INTRODUCTION

How a continuum of founder stem cells generates distinct phenotypic classes of differentiating cells during organogenesis is a question of major interest in developmental biology. During Drosophila neuroblast divisions, the temporal expression of Pou domain and zinc finger transcription factors governs the neural identity of daughter cells, which is subject to their spatial identity (Kambadur et al., 1998; Ishikii et al., 2001; Grosskortenhaus et al., 2006). Similarly, in the vertebrate CNS, radial glial cells generate distinct neurons that are spatially specified largely via an interplay between homeodomain and bHLH transcription factors (Maurange, 2012). Although less complex in terms of cellular diversity, little is known about the generation of distinct classes of committed progeny during vertebrate skeletal muscle development.

Skeletal muscle founder stem cells in the body arise from a transient epithelial dermomyotome (DM) within somites and express the paired box/homeodomain transcription factors Pax3 and Pax7 (Ben-Yair and Kalcheim, 2005; Kassar-Duchossoy et al., 2005; Relaix et al., 2005). They undergo myogenic specification to give rise to muscle progenitor cells by sequential expression of the bHLH myogenic regulatory factors (MRFs) Myf5, Mrf4 (also known as Myf6) and Myod, and, subsequently, the differentiation gene myogenin (Myog) (Rudnicki et al., 1993; Kassar-Duchossoy et al., 2004; Tajbakhsh, 2009). During early embryonic stages, Pax7 marks bi-potent cells in the DM that can give rise to muscle and dermis (Ben-Yair and Kalcheim, 2005; Lepper and Fan, 2010). Dermal stem/progenitors later downregulate Pax7 expression, in contrast to myogenic stem/progenitors, which maintain high levels of Pax7 during embryonic, foetal and postnatal myogenesis. This marker is then downregulated during myoblast differentiation (Tajbakhsh, 2009; Murphy and Kardon, 2011). Notably, embryonic [embryonic day (E) 9-14.5] and foetal (E14.5-18.5) myoblasts and differentiated cells are molecularly and phenotypically distinct (Cusella-De Angelis et al., 1994; Biressi et al., 2007a; Tajbakhsh, 2009). Embryonic myoblasts in the mouse fuse to form primary fibres from E11 and they establish the basic muscle pattern. Foetal myoblasts appear from E14.5 and subsequently form larger secondary fibres, and, unlike their embryonic counterparts, their differentiation is blocked by Tgfβ and β-catenin (Cusella-De Angelis et al., 1994; Hutcheson et al., 2009). Juvenile satellite cells are then observed under the myofibre basement membrane from E16.5 and they act as reservoirs of quiescent adult muscle stem (satellite) cells from 3 weeks postnatally. Although it is thought that a continuum of stem cells that resists differentiation assures these waves of distinct myogenic populations (Gros et al., 2005; Kassar-Duchossoy et al., 2005; Relaix et al., 2005; Tajbakhsh, 2009; Murphy and Kardon, 2011) and that distinct transcriptome dynamics defines their progeny (Biressi et al., 2007b), little, if any, information is available on how these processes are regulated within muscle stem/progenitor cells. The identification of the transcription factor Nfix, which regulates...
foetal and suppresses embryonic myoblast fate, was a major step in understanding how downstream muscle progenitor cell fate decisions are mediated (Messina et al., 2010).

