Activation of the skeletogenic gene regulatory network in the early sea urchin embryo

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SUMMARY

The gene regulatory network (GRN) that underlies the development of the embryonic skeleton in sea urchins is an important model for understanding the architecture and evolution of developmental GRNs. The initial deployment of the network is thought to be regulated by a derepression mechanism, which is mediated by the products of the pmar1 and hesC genes. Here, we show that the activation of the skeletogenic network occurs by a mechanism that is distinct from the transcriptional repression of hesC. By means of quantitative, fluorescent whole-mount in situ hybridization, we find that two pivotal early genes in the network, alx1 and delta, are activated in prospective skeletogenic cells prior to the downregulation of hesC expression. An analysis of the upstream regulation of alx1 shows that this gene is regulated by MAPK signaling and by the transcription factor Ets1; however, these inputs influence only the maintenance of alx1 expression and not its activation, which occurs by a distinct mechanism. By altering normal cleavage patterns, we show that the zygotic activation of alx1 and delta, but not that of pmar1, is dependent upon the unequal division of vegetal blastomeres. Based on these findings, we conclude that the widely accepted double-repression model is insufficient to account for the localized activation of the skeletogenic GRN. We postulate the existence of additional, unidentified repressors that are controlled by pmar1, and propose that the ability of pmar1 to derepress alx1 and delta is regulated by the unequal division of vegetal blastomeres.

KEY WORDS: Gene regulatory network, Primary mesenchyme, Sea urchin, alx1

INTRODUCTION

A prominent feature of the embryogenesis of indirectly developing sea urchins is the formation of an elaborate, calcified eskeleton. Recent studies have revealed a gene regulatory network (GRN) that controls the development of the skeletogenic large micromere primary mesenchyme cell (PMC) lineage (reviewed by Oliveri et al., 2008; Ettensohn, 2009). The PMC gene network is currently one of the most complete developmental GRNs and is being used to elucidate GRN architecture, the evolution of developmental programs, and developmental plasticity. For example, recent studies suggest that the evolution of skeletal development in echinoderms involved the co-option by the embryo of an ancestral, adult skeletogenic GRN via the invention of new regulatory connections (Gao and Davidson, 2008; Erwin and Davidson, 2009; Ettensohn, 2009). The regulative deployment of the PMC GRN in non-micromere lineages during gastrulation is a striking example of developmental plasticity, and has been shown to involve novel upstream inputs (Ettensohn et al., 2007). Such studies have focused attention on the molecular mechanisms that activate the skeletogenic GRN and highlight the need to clarify the initial regulatory inputs into this network.

The activation of the PMC GRN in the large micromere territory is dependent upon the stabilization of β-catenin. One important target of β-catenin is the transcriptional repressor pmar1, which is transiently expressed in the micromere lineage beginning at the 16-cell stage (Kitamura et al., 2002; Oliveri et al., 2002). Ectopic expression of Pmar1 causes most cells of the embryo to adopt a PMC-like fate (Oliveri et al., 2002; Oliveri et al., 2008). Because Pmar1 is a transcriptional repressor, it presumably activates the skeletogenic GRN indirectly, by blocking the expression of a second repressor. This second repressor is believed to be HesC, a member of the HES (hairy-enhancer-of-split) family (Revilla-i-Domingo et al., 2007). hesC transcripts are ubiquitous in the early embryo, but disappear from the vegetal region (including the presumptive PMCs) at the early blastula stage (Revilla-i-Domingo et al., 2007; Smith and Davidson, 2008). Overexpression of Pmar1 results in a decrease in the level of hesC transcripts, whereas morpholino (MO) knockdown of HesC leads to the ectopic expression of delta throughout the embryo and to an increase in the levels of alx1, ets1, and thr mRNAs (Revilla-i-Domingo et al., 2007). These findings support the model that the skeletogenic GRN is activated by a Pmar1/HesC double-repression ‘gate’, a model that has been widely accepted (Davidson and Levine, 2008; Oliveri et al., 2008; Ettensohn, 2009).

Alx1 is one of the earliest regulatory genes to be activated specifically in the large micromere lineage, and this gene plays a pivotal role in PMC specification (Ettensohn et al., 2003). Delta is a signaling molecule that mediates an interaction between the large micromere progeny and adjacent, non-skeletogenic mesoderm (NSM) cells (Sweet et al., 2002). The cis-regulatory control of delta has been analyzed in considerable detail (Revilla-i-Domingo et al., 2004; Smith and Davidson, 2008). By contrast, little is known concerning the regulation of the alx1 gene, other than a proposed input from the pmar1/hasC double-repression system. A positive regulatory input from ets1 has been demonstrated by MO knockdown experiments and quantitative PCR (qPCR) studies (Oliveri et al., 2008). Perturbation of Ets1 function by MO knockdown or by overexpression of a dominant-negative form of the protein blocks PMC ingestion and skeletogenesis, whereas overexpression of Ets1 transforms most cells of the embryo to a mesenchymal fate (Kurokawa et al., 1999; Rottinger et al., 2004; Oliveri et al., 2008). Rottinger et al. (Rottinger et al., 2004) provided
evidence that the phosphorylation of Ets1 by MAP kinase is essential for its function and showed that inhibition of MAP kinase signaling downregulates the expression of alx1. Together, these findings suggest that the MAP kinase pathway upregulates alx1 expression via the phosphorylation of Ets1.

