at tailbud stage did not reveal evident developmental abnormalities and in particular somite formation and segmentation seemed to be unaffected (Fig. 6D,D'). To detect possible alterations at cellular and molecular level in the injected side of the embryos, we further analyzed the expression of the genes involved in the early phases of myogenic commitment MyoD (n=56, Fig. 5F) and p27 (n=53; Fig. 5G), and the specific differentiation marker CA (n=60; Fig. 5H). The expression pattern of these genes at neurula stage appeared unaffected. The TUNEL assay, performed at the same stage, did not reveal any increase in apoptosis...
The apoptotic cells are in blue; red spots indicate the site of injection. -Mo injected embryo processed by TUNEL assay. whole mount in situ hybridization: (F) gal staining. The expression of the following markers was detected by neurula stage, the injected side of the embryos is visualized by the Red- arrowheads). (F-H) XCD44 expression is present in somites, cement gland (arrowhead) and, at lower level, in the cranial NCC (arrows). (C) Bisected embryo at stage 24 showing that in the trunk region XCD44 is localized exclusively in the somites. The notochord (n) at this stage does not express XCD44 mRNA. (D) Lateral view of stage 32 embryo: XCD44 mRNA is present in somites, branchial arches (arrow) and in the otic vesicle (arrowhead). A horizontal section at the level of the otic region is shown in the inset. (E) Lateral view of a stage 37 embryo showing the localization of XCD44 transcripts in the CNS (arrow), the dorsal somite tips (black arrowhead), the notochord and migrating hypaxial muscle cells (red arrowheads). (F-H) Dorsal view of XCD44-Mo injected embryos at neurula stage, the injected side of the embryos is visualized by the Red-gal staining. The expression of the following markers was detected by whole mount in situ hybridization: (F) Myod, (G) p27 and (H) CA. An example of a XCD44-Mo injected embryo processed by TUNEL assay. The apoptotic cells are in blue; red spots indicate the site of injection.

Fig. 5. XCD44 gene expression pattern. (A) XCD44 expression during Xenopus development analyzed by RT-PCR. (B) Dorsal view of a stage 20 embryo showing XCD44 mRNA localization in the presomitic mesoderm. (C) Lateral view of a stage 24 embryo: XCD44 gene expression is detected in somites, cement gland (arrowhead) and, at lower level, in the cranial NCC (arrows). (C) Bisected embryo at stage 24 showing that in the trunk region XCD44 is localized exclusively in the somites. The notochord (n) at this stage does not express XCD44 mRNA. (D) Lateral view of stage 32 embryo: XCD44 mRNA is present in somites, branchial arches (arrow) and in the otic vesicle (arrowhead). A horizontal section at the level of the otic region is shown in the inset. (E) Lateral view of a stage 37 embryo showing the localization of XCD44 transcripts in the CNS (arrow), the dorsal somite tips (black arrowhead), the notochord and migrating hypaxial muscle cells (red arrowheads). (F-H) Dorsal view of XCD44-Mo injected embryos at neurula stage, the injected side of the embryos is visualized by the Red-gal staining. The expression of the following markers was detected by whole mount in situ hybridization: (F) Myod, (G) p27 and (H) CA. An example of a XCD44-Mo injected embryo processed by TUNEL assay. The apoptotic cells are in blue; red spots indicate the site of injection.

XHas2 and XCD44 are required for hypaxial muscle cell migration

During muscle formation, a specific cell population that originates from the ventral part of each somite migrates extensively to form the ventral body wall musculature. As HA has been suggested to be fundamental for embryonic cell movements, we asked whether loss of function of XHas2 and/or XCD44 could lead to an altered migration of these hypaxial muscle cells. In 66% of XHas2-Mo injected embryos (n=145), hypaxial muscle cell precursors appeared impaired in their ventral migration and remained confined to the ventral aspect of the somite (Fig. 6A-B’), or migrated less extensively, as determined by identification of the cells through CA hybridization and 12/101 antibody staining. Moreover, in XHas2-Mo injected embryos, we analyzed the expression of XPax3, known to be transiently upregulated in the ventral part of somites before hypaxial cells migration and then its expression is maintained in the migrating hypaxial muscle cells by stage 35-37 (Martin and Harland, 2001). In XHas2-Mo-injected embryos, XPax3 expression persisted in the ventral part of somites and migrating hypaxial cells expressing XPax3 were not detectable in the injected side of the embryo (68%, n=90; Fig. 6C,C’). These observations suggested that, when deprived of XHas2, hypaxial muscle cells were unable to commence their proper migration. A summary of the data obtained in XHas2 and XCD44 loss-of-function experiments during muscle development is reported in Table 1.