The Notch signalling pathway plays crucial roles in regulating the fate of stem cells in diverse tissues in metazoans (Fre et al., 2005; Androussis-Theotokis et al., 2006; Louvi and Artavanis-Tsakonas, 2006; Farme and Clarke, 2007). Notch was shown to be essential for myogenic stem cell fate and differentiation throughout embryogenesis and in the adult, as both embryonic and adult muscle stem cells mutant for Rbpj, the downstream effector of canonical Notch signalling, differentiate precociously (Kuang et al., 2007; Schuster-Gossler et al., 2007; Vasyutina et al., 2007; Brack et al., 2008; Bjornson et al., 2012; Mourikis et al., 2012). It has been demonstrated that differentiating myogenic cells upregulate the Notch ligand delta-like 1 (Dll1) and stimulate Notch activity in the upstream population to assure their maintenance (Delfini et al., 2000; Hirsinger et al., 2001; Schuster-Gossler et al., 2007; Mourikis et al., 2012), in accordance with what has been shown in the nervous system (Henrique et al., 1997; Dong et al., 2012). Consistent with this notion, our previous studies have indicated that the muscle stem cell population requires the presence of differentiating cells for their maintenance, such that a lack of differentiated cells results in the loss of upstream Pax7+ cells in the foetus (Kassar-Duchossoy et al., 2005). Although active Notch signalling has been shown to block myogenic differentiation (Kopan et al., 1994; Shawber et al., 1996; Delfini et al., 2000; Hirsinger et al., 2001; Sun et al., 2008), a recent study in dorsal somitic muscle progenitor cells in the chick embryo reported that transient, but not sustained, activation of Notch is required for the expression of Myod and Myf5 and for lineage commitment and differentiation (Rios et al., 2011). In addition, Notch signalling influences lineage diversification in the multipotent cells of the dorsal DM, where specifically in the lateral DM its activity biases progenitors toward a smooth muscle fate (Ben-Yair and Kalcheim, 2008). Therefore, although numerous studies point to Notch as a crucial regulator of myogenesis, it is not clear how this or other signalling pathways impact on the temporal release of distinct myogenic cells in vivo.

Using a combination of genetic tools and transcriptome analysis, we show that Notch is active throughout development in the muscle founder stem cell population. We demonstrate that constitutive Notch activity is sufficient to autonomously maintain and self-renew muscle stem/progenitor cells, in spite of the complete abrogation of committed and differentiated cells. Notably, we demonstrate that these replicating embryonic stem/progenitors respond to foetal environmental cues as development proceeds, and, despite the ectopic expression of markers of the adipocyte, pericyte and osteoblast lineages, they adopt a foetal muscle fate after the release of Notch activity.

MATERIALS AND METHODS

Animals

Mouse line Tg:Pax7-nGFP was described previously (Sambasivan et al., 2009). Reporter line R26R(CreERT2stop-mEGFP) (R26R(TmCE)) (Muzumdar et al., 2007) was purchased from Jackson Laboratories (stock 007576). Cre recombinase lines were described and kindly provided by the corresponding laboratories: Myf5Cre [M. R. Capecchi (Haldar et al., 2008)]; En1Cre [A. Joyner (Kimmel et al., 2000)]; R26R(Cre) (P. Soriano (Soriano, 1999)]; R26R(Cre-EGFP) [J. P. Martinez-Barbera (Ivanaova et al., 2005)]; R26R(Cre-NCAM-EGFP) [D. Melton; Jackson Laboratories, stock 008159 (Murtaugh et al., 2003)]; RbpjF/+ [T. Honjo (Han et al., 2002)]. Animal experiments were performed as per European Community guidelines.

Immunofluorescence and imaging

Embryos were fixed for 1 hour in 2% paraformaldehyde and 0.1% Triton X-100 and equilibrated in 15% sucrose/PBS overnight. Samples were embedded in 7% gelatin/15% sucrose, frozen in a 2-methylbutylate liquid nitrogen bath and cryosectioned at 16-20 µm. Antibodies used were: GFP (chicken: Abcam 13970; 1/1000); Pax7 [rabbit (Aviva Biosystems AR32742; 1/750) and mouse (DSHB; 1/20)]; Myod (mouse: Dako M3512; 1/50); myogenin (DSHB F5; 1/100); Myf5 (Santa Cruz Biotechnology sc-302; 1/1200); MyHC (rabbit; kindly provided by G. Cossu, University College London, UK; 1/750); p57 (Santa Cruz Biotechnology sc-8298; 1/200); Nfix (gift from G. Messina, University of Milan, Italy; 1/300); Me2c2 (gift from S. Molinari; Cell Signaling 5030; 1/100); calcitonin receptor (AbD Serotech AHP635; 1/100); laminin (Sigma 9393; 1/1000). Confocal images were acquired using a Leica SPE confocal microscope and Leica Application Suite (LAS) or Zeiss Axioplan and Axiovision software. Images were assembled using Adobe Photoshop and Adobe InDesign.