The micromeres arise as a consequence of an unequal cell division at the vegetal pole. This stereotypical pattern of cleavage plays an important role in PMC specification. The unequal fourth cleavage division is a consequence of the displacement of the nuclei and mitotic spindles of the four vegetal blastomeres of the 8-cell stage embryo toward the vegetal pole (Dan and Tanaka, 1990). These cytological changes might be dependent upon a specialized microtubule attachment site in the vegetal cortex. Pharmacological agents have been used to inhibit the displacement of the mitotic spindles toward the vegetal pole, thereby equalizing cleavage and producing micromere-less embryos (Tanaka, 1976; Dan, 1979; Tanaka, 1979; Langelan and Whiteley, 1985). Micromere-less embryos show a striking reduction in the development of the skeleton. These studies preceded the recent elucidation of the skeletogenic GRN, and no linkage between unequal cleavage and specific steps in the molecular specification of PMCs has been established.

Here, we focus on the initial deployment of the large micromere PMC GRN. Our findings lead to a significant revision of the current model of the activation of this GRN. We show that the lineage-specific expression of at least two early genes in the network, alx1 and delta, occurs by a mechanism that is distinct from the transcriptional repression of hesC. We confirm that alx1 is regulated by MAPK signaling and by the transcription factor Ets1, but show that these inputs influence only the maintenance of alx1 expression, and not its activation, which occurs by a distinct mechanism. By experimentally altering normal cell division patterns, we show that the initial expression of alx1 and delta is linked tightly to the unequal cleavage of vegetal blastomeres. Surprisingly, the activation of pmar1 is not dependent upon unequal cleavage.

MATERIALS AND METHODS

Animals

Adult *Lytechinus variegatus* were obtained from the Duke University Marine Laboratory (Beaufort, NC, USA) and from Reeftopia Inc. (Key West, FL, USA). Adult *Strongylocentrotus purpuratus* were obtained from Patrick Leahy (California Institute of Technology, USA). Embryos were cultured at 23°C (*L. variegatus*) or 15.5°C (*S. purpuratus*) in temperature-controlled incubators.

Constructs and mRNA injections

Capped mRNAs were synthesized using the SP6 mMessage mMachine RNA Transcription Kit (Ambion) and were microinjected into fertilized eggs as described by Cheers and Ettensohn (Cheers and Ettensohn, 2004). A C-terminal, GFP-tagged form of Pmar1 (coding region only) was cloned into the BamHI and XhoI sites of the pCS2+ vector.

Equalization of cleavage

The fourth and fifth cleavage divisions were equalized by treating *L. variegatus* embryos for 1 hour with sodium dodecyl sulfate (SDS) at a concentration of 30 μg/ml, beginning at the 4-cell stage (Langelan and Whiteley, 1985). The embryos were then transferred to artificial sea water (ASW) without SDS and were allowed to continue development.

Polymerase chain reaction (PCR)

Total RNA was isolated using the NucleoSpin RNA II Kit (Clontech). cDNA synthesis was carried out using the RETROscript Kit (Ambion) and HiFi Taq polymerase (Invitrogen). Quantitative PCR (qPCR) was performed using an ABI 7300 real-time PCR system and SYBR-Green/ROX Master Mix (Bio-Rad). PCR primers are shown in Table S1 in the supplementary material.

Whole-mount in situ hybridization (WMISH)

Conventional WMISH was carried out as described previously (Ettensohn et al., 2007). For single-color, fluorescent WMISH (F-WMISH), embryos were incubated in a blocking buffer that comprised 5% lamb serum in phosphate buffered saline containing 0.1% Tween-20 (PBST) for 30 minutes at room temperature (RT), followed by incubation in a 1:1500 dilution of horseradish peroxidase (HRP)-conjugated anti-digoxigenin antibody (Roche) in blocking buffer for 30 minutes at RT. The embryos were then incubated in a 1:100 dilution of FITC-Tyramide Signal Amplification Solution (Fluorescein-TSA Plus Fluorescence System, PerkinElmer) in the diluting buffer provided with the kit for 4 minutes at RT. The embryos were counterstained with Hoechst 33342 (0.5 μg/ml) in PBST for 5 minutes, followed by several washes with PBST. For two-color F-WMISH, embryos were incubated overnight with a mixture of a (DIG)-11-UTP-labeled probe and a fluorescein-labeled probe. After incubating the embryos in blocking buffer as described above, the embryos were incubated in a 1:750 dilution of HRP-conjugated anti-fluorescein antibody in PBST for 2 hours, followed by a 4-minute incubation (RT) with a 1:100 dilution of Cy3-TSA in the diluting buffer provided with the kit (Cy3-TSA Plus Fluorescence System, PerkinElmer). Peroxidase activity was quenched by incubating the embryos in 5% (v/v) H2O2 in PBST for 30 minutes. The transcripts for the second gene were then detected using the HRP-conjugated anti-digoxigenin antibody and the fluorescein-TSA Plus Fluorescence System, as described above.