We next sought to define whether the HA/XHas2 role in muscle cells mobility was mediated by the XCD44-HA interaction. The 80% of the XCD44-Mo injected embryos analyzed at stage 37 by immunohistochemistry with the 12/101 antibody (n=95) showed an altered migratory pattern of hypaxial muscle cell precursors that was highly reminiscent of that observed in the XHas2-Mo injected embryos, while the trunk muscle mass seemed to develop normally (Fig. 6D,D’). To verify whether the hypaxial muscle cells were simply delayed in their migration or whether the ventral muscle formation was finally affected, we examined the ventral body wall muscles at stage 43 (Fig. 6E,E’) and found that 70% of the XCD44-Mo injected embryos indeed failed to develop a properly organized ventral musculature (n=64; Fig. 6F,F’). These embryos therefore recapitulated the XHas2-Mo phenotype observed at this stage of development (Fig. 6G,G’).

XHas2 knock down impairs trunk neural crest cell migration

As we have previously found that XHas2 is expressed in premigratory trunk NCC (Nardini et al., 2004), we investigated here whether downregulation of the enzyme could also interfere with the migratory process of these precursor cells. XHas2-Mo-injected embryos were therefore hybridized with XGremlin to visualize migrating NCC (Hsu et al., 1998). In 70% (n=125) of these embryos, NCC failed to progress along their normal migratory pathways, resulting in randomly dispersed cells along the flank of the embryo, when compared with the control side (Fig. 7A-C). This observation did not allow us to discern if the detected phenotype was a direct consequence of the loss of XHas2 activity in NCC, or a secondary alteration resulting from the abnormal development of somites in XHas2-Mo-injected embryos. In order to approach this aspect, we performed double in situ labelling of the somites, using the muscle-specific antibody 12/101 and the XGremlin probe to detect migrating NCC. Through this analysis, we could assert that the perturbation of NCC migration was consistently associated with the somitic mass reduction and segmentation abnormalities (n=120; Fig. 7D,D’). In accordance, XHas2-Mo-injected embryos exhibiting a mild muscle phenotype did not show an altered NCC migration. Although XCD44 is implicated in cell migration and mobility, XCD44-Mo-injected embryos did not show disturbed migration of trunk NCC (Fig. 7E,E’).

DISCUSSION

Deletion of the murine Has2 gene causes early interruption of gestation due to severe cardiac defects (Camensich et al., 2000). On one hand, this finding asserts the indispensable role of HA during embryonic development but, on the other hand, it leaves the precise role of the glycosaminoglycan during embryogenesis unresolved. To address this problem, we made use of a different vertebrate model in which functional abrogation of selected genes may be effectively performed in a more accessible embryo. Thus, after having
accomplished the cloning and characterization of the expression pattern of the three known Has genes during Xenopus development (Vigetti et al., 2003; Nardini et al., 2004), we have addressed here the function of XHas2 in the early developmental processes by exploiting a targeted knockdown approach at the post-transcriptional level. Our data highlight a crucial role of HA/XHas2 in promoting survival and differentiation of myoblast cells, as well as in the somite formation. Our findings also assert a previously proposed key role for HA in mediating precursor cell migration with particular reference to muscle cell precursors of the ventral body wall and trunk NCC. Recently, a similar loss-of-function study performed in zebrafish embryos showed that Has2 knockdown affected gastrulation (Bakkers et al., 2004). However, no gastrulation defects have been detected following XHas2 knockdown in Xenopus, or deletion of the murine gene. This could in part be due to a complementary activity of Has1, which is found to be an early transcribed HA synthase both in Xenopus and mammals, but absent in the early zebrafish embryo. It may also be further speculated that such a developmentally related discrepancy in Has gene expression between tetrapods and teleosts may underlie a possible evolutionary divergence in the specific requirement of HA in different tissues and in specific time-windows of development.