Quantitative RT-PCR (RT-qPCR)

To maximise recovery, total RNA was extracted from FACS-isolated cells directly into the cell lysis buffer (RLT) of the Qiagen RNeasy Micro Kit. The equivalent of 1.5×10⁶ cells were used for transcript amplification. cDNA was prepared by random-primed reverse transcription (Super Script II, Invitrogen 18064-014) and real-time PCR was performed using SYBR Green Universal Mix (Roche 13608700) or TaqMan Universal Master Mix (ABI Prism 7700 and StepOne-Plus; Perkin-Elmer and Applied Biosystems). Gapdh transcript levels were used for normalisation of each target (Livak and Schmittgen, 2001). At least three biological replicates were used for each condition. For SYBR Green, custom primers were designed using Primer3Plus online software. Serial dilutions of total cDNA from E12.5 whole embryos and placentas were performed to calculate the amplification efficiency of all primers. Primer sequences are listed in supplementary material Table S1.

siRNA transfection and lentivirus transduction of primary myogenic cells

For siRNA transfections, FACS-isolated GFP+ cells from E18.5 control and mutant embryos were plated on Matrigel-coated 96-well dishes at 15,000 cells per well in DMEM/MCDB (1:1), 20% foetal calf serum medium without antibiotics. Cells were transfected with 10 pmol siRNAs (GFP-22 siRNA stock number 1022064; negative control siRNA stock number 1027280; Qiagen) using Lipofectamine RNAiMax reagent (Invitrogen) as per manufacturer’s instructions. For longer chase periods, cells were retransfected every 2-3 days. For the production of lentiviruses, murine Me2c2 was amplified by PCR from a plasmid kindly provided by G. Messina and cloned into the entry vector pENTR11. The expression vector was subsequently generated using the Gateway LR Clonase Kit (Life Technologies, 11791-100). For viral transduction, primary cells were incubated with lentiviruses at an MOI of 50 for 6 hours in OptiMem (Life Technologies) containing 10 µg/ml polybrene. Subsequently, medium was aspirated and cells incubated in DMEM/MCDB (1:1), 20% foetal calf serum medium.

In situ RNA hybridisation

For the detection of mRNA by in situ hybridisation (ISH) (Tajbakhsh et al., 2001), riboprobes were produced with T7 RNA polymerase from the following plasmids: for HeyL, IMAGE clone 40142873 was used linearised with SacI; for Hey1, a plasmid kindly provided by R. Kageyama was used as previously described (Hirata et al., 2001).

EDU administration in vivo

For proliferation experiments in vivo, 5-ethyl-2’-deoxyuridine (EdU; Invitrogen E10187) was injected twice: first at 50 µg/g body weight, then after 12 hours at 75 µg/g body weight; mice were then sacrificed 6 hours later. EdU was detected using the Click-iT EdU Cell Proliferation Assay Kit (Life Technologies C10350) as per manufacturer’s instructions.
Transcriptome analysis
Expression profile data were generated using limb skeletal muscle stem/progenitor cells from transgenic Tg:Pax7-nGFP mice (R.S. and S.T., unpublished). The full dataset will be published elsewhere, but is available upon request. Briefly, E12.5 and E17.5 embryos were dissociated and GFP-positive stem/progenitors were isolated by FACS. Fragmented biotin-labeled cRNA samples were hybridised on GeneChip Mouse Genome 430_2 arrays (45,000 probe sets) as recommended by the manufacturer (Affymetrix). For each developmental stage, three biological replicates were hybridised. Raw data were pre-processed using the GC-Robust MultiChip Analysis (GCRMA) algorithm to correct background, to adjust intensity distribution over the arrays and to convert probe intensity summarisation into a unique probe set signal. Local pooled error tests (Jain et al., 2003) were conducted in order to identify significant differences in gene expression between groups. The Benjamini-Hochberg multiple summarisation into a unique probe set signal. Local pooled error tests (Jain et al., 2003) were conducted in order to identify significant differences in gene expression between groups. The Benjamini-Hochberg multiple correction test (Benjamini and Hochberg, 1995) was applied to control for the number of false positives with an adjusted 5% statistical significance threshold.