Microscopy and quantitative image analysis

Embryos labeled by F-WMISH were examined using a Zeiss LSM 510 metal/UV DuoScan spectral confocal microscope and a 40× oil immersion lens. Embryos that had been double-labeled with hesC and alx1 probes were used to measure the levels of hesC mRNA in the large micromere territory and in the remainder of the embryo. ImageJ was used to generate two-dimensional projections of small stacks (3-5 images with a 1 μm spacing) of confocal sections that approximately bisected the region of alx1 expression (the large micromere territory). For each projection, we used ImageJ to calculate the average pixel intensity of hesC signal in the cells that also expressed alx1 and in the remainder of the embryo. These two values were obtained from a total of 6-12 confocal image stacks, each of which was collected from a different embryo. We then calculated the mean and standard deviations of the values for the two regions and compared them using a paired, two-sided t-test. In control experiments using single probes, we confirmed that there was no detectable spillover between the alx1 and hesC channels. In addition, controls processed in the absence of probe indicated that there was no detectable background signal in either channel. In all experiments, pixel intensities were below saturation.

RESULTS

The activation of alx1 and delta precedes the clearing of hesC transcripts from the large micromere territory

Several early genes in the skeletogenic GRN, including alx1, tbr, delta and ets, are thought to be activated via the transcriptional repression of hesC (Oliveri et al., 2008). Tbr and ets mRNAs are abundant maternally and are ubiquitous in the early embryo, making it difficult to pinpoint the time at which these genes are first activated in the large micromere territory. alx1 and delta, by contrast, are expressed only zygotically. We reported previously that Spalx1 mRNA accumulates in the four large micromeres in the first cell cycle after these cells are born (Ettensohn et al., 2003). This early onset of expression suggested to us that the activation of alx1 transcription might precede the loss of hesC mRNA from vegetal blastomeres.

To compare directly the dynamic patterns of Spalx1 and SphesC expression in the same embryo, we used two-color F-WMISH. The domain of Spalx1 expression served as an unambiguous marker of the large micromere territory. Quantification of the F-WMISH signals confirmed that when Spalx1 mRNA was first detectable at
the 56-cell stage (8 hours post-fertilization, or hpf), the level of SphesC mRNA in the large micromere territory was equivalent to that in the other cells of the embryo (Fig. 1A, A', F). At the mid-blastula stage (10-12 hpf), SphesC transcripts were downregulated in the central region of the vegetal plate; i.e. in a region that contained the large micromere, as shown by a decrease in the average pixel intensity of the F-WMISH signal (Fig. 1B, B', F).

To determine whether this temporal pattern of gene expression was shared by other sea urchin species, we carried out a similar analysis using L. variegatus embryos. LvhesC was cloned using degenerate RT-PCR and RACE (random amplification of cDNA ends). A comparison between SphesC and LvhesC revealed that the two genes were ~80% identical at the nucleotide level (see Fig. S1 in the supplementary material) and showed that they encoded proteins with ~85% amino acid identity (see Fig. S2 in the supplementary material). Phylogenetic analysis using ClustalW and the Phylogenetic Analysis Using Parsimony (PAUP) software demonstrated that LvhesC and SphesC are orthologous genes (see Fig. S3 in the supplementary material). We examined the developmental expression of LvhesC by WMISH and found that the pattern was very similar to that of SphesC (see Fig. S4 in the supplementary material).

F-WMISH confirmed that Lvalx1 was activated specifically in the eight daughter cells of the large micromeres, beginning at ~5 hpf (seventh cleavage), as reported previously (Ettensohn et al., 2003). Quantitative, two-color F-WMISH showed that, at this stage, the level of LvhesC mRNA in the large micromere progeny was equivalent to that in the remainder of the embryo (Fig. 1C, C', F). At the hatched blastula stage (8 hpf), LvhesC transcripts were downregulated in the central region of the vegetal plate (Fig. 1D, D', F). LvhesC expression also declined in the apical plate region, as has been described in S. purpuratus (Smith and Davidson, 2008).