During embryogenesis, HA is thought to play multiple roles in the regulation of cell behaviour which are brought about by its interaction with diverse ECM molecules, or via the direct activation of intracellular signal transductions mediated by

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<th>Table 1. Summary of the muscle phenotypes observed at different developmental stages in XHas2 and XCD44 loss of function experiments</th>
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* normal; -- reduced; + increased.
The number of processed embryos is provided in the text.
specific cell-surface receptors. Moreover, the analysis of the Has2 role during mouse heart development has shown that HA is necessary for neuregulin binding and activation of Erb receptors (Camenisch et al., 2002). To better understand the possible mechanisms involved in the HA function during Xenopus somitogenesis and cell migration events, we cloned and analyzed the role of CD44 during Xenopus development. So far, the localization of CD44 transcripts during vertebrate development has not been reported and its role during embryogenesis is still unclear.

**Activin is an upstream regulator of XHas2 transcriptional activation**

The genetic cascade upstream of the transcriptional control of Has genes in vertebrates is completely unknown. We find that in accordance with its localization in the involuting mesoderm of the gastrula, XHas2 expression is controlled by the activin signalling pathway, confirming that XHas2 transcription is associated with mesoderm formation. Furthermore, as XHas2 transcription is turned on within 1 hour of activin treatment of animal caps in vitro, it is tempting to suggest that XHas2 may represent a novel direct target of activin signalling.

**XHas2 but not XCD44 activity is required during early somitogenesis**

Tailbud Xenopus embryos that received a unilateral injection of XHas2 morpholino at the two-cell stage failed to correctly organize their flank musculature. In fact, in a mild version of the observed phenotype, embryos had smaller somites with a morphology deviating from the typical chevron-like arrangement observed in their normal counterparts. In severely affected phenotypes, the segmental organization of the myotomes appeared disrupted, with the individual somites remaining unsegregated and deprived of intersomitic boundaries. These observations raised the possibility that XHas2 abrogation, could affect the structural integrity of the inter- and intra-somitic ECM, which in turn could have interfered with the establishment of correct cell-cell contacts between the forming myoblasts (Gurdon et al., 1993; Cossu et al., 1995). In situ analyses confirmed the decreased HA accumulation within the myocyte pericellular matrix as a consequence of the XHas2 abrogation. It is also likely that this loss might has perturbed the intercellular connections that are thought to be crucial for proper formation of the somites, as cells normally undergo a coordinate 90° rotation and realign along the anteroposterior axis of the embryo (Keller, 2000).

As XHas2 is expressed in the pre-somitic mesoderm, we asserted whether altered somitogenesis caused by loss of XHas2 activity was connected to an interference with the early phases of myogenic differentiation. When examined at neurula stage, XHas2-deprived embryos showed a significant loss of MyoD expression and a substantial increase in the apoptosis confined to the region where XHas2 has been abrogated. Conversely, in the same area of the embryo, myoblast proliferation and the expression of the precocious muscle marker MyoD appeared unaffected. At the same developmental stage, we also detected a downregulation of p27, known to be a hallmark of the cell-cycle exit of myoblasts and their subsequent differentiation (Vernon and Philpott, 2003). These data strongly suggested that XHas2 activity was not essential for the early myogenic commitment, or for myoblasts proliferation, but that it was required for the survival and differentiation of the early muscle precursors. Indeed, the role of XHas2 in preventing these cells from undergoing apoptosis seems to be restricted to a specific developmental period, which coincides with the early steps of myogenic differentiation in the presomitic mesoderm. The effect of HA on survival and differentiation of presomitic mesodermal cells...
could have exerted through a structural supportive effect of the ECM, or alternatively HA produced by the myoblast cells could activate intracellular signals via binding to specific receptors such as CD44.