Statistical analysis
For statistical comparison of Pax7-nGFPHi, Pax7-nGFPMid and Pax7-nGFPLo and quantifying cell populations, Student’s t-test (two-tailed) was performed using PRISM software (GraphPad). A minimum of three replicates were analysed for all experiments presented.

RESULTS
A subpopulation of myogenic cells with elevated Pax7 expression is specified by active Notch signalling
To determine the specific stage of myogenic lineage progression when Notch signalling is highest, we used a transgenic mouse line that expresses nGFP under the control of the regulatory elements of Pax7 (Tg-Pax7-nGFP) (Sambasivan et al., 2009) to perform a refined fractionation of myogenic cells during development (Fig. 1A; top 20% Pax7Hi, intermediate 40% Pax7Mid, bottom 20% Pax7Lo). RT-qPCR analysis of the subfractions showed that GFP reporter expression provided a faithful readout of the lineage progression status, with the gradual loss of Pax7 and Myf5 and the gain of commitment and differentiation markers (Myod, Myog) in Pax7Lo cells (Fig. 1B). At embryonic (E11.5) and, more prominently, at foetal (E18.5) stages, the Pax7Hi population had higher Notch activity, as measured by expression of the Notch target HeyL, Hey1 and Nrarp, compared with the cells with lower levels of GFP (Fig. 1B). In addition, in the Pax7Hi cells, higher expression of Notch1 and Notch3, the ligand jagged 1 (Jag1), and specifically the Notch glycosyltransferase lunatic fringe (Lfrng) was observed, whereas theDll ligand was significantly reduced (Fig. 1B). A similar pattern of expression was observed in Pax7-nGFP cells isolated from postnatal day (P) 8 and adult (post-injury) activated satellite cells (Mourikis et al., 2012). Upon analysis of purified embryonic cells overexpressing a constitutively active form of Notch1 (NICD) in vivo, a similar transcriptional response to that of the Pax7Hi population was observed (supplementary material Fig. S1A). Taken together, these results indicate that irrespective of the developmental stage, the Pax7Hi fraction corresponds to the stem/progenitor population and is characterised by elevated endogenous Notch activity.

Based on these observations, we hypothesised that sustained Notch activity in the DM would retain cells in a state of elevated Pax7 expression that is compatible with muscle, but not dermal, stem/progenitor cells. To test this, we used an En1Cre;R26Rstop-NICD-nGFP (hereafter En1Cre-NICD) embryos showed significant expansion of the muscle founder stem cell population, manifested first by an expansion of Pax3+ cells in the DM, and later of Pax3+Pax7+ cells in the myotome after epithelial-to-mesenchymal transition of the DM (Fig. 1D,E). This occurred at the expense of myogenic commitment and terminal differentiation (no Myod and no Myog, respectively; Fig. 1F; control in supplementary material Fig. S1B). Consistent with previous findings that genetic regulation of Myf5 is distinct from that of Myod (Tajbakhsh et al., 1997; Tajbakhsh and Buckingham, 2000), Myf5 continued to be co-expressed in essentially all GFP+/Pax7+ cells (Fig. 1F; designated as stem/progenitors). Interestingly, HeyL (upregulated ~40-fold), and not Hes1, was the major responding gene to NICD (supplementary material Fig. S1C).

When Notch signalling was compromised in En1Cre;RbpflacSTOP::R26RFlacCreERT2 (hereafter En1Cre-NICD) embryos, Alx4+ dermal progenitors emerged at E11.5 as in wild-type embryos (supplementary material Fig. S1D), suggesting that Notch signalling is not essential for dermal lineage commitment. Accordingly, we obtained similar results using a Myf5Cre line (Haldar et al., 2008), which drives expression in some dermal progenitor cells that share a common and recent ancestry with myogenic stem/progenitors (supplementary material Fig. S1D). This observation led us to propose that Notch signalling is dispensable for the dermis/muscle cell fate choice of the founder stem cells, at least in the En1+ population found in the central portion of the DM. Instead, constitutive NICD suppressed the expression of the early dermal progenitor marker Alx4 as well as the later marker Dermo1 (Twist2 – Mouse Genome Informatics) (Fig. 1G) (Scalp et al., 2001; Cinnamon et al., 2006). However, it did not impair their migration dorsally underneath the ectoderm (Fig. 1D). Therefore, elevated Notch activity in multipotent DM cells biases their fate toward skeletal myogenesis, while concomitantly blocking their differentiation.