Fig. 1. Accumulation of alx1 transcripts precedes the clearing of hesC mRNA from the large micromere territory. Two-color F-WMISH was performed using digoxigenin-labeled hesC probes (green) and fluorescein-labeled alx1 or delta probes (red). Each image is a projection of 3-5 confocal sections. (A-B') Spalx1 and SphesC expression in S. purpuratus, shown at 8 hpf (56-cell stage; A, A') and 10-12 hpf (mid-blastula stage; B, B'). (C-D') Lvalx1 and LvhesC expression in L. variegatus, shown at 5 hpf (128 cell stage; C, C') and 8 hpf (mid-blastula stage; D, D'). (E, E') Ldelta and LvhesC expression at 5 hpf (128-cell stage). Arrowheads in B' and D' indicate the vegetal region of hesC clearing. (F) Quantification of hesC F-WMISH signal. Average pixel intensities were determined for the large micromere territory (i.e. the alx1-expressing region) and for the remainder of the embryo, as illustrated in A and A' (see Materials and methods). For each species and time point analyzed, data from 6-12 different embryos were used to calculate mean average pixel intensities for the two regions (red and green bars). Black bars show standard errors. (G, H) qPCR analysis of alx1, delta and hesC expression in S. purpuratus (G) and L. variegatus (H). For each time point, the average Ct value for each gene was normalized against the average Ct value of an internal standard mRNA (ubiquitin for L. variegatus and z12 for S. purpuratus). Values shown on the y-axis reflect relative numbers of hesC transcripts at the various stages, with the maternal expression level arbitrarily set to 1.
These studies confirmed that in *L. variegatus*, as in *S. purpuratus*, *alx1* was activated selectively in the large micromere progeny prior to the clearing of *hesC* transcripts from these cells.

In *L. variegatus*, expression of *delta* in the large micromere territory begins at ~5 hpf (Sweet et al., 2002). We carried out two-color F-WMISH analysis of *L. variegatus* embryos labeled with *Lvdelta* and *LvhesC* probes, and found that expression of *LvDelta* in the large micromere territory also preceded the clearing of *LvhesC* transcripts from the vegetal region (Fig. 1E,E′). Although we did not carry out equivalent, double-label F-WMISH studies of *delta* and *hesC* expression in *S. purpuratus*, it has already been reported that *Sdelta* is first transcribed at the late fifth cleavage stage (8 hours to 8 hours, 40 minutes after fertilization) (Smith and Davidson, 2008). This is the same cleavage division at which we first detect Spalx1 expression in the large micromeres, and 2-3 hours before *S hesC* mRNA clears from the micromere territory (Fig. 1A,A′,F). Therefore, these studies indicate that at least two early genes in the skeletogenic GRN, *alx1* and *delta*, are activated in the large micromeres prior to any measurable decline in *hesC* transcript levels.

In *S. purpuratus*, *hesC* transcripts are present maternally at relatively low levels (~500 transcripts/egg) and increase sharply in abundance beginning at about the 56-cell stage, indicating that zygotic transcription of the gene is taking place by this stage (Revilla-i-Domingo et al., 2007). We used qPCR to compare directly the temporal patterns of *hesC*, *alx1* and *delta* expression in both *S. purpuratus* and *L. variegatus* (Fig. 1G,H). Activation of *alx1* and *hesC* transcription occurred at approximately the same time in both species, while *delta* lagged slightly behind. Significantly, at the same developmental stages that were used for our quantitative F-WMISH analysis of *hesC* expression prior to vegetal clearing (i.e. at 8 hpf in *S. purpuratus* and 5 hpf in *L. variegatus*), *hesC* transcript levels were more than 10-fold higher than maternal levels. Therefore, these qPCR studies showed that, in both species, *hesC* transcripts that were visualized by F-WMISH at the developmental stages shown in Fig. 1 were predominantly zygotic in origin. We conclude that *hesC* is transiently transcribed in the large micromere territory and that the lineage-specific activation of the skeletogenic GRN occurs at a stage when *hesC* mRNA is uniformly distributed throughout the embryo.

**Ets1 is not required for the onset of Lvalx1 expression, but is required for its maintenance**

The observation that *Lvalx1* is activated before the clearing of *LvhesC* transcripts from the large micromere territory prompted us to examine other factor(s) that might trigger the onset of *Lvalx1* expression. Ets1 has been identified as a positive regulator of *alx1* (Rottinger et al., 2004; Oliveri et al., 2008) and the presence of maternal *ets* transcripts was demonstrated previously in the sea urchin (Kurokawa et al., 2000; Oliveri et al., 2008). To test whether maternal Ets1 protein plays a role in activating *alx1*, we carefully compared the spatial and temporal patterns of expression of the mRNAs and proteins encoded by *Lvets1* and *Lvalx1*. WMISH studies confirmed that *Lvets1* mRNA was expressed ubiquitously in *L. variegatus* embryos until ~6 hpf (mid-blastula stage; Fig. 2A). At this developmental stage, very strong expression of *Lvalx1* mRNA was apparent in the large micromere territory in sibling embryos (Fig. 2C). At the hatched blastula stage (8 hpf), *Lets1* mRNA, like *Lvalx1* mRNA, was restricted to the large micromere lineage (Fig. 2B,D).