The pre-somitom expression of XCD44 supported the above idea and was consistent with findings in other cellular systems showing that HA-mediated activation of CD44 exerts an anti-apoptotic effect through phosphorylation of FAK, activation of RhoB (Fujita et al., 2002) and upregulation of specific anti-apoptotic genes (Marhaba et al., 2003). However, abrogation of XCD44 through morpholino injection revealed an unaffected early myogenesis and undisturbed formation of the trunk musculature at tailbud stages. Moreover, in XCD44 morpholino-injected neurula embryos, there was no increase in apoptotic rate, suggesting that the XHas2 generated HA prevented early myoblast death by a different mechanism than through CD44 signalling. However, proper assembly of the mesodermal ECM is likely to be required for bringing about community effects, for proper diffusion/gradient formation of morphogens, and/or for a normal action of other instructive signals responsible for the differentiation and survival of myogenic precursors. For example, it has been demonstrated that members of the TGFβ superfamily are more stable if complexed with HA, whereas they are rapidly degraded in matrices depleted of HA (Loci et al., 1995).

Comprehensively, our results suggest two possible scenarios for the HA/XHas2 function during muscle development. First, HA/XHas2 seem to have an early key role in the presomitom mesoderm where they support myoblast survival. XHas2 depletion alters the muscle differentiation programme leading, in turn, to the development of embryos with strongly compromised somite arrangement. Second, the mild muscle phenotype observed in some of these embryos suggested an additional later role of XHas2 in contributing to the formation of a hydrated ECM necessary for cell-cell contacts and morphogenetic movements. In this regard, it is interesting to note that the XHas2 knockdown phenotype observed at tailbud stages was highly reminiscent of the one obtained by functional abrogation of type I cadherins (Giacomello et al., 2002), or paraxial proto-cadherins (Kim et al., 2000), which are cell adhesion molecules known to be essential for somitogenesis. The possibility to abrogate gene function in a time-regulated manner in Xenopus, or through conditional gene deletion in mice should allow the clarification of this aspect.

**Hyaluronan is crucial for proper trunk NCC migration**

XHas2-deprived embryos showed altered trunk NCC migration, corroborating a proposed pivotal role of HA during NCC development (Perris et al., 1996; Perris, 1997; Perris and Perissinotto, 2000; Epperlein et al., 2000). In fact, previous experimental evidence from our group have indicated that different local accumulations of HA-versican complexes may define migration-permissive and non-permissive environments for NCC migrating in the trunk region of the embryo (Perris et al., 1991; Perissinotto et al., 2000). It is noteworthy that Xenopus migrating trunk NCC do not express XCD44 and that depletion of the receptor in somitic cells does not influence the NCC movements. Although the presence of HA in the extracellular environment seems to be crucial for allowing proper NCC migration, it is not clear if the impaired movement of trunk NCC observed in XHas2-depleted embryos was due to a failure of these cells to synthesize and secrete HA, or to a structural deficit caused by its loss from the ECM of the NCC migratory pathways. An alternative possibility could be that the altered NCC migration could result from a morphogenetic loss of the structural integrity of the somites through which the cells migrate.

As a locally and temporally controlled tissue-specific knockdown of a gene is technically difficult to accomplish in Xenopus, we performed a double in situ labelling to simultaneously visualize muscle cell and migrating trunk NCC. Although further studies are needed to fully clarify this issue, the results suggest that defective NCC migration consistently coincides with areas of severe somitic malformation. This latter result may suggest that both a correct structure of somite and a HA enrichment of the ECM, contributed by NCC and myocytes, are necessary to create a specific environmental condition necessary to allow NCC migration. It is also plausible that there may be a different threshold requirement of XHas2 activity in muscle cell precursors and NCC, whereby a partial loss of HA production may be sufficient to alter muscle formation (mild phenotype), but only a virtually complete depletion of matrix HA may interfere with both muscle development and NCC migration.

On the basis of our data, we suggest two different modes through which HA may govern cell migratory phenomena during embryogenesis: by directly influencing the migration process in cells expressing the HA receptor CD44, such as in the case of hypaxial cells; and by serving a structural function in the ECM through its linkage to different proteoglycans that may participate in the elaboration of permissive and non-permissive routes for NCC movement.
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References