Maintenance of early myogenic stem/progenitors throughout development by constitutive Notch activity
Given that constitutive allelic expression of NICD maintains the upstream myogenic stem/progenitor population cell-autonomously, we used NICD as a tool to interrogate the distinct spatiotemporal behaviours of these cells and their relationship with other myogenic subpopulations. Since Myf5 is the earliest MRF to be expressed in somitic and cranial mesoderm, we crossed constitutively expressing Myf5Cre mice (Haldar et al., 2008) to trigger the expression of NICD in these muscle progenitors. Myf5Cre;R26RSTOP::NCD-nGFP/+ embryos (hereafter Myf5Cre-NICD) were highly oedemic (Fig. 2A; starting at E16.5), lacked skeletal muscles and died perinatally. Analysis of head and trunk muscle at these embryos at E18.5 showed a total lack of skeletal muscles, and, instead, a dramatic expansion of Pax7+/Myf5+/Myog muscle cells that we refer to as stem/progenitors. Interestingly, the patterning of these cells followed that of the presumed muscle masses in both head and trunk regions (Fig. 2B). This demonstrates that, in contrast to Wnt and Shh signalling, which inhibit myogenesis in the head but promote myogenesis in the trunk (Tzaghor et al., 2003), there is no such disparity in the effect of Notch signalling on cranial and somitic myogenic cells. Furthermore, it shows that expression of NICD is sufficient to maintain their viability and self-renewal capacity in the absence of downstream committed progeny.
Temporal specification of muscle stem cells

Fig. 1. High Notch activity defines an upstream, undifferentiated myogenic population with elevated Pax7 expression. (A) Fractionation by FACS of GFP^+ cells from E11.5 Tg:Pax7-nGFP mouse embryos into Pax7^Hi (20% of population), Pax7^Mid (40%) and Pax7^Lo (20%). Intensity of the GFP signal reflects activity of the Pax7 promoter. (B) Expression of muscle and Notch signalling factors in the Pax7^Hi and Pax7^Lo fractions measured by RT-qPCR. Data are presented as a heatmap, relative to expression in Pax7^Mid cells (2^−ΔΔCt). All genes listed were differentially expressed between Pax7^Hi and Pax7^Lo samples with statistical significance (n=3 embryos/genotype). (C) Distribution of En1^Cre targeted cells in an interlimb transverse section of an E10.75 En1^Cre:R26RmT/mG embryo. Marked GFP^+ cells are detected in both dermal (arrowhead) and muscle (arrow) lineages. Dotted line delineates dermomyotome (DM) from myotome. The boxed region in the diagram indicates the anatomical location. (D) Anti-Pax3 and anti-Pax7 immunostaining on serial sections of En1^Cre-NICD (nuclear GFP) and control (En1^Cre:R26RmT/mG; membrane GFP) embryos. NICD overexpression results in expansion of the Pax3 but not the Pax7 expression domain (see arrows and insets). Asterisks indicate GFP^+ cells in the dermal compartment. (E) Quantification of the effect of NICD overexpression on Pax3 and Pax7 at E10.5 and E11.5. Values are presented as percentage of Pax3 or Pax7 co-expression with GFP over total number of GFP^+ cells. (F) Interlimb sections of E11.5 En1^Cre-NICD embryos stained with antibodies against Myf5, Myod and Myog. The boxed region in the upper left panel designates the anatomical location shown in the other panels. (G) (Left) Whole-mount RNA in situ hybridisation (ISH) for Alx4 on E10.75 embryos. The En1 targeting domain is indicated by arrows. (Right) RT-qPCR for the dermal markers Alx4 and Dermo1, using FACS-isolated cells from En1^Cre-NICD and control (En1^Cre:R26RmT/mG) E10.75 embryos. Error bars indicate s.e.m.; n=3 embryos/genotype. *P<0.05, **P<0.01, ***P<0.001. NT, neural tube; PE-A, phycoerythrin. Scale bars: 100 µm in C and in F upper left; 80 µm in D; 40 µm in remainder of F; 30 µm in D insets; 15 µm in F insets.
The complete lack of musculature in *Myf5*−/−;NICD embryos was unexpected given two previous reports showing the presence of a Myf5-independent Myod+ subpopulation that rescues myogenesis after diphtheria toxin ablation (DTA) of Myf5+ cells (Gensch et al., 2008; Haldar et al., 2008). Quantification of forelimb musculature of *Myf5*−/−;NICD embryos at E12.5 showed an initial modest increase in non-targeted (GFP−) myoblasts that were Pax7+/Myod+ to 7±0.7% (essentially undetectable in control), whereas 92±0.3% of the GFP+ population was Pax7+/Myod− (Fig. 2C,D; 24±2.6% in control). Further analysis revealed that the small fraction of GFP+/Myod+ cells was neither sustained nor expanded at later stages of development, but instead differentiated to form rudimentary myofibres (Fig. 2B, bottom right, arrows). That the Myod+ subpopulation did not rescue myogenesis in this model was evident in a comparison of *Myf5Cre/+:R26Rstop-DTA/+* (cell ablation and Myod rescue) and *Myf5 Cre/+:R26Rstop-NICD-nGFP/+* (skeletal muscle agenesis) foetuses. In the DTA ablation model, a partial rescue of muscle differentiation was observed in the body, whereas in the constitutive NICD model no significant rescue of skeletal myogenesis was detected by the Myf5-independent population (Fig. 2E). Taken together, these results demonstrate that
constitutive Notch is sufficient to maintain a self-renewing population of muscle stem/progenitors while inhibiting differentiation throughout embryogenesis. Although undifferentiated, these Myf5-NICD+ cells inhibited the expansion of the presumed Myf5-independent Myod+ population, indicating that negative cross-regulation between these subpopulations can occur primarily at the stem/progenitor cell level, thereby resulting in failure of myogenic rescue in this scenario.