We used a polyclonal antiserum that recognizes LvEts1 (Ettensohn et al., 2007) to examine the distribution of this protein at different developmental stages. Immunostaining studies showed that LvEts1 was not detectable in nuclei at 6 hpf (Fig. 2E). At 8 hpf, however, the protein was concentrated in the nuclei of every blastomere and was visibly enriched in the nuclei of the large micromere progeny (Fig. 2F). We considered it probable that this dominant-negative form would interfere with the function of both maternal and zygotic pools of endogenous LvEts1 protein. Consistent with previous findings in a different species (Kurokawa et al., 1999), embryos injected with mRNA encoding dnLvEts1 failed to form PMCs and completely lacked skeletal elements, even after prolonged periods in culture (Fig. 3A,B). F-WMISH analysis showed, however, that there was no change in *Lvalx1* expression at 6 hpf in dnLvEts1-expressing embryos as compared with sibling control embryos that had been injected with 20% glycerol (Fig. 3C,E). Soon thereafter,
the expression of \textit{Lvalx1} declined markedly in embryos expressing d\textit{nLvEts1}, and by 8 hpf, \textit{Lvalx1} transcripts were no longer detectable by F-WMISH (Fig. 3D,F). These findings indicate that \textit{LvEts1} is required for the maintenance, but not for the activation, of \textit{Lvalx1} expression.

Misexpression of wild-type \textit{Ets1} results in the formation of supernumerary mesenchymal cells (Kurokawa et al., 1999; Rottinger et al., 2004). The precise fate of these cells is unclear; it has been reported that they express some skeletogenic genes but not others (Kurokawa et al., 1999). Based on these findings, it seemed possible that misexpression of \textit{Ets1} might be sufficient to activate \textit{alx1} in non-micromere-derived cells. We tested this possibility by injecting mRNA (8 mg/ml) encoding wild-type \textit{LvEts1} into fertilized eggs. We chose this concentration because it reliably induced the formation of large numbers of supernumerary mesenchymal cells in ~75-80\% of injected embryos. \textit{Lvalx1} expression was analyzed by WMISH at the hatched blastula stage and during the phase of supernumerary mesenchymal cell ingestion. These studies showed that there was no expansion of the expression domain of \textit{Lvalx1} at either developmental stage (Fig. 4C,D). In contrast, >50\% of the injected embryos showed a moderate reduction in the number of cells expressing \textit{Lvalx1} as compared with sibling uninjected embryos (n=35 at each developmental stage). We also examined skeletogenic specification in these embryos by immunostaining with monoclonal antibody 6a9, an antibody that recognizes MSP130 family proteins. Again, we observed no increase in the numbers of skeletogenic cells (data not shown). These findings indicate that the striking conversion of cells to a mesenchymal phenotype induced by the misexpression of \textit{Ets1} is not accompanied by the ectopic activation of \textit{alx1}. Taken together, our studies suggest that \textit{LvEts1} is neither necessary nor sufficient for the initial activation of \textit{Lvalx1}, although the protein plays an important role in maintaining \textit{Lvalx1} expression in the large micromere territory.

**MAPK signaling is required for the maintenance, but not for the activation, of \textit{Lvalx1} expression**

Rottinger et al. (Rottinger et al., 2004) showed that \textit{alx1} expression was inhibited when embryos were treated with U0126, a MEK inhibitor. They provided evidence that one important role of MAPK signaling is to promote the phosphorylation of \textit{Ets1}. Previous work showed that U0126 has the same general effects on embryonic development (i.e. a complete inhibition of PMC formation and skeletogenesis) in \textit{L. variegatus} as it does in other species, and is effective at similar concentrations (Ettensohn et al., 2007). We analyzed the effect of U0126 on \textit{alx1} expression in \textit{L. variegatus}, focusing specifically on the initial phase of expression. Embryos treated continuously with 6 μM U0126 from the 2-cell stage exhibited strong \textit{Lvalx1} expression at 7 hpf (late blastula stage) (Fig. 5C). Such embryos were indistinguishable from control embryos treated with DMSO alone (Fig. 5A). By contrast, by 9 hpf (hatched blastula stage), no \textit{Lvalx1} expression was detectable in U0126-treated embryos (Fig. 5B,D). The effects of U0126 on \textit{Lvalx1} expression were therefore very similar to those of \textit{dnlvEts1} and reinforced the view that the activation and the maintenance of \textit{Lvalx1} expression are controlled by different mechanisms.

**The expression of \textit{Lvalx1} and \textit{Lvdelta}, but not that of \textit{Lypmar1}, is dependent upon unequal cell division**

To determine whether the unequal cleavage divisions that occur at the vegetal pole influence the activation of \textit{alx1} expression, we equalized both the fourth and fifth cleavage divisions using low

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**Fig. 3. LvEts1 is required for the maintenance, but not for the activation, of \textit{Lvalx1} expression.** (A) Control pluteus larva at 72 hpf. Arrowhead indicates skeletal rods. (B) Sibling embryo expressing \textit{dnlvEts1}, also at 72 hpf. \textit{dnlvEts1} mRNA-injected embryos fail to form skeletal elements even after prolonged periods in culture. (C-F) \textit{Lvalx1} expression in embryos overexpressing \textit{dnlvEts1}. (C,D) Control embryos injected with 20\% glycerol alone and examined at 6 hpf (mid-blastula stage; C) and 8 hpf (hatched blastula stage; D). (E,F) Embryos injected with \textit{dnlvEts1} mRNA and examined at 6 hpf (E) and 8 hpf (F). Each panel is a merged image of a 2-projection of several confocal slices and a single DIC image taken at the midpoint of the stack. \textit{dnlvEts1} mRNA-injected embryos exhibit normal levels of \textit{Lvalx1} expression at 6 hpf (compare C with E), but by 8 hpf, \textit{Lvalx1} expression is no longer detectable (compare D with F).

**Fig. 4. Misexpression of \textit{Lvets1} mRNA converts many cells of the embryo to a mesenchymal fate but \textit{Lvalx1} expression remains restricted to the large micromere lineage.** \textit{Lvalx1} expression was examined in \textit{Lvets1} mRNA-injected embryos when sibling control embryos were at the mesenchyme blastula (MB) or early gastrula (EG) stages. (A,B) Control embryos showing normal expression of \textit{Lvalx1} at the MB stage (A) and the EG stage (B). (C,D) \textit{Lvets1} mRNA-injected embryos showing that \textit{Lvalx1} expression is restricted to the PMCs at the MB stage (C) and later in development, when additional mesenchymal cells form (D).
Fig. 5. The MAPK pathway is required for the maintenance of Lvalx1 expression. Embryos were treated with 6 μM U0126 and Lvalx1 expression was assayed at 7 hpf (hatched blastula stage) and 9 hpf (pre-ingression blastula stage). Each panel is a merged image of z-projections of confocal stacks (green, Lvalx1; blue, Hoechst). (A, B) DMSO-treated control embryos showing normal Lvalx1 expression (green) at 7 hpf (A) and 9 hpf (B). (C, D) U0126-treated embryos showing normal expression of Lvalx1 at 7 hpf (C) but a striking loss of Lvalx1 expression by 9 hpf (D).

concentrations of SDS. Approximately 72% of SDS-treated embryos (L. variegatus) underwent an equal fourth cleavage division and ~67% of the treated embryos underwent equal divisions at both the fourth and fifth cleavages (Fig. 6A-D). The remaining embryos formed variable numbers of micromeres. As reported by Langelan and Whiteley (Langelan and Whiteley, 1985), SDS-treated embryos lacked PMCs, gastrulated in a delayed fashion and formed spicules after a considerable delay (Fig. 6E-H). Skeleton formation in these embryos was probably a consequence of the transfating of non-micromere-derived cells. F-WMISH analysis of SDS-treated embryos revealed a striking reduction in Lvalx1 expression (Fig. 7D,E) compared with sibling controls (Fig. 7A,B) at 8 hpf (hatched blastula stage) and 10 hpf (pre-ingression blastula stage). Only 30-35% of the SDS-treated embryos exhibited any detectable Lvalx1 expression at these stages. At 12 hpf, when sibling control embryos were at the mesenchyme blastula stage (Fig. 7C), Lvalx1 expression was detectable in ~50% of the SDS-treated embryos, but usually in a much smaller number of cells than in control embryos (Fig. 7F). The residual expression of Lvalx1 at early developmental stages in SDS-treated embryos is probably a consequence of the incomplete effect of the detergent on the pattern of cleavage.

We next asked whether the effect of the cleavage pattern on Lvalx1 activation might be mediated by pmar1. Two hundred control embryos and 200 sibling SDS-treated embryos were collected at 6 hpf (mid-blastula stage) and the expression of Lvpmar1, Lvalx1 and Lvdelta was assessed by RT-PCR using equivalent serial dilutions of the cDNA samples. SDS had no effect on Lvpmar1 expression, but the expression of Lvalx1 and Lvdelta was clearly reduced (Fig. 7G). We also examined Lvpmar1 expression at earlier developmental stages (3-4 hpf) and found, in three independent trials, that equal cleavage had no effect on transcript levels (data not shown). The effect of SDS on Lvpmar1, Lvalx1 and Lvdelta expression was confirmed by qPCR (Fig. 7H). These experiments showed that, although pmar1 is ordinarily expressed specifically in the micromeres immediately after they form, unequal cleavage is not required for the transcriptional activation of this gene. The level of Lvpmar1 expression on a per-embryo basis was not affected by SDS-treatment, but the level of expression per cell might have been altered owing to changes in cell size. Unlike Lvpmar1, Lvalx1 and Lvdelta were dependent on unequal cell division for their activation; this might have been a consequence of changes in the level of pmar1 expression per cell, or could have occurred by other mechanisms.