The Myf5Cre-NICD model also permitted us to address a longstanding question in the field of Notch signalling and myogenesis (Shawber et al., 1996; Nofziger et al., 1999): is the block of differentiation by Notch accomplished via canonical signalling or independently of Rbpj? To resolve this issue, we generated compound mice that express NICD in an Rbpj null background (Myf5Cre/+:R26Rstop-NICD-nGFP/+:Rbpjflox/–) and scored for the expression of Myod and Myog in the myotome. In the absence of Rbpj, constitutively activated Notch1 did not inhibit cell differentiation in the trunk or head muscles. Instead, cells differentiated more rapidly than controls, reproducing the phenotype that we observed in Rbpj null mice (Fig. 2F,G; supplementary material Fig. S2A-C). Therefore, an Rbpj-independent pathway does not appear to be manifested for muscle progenitor cell differentiation in this scenario.

Self-renewing embryonic myogenic stem/progenitor cells arrested in lineage progression adopt foetal phenotypes in the foetus

Given that Notch signalling blocked differentiation and sustained the muscle stem/progenitor population from embryo to foetus, we examined whether this population would be responsive to the foetal environment and adopt foetal cell fate characteristics. The shift from embryonic to foetal development is a critical step during skeletal myogenesis, in which molecularly and phenotypically distinct foetal myoblasts generate secondary myofibres (Biressi et al., 2007b). We showed previously, using a differential transcriptome comparison between embryonic and foetal Myf5GFP-P/+ myogenic cells from the limbs, that different classes of genes distinguish these two myoblast populations (Biressi et al., 2007b). This led to the identification of the transcription factor Nfix as a crucial determinant of the foetal myoblast fate (Messina et al., 2010). To complement this study and identify novel markers of the ancestral Pax7+ muscle stem/progenitor population, we performed
a differential transcriptome analysis between FACS-isolated embryonic (E12.5) and foetal (E17.5) Pax7-nGFP cells. We identified a number of differentially expressed genes that were not observed previously (Fig. 1A,B). RT-qPCR analysis of control cells isolated by FACS from E12.5 and E18.5 Myf5Cre/+:R26RmT-mG/+ samples confirmed the temporal specificity of these transcripts in embryonic and foetal progenitors (Fig. 3A,B; supplementary material Fig. S3A,B).