Pmar1 protein is stable in both the large and small micromeres. Pmar1 mRNA is detectable in the micromeres immediately after they are born and continues to be expressed in both the large and small micromeres until the blastula stage (Oliveri et al., 2002). By contrast, alx1 and delta are activated specifically in the large micromeres and are restricted to this lineage throughout later development (Sweet et al., 2002; Ettensohn et al., 2003). Misexpression studies show that Pmar1 is sufficient to activate the GRN widely throughout the embryo; why then does Pmar1 not ordinarily activate alx1 and delta in the small micromeres? One possibility is that, despite the presence of pmar1 mRNA in the small micromeres, post-transcriptional mechanisms prevent the accumulation of functional Pmar1 protein in these cells.
First, to further support the idea that pmar1 provides a positive regulatory input into alx1, we used F-WMISH to show that overexpression of Lvpmar1 was sufficient to activate Lvalx1 throughout the embryo (Fig. 8A,B). This finding supported earlier studies demonstrating an increase in alx1 mRNA levels as measured by qPCR (Ettensohn et al., 2003), and experiments showing that misexpression of pmar1 induces the ectopic activation of delta (Oliveri et al., 2002). Selective protein degradation regulates the expression of other transcription factors in the sea urchin embryo (Weitzel et al., 2004; Angerer et al., 2005). Therefore, to test whether Pmar1 might be selectively degraded in the small micromeres, we microinjected mRNA encoding a GFP-tagged form of LvPmar1 (cDNA region only) into fertilized eggs and monitored the expression of fluorescent protein in living embryos by confocal microscopy. LvPmar1-GFP was expressed in all cells of the embryo during cleavage, including both the large and small micromere lineages (Fig. 8C,D), and continued to be stably expressed in both territories until at least the blastula stage, after the onset of Lvalx1 expression. This pattern of protein expression contrasts with that of other GFP-tagged transcriptional regulators; for example, β-catenin-GFP is rapidly degraded in animal blastomeres during early cleavage (Weitzel et al., 2004). These findings argue against the hypothesis that LvPmar1 is degraded selectively in the small micromeres and indicate that other mechanisms prevent the activation of the GRN in these cells.

**DISCUSSION**

Much progress has been made in dissecting the GRN that underlies the development of the skeletogenic primary mesenchyme (Oliveri et al., 2008; Ettensohn, 2009). The identification of Pmar1 as an important early activator of this pathway, combined with evidence that this protein functions as a transcriptional repressor, led to the hypothesis that Pmar1 activates the GRN by blocking the expression of a second repressor. HesC has been identified as this second repressor based on the following criteria: (1) hesC transcript levels are downregulated following forced misexpression of Pmar1; (2) hesC transcripts disappear from the micromere territory during early development; and (3) MO-mediated inhibition of HesC translation results in an increase in mesenchymal cells and in the ectopic expression of delta (Revilla-i-Domingo et al., 2007). Based on these findings, hesC has been considered the linchpin of a double-repression gate, and the evolutionary invention of the pmar1/ hesC gate has been put forward as a pivotal event during the evolution of skeletogenesis in sea urchins (Davidson and Levine, 2008; Gao and Davidson, 2008).

Our WMISH studies show that the activation of alx1 and delta selectively in the large micromere territory occurs prior to the clearing of hesC mRNA from these cells. We considered the possibility that maternal hesC transcripts might be non-translatable, or could encode a non-functional form of the HesC protein, and that WMISH signal from maternal transcripts might prevent us from detecting a local repression of zygotic hesC transcription. qPCR studies, however, showed that levels of maternal hesC transcripts were low (see also Revilla-i-Domingo et al., 2007) and that at the developmental stages that were used for quantitative F-WMISH analysis, most hesC transcripts were zygotic in origin. Therefore, our combined qPCR and WMISH data indicate that hesC is transiently transcribed in the large micromere territory and that alx1 and delta are expressed selectively by these cells at a stage when zygotic hesC transcripts are ubiquitous. Our qPCR analysis also showed that the activation of alx1 occurred at approximately the same time as the activation of hesC (Fig. 1G,H). It is therefore difficult to envision how regional differences in hesC transcription, which would require some time to produce differences in HesC protein levels, could influence the early spatial pattern of alx1 expression. These considerations, however, do not preclude an essential role for hesC repression in the later maintenance phase of alx1 expression (see below).
Considerable evidence indicates that pmarl is a pivotal regulator of the micromere-PMC GRN. Misexpression of pmarl is sufficient to activate the skeletogenic GRN in non-micromere-derived cells (Oliveri et al., 2002; Oliveri et al., 2003; Nishimura et al., 2004; Yamazaki et al., 2005; Yamazaki et al., 2009) (this study). It has been more difficult to test directly the function of pmarl in the large micromere territory (where the gene is ordinarily expressed) owing to the difficulty in blocking the expression of multiple tandem pmarl genes using MOs. A VP16-Pmar1 fusion protein, which probably acts in a dominant-negative fashion, blocks PMC formation and reduces the levels of several skeletogenic mRNAs, at least at late developmental stages (Yamazaki et al., 2005). This loss-of-function analysis supports the view that pmarl is required for the deployment of the skeletogenic GRN in the large micromere territory. Pmar1 (a known repressor) presumably mediates the activation of alxl, delta and other early genes in the network by blocking the expression of a second repressor, as discussed by Oliveri et al. (Oliveri et al., 2002). Our findings therefore point to one of two possibilities: (1) the existence of an as-yet-unidentified repressor downstream of pmarl but distinct from hesC, or (2) a pmarl-independent mechanism of GRN activation, which might be reinforced later in development by the pmarl-hesC derepression system.

The conclusion that the skeletogenic GRN is activated by mechanisms that are independent of hesC repression seems at odds with evidence that inhibition of hesC function is sufficient to activate the GRN ectopically (Revilla-i-Domingo et al., 2007; Smith and Davidson, 2008). It should be noted that in a recent structure-function analysis of Pmar1, one mutant construct (N-HD-A-C) that lacked a portion of the C-terminal region of the protein was reported to downregulate hesC mRNA levels throughout the embryo without expanding the expression of alxl, tbr or etsl (Yamazaki et al., 2009).

This observation suggests that downregulation of hesC might not be sufficient to activate the skeletogenic GRN in non-micromere lineages. If, as the earlier data suggest, inhibition of hesC function is sufficient to activate the network, then one interpretation is that alxl, delta and other early genes can be activated by more than one regulatory mechanism. According to this view, the repression of hesC is sufficient to activate these genes in non-micromere lineages, but during normal development (i.e. in the large micromere lineage), a separate regulatory pathway is used very early in development that activates the network, essentially bypassing hesC repression, which is relegated to a maintenance function. A prediction of this view is that genes such as alxl and delta will have multiple activation modules, any one of which can activate transcription once engaged. The cis-regulatory architecture of alxl has not been described, but delta has been analyzed extensively in this regard (Revilla-i-Domingo et al., 2004; Revilla-i-Domingo et al., 2007; Smith and Davidson, 2008). Consistent with the above model, two separate regulatory modules have been identified that are sufficient to drive expression of delta in the micromere territory; both modules are responsive to pmarl but only one contains putative HesC binding sites.

Our findings reinforce the view that the activation and the maintenance of alxl expression are controlled by very different mechanisms. Positive inputs into alxl from MAP kinase signaling and from etsl (inputs that might be related to one another) regulate the maintenance, but not the onset, of alxl expression. One essential early input into alxl that we have identified is a cellular, rather than molecular, one; namely, the unequal cleavage of vegetal blastomeres. It was shown previously that PMC specification is influenced by the cleavage pattern (Langeland and Whiteley, 1985), but this work predated the elucidation of the skeletogenic GRN, and ours is the first effort to analyze the molecular step(s) at which unequal cell division impinges on the network. Surprisingly, although pmarl is ordinarily activated in the micromeres immediately as they form, unequal cleavage is not required for the transcriptional activation of pmarl. Instead, a molecular step between pmarl expression and the activation of alxl and delta is linked to unequal cleavage. Whatever the regulatory connection, it is likely to be a novel feature of echinoderm development. The embryos of a related group of echinoderms, the ophiuroids (brittle stars), exhibit equal cleavage, but nevertheless form PMCs and an embryonic skeleton [see Tominaga et al. (Tominaga et al., 2004) and references therein]. Evolution has evidently experimented freely with the upstream regulation of the skeletogenic GRN (Gao and Davidson, 2008; Ettensohn, 2009).

A key unanswered question is why the skeletogenic GRN is activated only in the large micromere territory, when pmarl mRNA is present in both the large and small micromeres (Oliveri et al., 2002). A variety of mechanisms can be envisioned that involve the asymmetric segregation of polarized maternal determinants, differences in nucleus-to-cytoplasm ratio and other mechanisms. Interestingly, during normal development, hesC expression persists in the small micromere territory after it is extinguished elsewhere in the vegetal plate (see Fig. S4 in the supplementary material) (Smith and Davidson, 2008). This suggests that Pmar1 protein is not present (or is inactive) in the small micromeres. Other transcriptional regulators undergo polarized, proteolytic degradation along the animal-vegetal axis of the sea urchin embryo (Weitzel et al., 2004; Angerer et al., 2005). Our analysis of the expression of Pmar1-GFP argues against the hypothesis that this protein is selectively degraded in the small micromeres, but other modes of post-transcriptional
regulation might be involved. Even if Pmar1 protein is present in the nuclei of both large and small micromeres, separate regulatory mechanisms might operate in the small micromeres that override the double-repression system and prevent the deployment of the skeletogenic GRN. The small micromeres express several germline markers (Juliano et al., 2006; Voronina et al., 2008) and in other animals the prospective germline is globally transcriptionally repressed during early development (Nakamura and Seydoux, 2008).

The regulative deployment of the skeletogenic GRN by NSM cells requires the ectopic activation of alx1 via novel, pmar1-independent regulatory inputs (Ettensohn et al., 2007; Ettensohn, 2009). Several of the molecular conditions that might be envisioned to be required for the expression of alx1 (i.e. activation of MAPK, expression of Ets1 and downregulation of hesC) appear to ordinarily be present in NSM cells, yet alx1 is not expressed. Although it has not been tested directly, it seems unlikely that unequal cell division, which is essential for the activation of alx1 in the micromere lineage and is a consequence of maternal cortical polarity, plays a role in the ectopic activation of alx1 in transfating cells. Further analysis of the molecular mechanisms that activate the skeletogenic GRN, and the identification of additional inputs that are unique to the endogenous or regulative pathways, will shed light on this example of developmental plasticity.

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