To assess the phenotype of Myf5Cre-NICD cells that persist in the foetus, we used lineage priming (Enver and Greaves, 1998) as an assay to determine their temporal state and commitment status. Strikingly, and in accordance with the control, Myf5Cre-NICD cells isolated from the foetus (E18.5) showed an upregulation of all foetal markers, but not embryonic markers (Fig. 3B; supplementary material Fig. S3A,B). Notably, the embryonic (E12.5) Myf5Cre-NICD cells expressed the embryonic markers at levels comparable to the control and did not express any of the foetal markers at this stage (Fig. 3A). These results suggest that the upstream embryonic population of Pax7+/Myf5+ cells maintained by constitutive allelic expression of NICD was receptive to the changing environmental signals of the foetus, and consequently adopted a foetal phenotype while concomitantly losing embryonic molecular markers.

Embryonic to foetal myogenic specification is regulated through Nfix-mediated transcriptional regulation. Analysis of Nfix as well as members of its transcriptional core regulatory group showed that Nfix and Pkcθ (Prkcg – Mouse Genome Informatics) transcripts were upregulated both in control and Myf5Cre-NICD cells at E18.5 compared with E12.5 (Fig. 4A). Importantly, embryonic slow myosin heavy chain, a marker specific for embryonic but not foetal myoblasts, was not expressed in Myf5Cre-NICD cells at E18.5 (Fig. 4A). Interestingly, however, the downstream targets of Nfix, such as muscle creatine kinase (Ckm) and β-enolase (Eno3), were not significantly induced in the Myf5Cre-NICD cells at E18.5 in spite of the presence of robust levels of Nfix protein (Fig. 4B), its co-factor Pkcθ and myocyte-specific enhancer factor 2a (Mef2a) (supplementary material Fig. S4A). We also found that another Mef parologue, Mef2c, which promotes myogenic differentiation, was strongly repressed in the Myf5Cre-NICD cells (Fig. 4C; supplementary material Fig. S4A). Although it normally does not bind to Nfix (Messina et al., 2010), we tested whether restoring Mef2c expression in the presence of NICD would rescue myogenesis and permit the induction of the differentiation marker Ckm. Exogenous overexpression of Mef2c did not promote the expression of Ckm, although some upregulation of Eno3 was observed (supplementary material Fig. S4B,C), suggesting that activated Notch interferes with the transcriptional activity of Nfix at different levels. These findings indicate that Myf5Cre-NICD cells arising in the embryo undergo normal ontology and adopt the correct temporal fate. However, their lineage progression to the myoblast and differentiation stages is abrogated by the constitutive expression of NICD.

**Foetal myoblasts arrested during lineage progression retain robust myogenic potential**

We showed above that myoblasts expressing activated Notch remain undifferentiated and respond effectively to ontologically
changing environmental signals for their temporal specification. Given that these cells arose in the somitic DM and that they were initially multipotent for several lineages, we wondered whether this property was retained after their exit from the DM under continuous NICD expression. We isolated Myf5Cre-NICD cells at E18.5 and examined the expression of specific markers for multiple lineages. We found that NICD-expressing cells retain their myogenic potential despite the expression of markers of diverse lineages. This suggests that the temporal specification of muscle stem cells is a dynamic process that is sensitive to environmental cues.

Fig. 5. Foetal NICD-expressing cells retain their myogenic potential despite the expression of markers of diverse lineages. (A) Relative expression of osteoblast (blue), pericyte (dark red; AP, alkaline phosphatase), dermoblast (green) and adipocyte (orange) markers and also of markers of endothelial cells (Cd31; also known as Pecam1), mesenchymal cells (Thy1) and smooth muscle cells (Sm22a; also known as Tagln). Transcript levels in Myf5Cre-NICD are presented relative to control (2^-ΔΔCt). Error bars indicate s.d.; n=3 embryos/genotype. (B) Anti-Pparγ nuclear staining of E18.5 control (Myf5Cre/+:R26RmT-mG/) and Myf5Cre-NICD at the forelimb level. Note the presence of NICD-expressing cells co-expressing Pparγ (asterisk). (C) (Left) Silencing the NICD-ires-nEGFP transgene by siRNA. The siGFP targets the EGFP sequence of the bicistronic transcript, leading to the degradation of the entire mRNA. (Right) The levels of NICD-ires-nEGFP transcripts as determined using primers targeting the NICD-ires (a) or the ires-nEGFP (b) junction sequences. Scrambled siRNA was used as transfection controls. Samples were collected after two 48-hour pulses of siRNA transfections. Error bars indicate s.e.m.; n=3 embryos/genotype. (D) siGFP transfection of FACS-isolated cells from Myf5Cre-NICD E18.5 foetuses. Scrambled siRNA was used as negative control. Efficient EGFP knockdown specifically in siGFP-treated samples resulted in the appearance of Myog+ cells by day 6 and the formation of multinucleated fibres by day 12. (E) Induction of the Nfix targets, but not Nfix, after silencing of the NICD transgene. Values of scrambled control are represented as 1. Data are presented as ratios of siGFP-treated over scrambled siRNA-treated samples (2^-ΔΔCt). Error bars indicate s.d.; n=3 embryos/genotype. *P<0.05, **P<0.01, ***P<0.001. Scale bars: 25 µm in B; 100 µm in D, top; 300 µm in D, bottom.
lineages by RT-qPCR or immunofluorescence. Notably, pericyte, adipocyte and osteoblast markers genes were detected in the Myf5Cre-NICD cells (Fig. 5A). Interestingly, although we observed the expression of more upstream lineage markers for these cell types, this was not accompanied by induction of the downstream differentiation cascade. For example, peroxisome proliferator-activated receptor gamma (Pparγ), which marks differentiating adipocytes, was induced robustly in the Myf5Cre-NICD cells. However, the preadipocyte factor C/EBP-δ (Cebpδ) was slightly reduced, whereas no induction was seen for the Pparγ target C/EBP-α (Cebpα), indicating that further differentiation was blocked. Strikingly, Pparγ protein was also observed in Myf5Cre-NICD cells in vivo, but these cells were located only on the periphery of the myogenic zone, sometimes adjacent to adipogenic regions (Fig. 5B; data not shown). This suggests that other local signals promote further transdifferentiation and cell commitment of this pre-myogenic population.

To assess the myogenic differentiation potential of these cells, NICD expression from the R26RNICD-αGFP locus was suppressed by targeting the NICD-ires-nGFP bi-cistronic transcript with siGFP. This approach allowed the knockdown of the transgene expressing NICD (Fig. 5C) while leaving endogenous Notch signalling intact. After 12 days in culture, Myog+ cells and multinucleated myotubes were observed in the siGFP-treated cells, but not in the cells with control/scrambled siRNA (Fig. 5D). Notably, many of these myotubes were larger than embryonic myotubes, which typically have only a few differentiated nuclei. Furthermore, these siGFP-treated cells expressed genes specific for foetal myogenesis (Fig. 5E; Ckm and Eno3). Taken together, these results indicate that constitutive NICD expression does not compromise the ability of myogenic stem/progenitor cells to adopt foetal myoblast and differentiated phenotypes, in spite of their initial expression of genes of multiple cell lineages.

**Distinct roles for Notch signalling during maturation of muscle stem cells**

We showed above that constitutive expression of NICD maintains muscle stem/progenitors at the expense of differentiation. These cells continued to proliferate and prefigured muscle mass formation. Given that these cells lose embryonic characteristics and adopt those found in the foetus, we asked whether they adopted later properties that characterise the emerging satellite cell population. A prominent feature of satellite cells is their quiescent state. We examined the cell cycle status of control and Myf5Cre-NICD cells (Pax7+/GFP+) by exposing E12.5 and E18.5 embryos to the nucleotide analogue EdU (see Materials and methods) and measured cells that were double positive for Pax7 and EdU. In accordance with the phenotypes described above during early myogenesis, activated Notch sustained stem/progenitor cell proliferation (Fig. 6A) at the expense of differentiation (Fig. 1C; Fig. 2B-D), with 71.7±3.8% and 83.9±2.9% of Pax7+/EdU+ cells in Myf5Cre-NICD and control embryos, respectively (Fig. 6A,B). Strikingly, at E18.5, activated Notch continued to block cell differentiation, yet unexpectedly it had a strong negative impact on proliferation such that the majority of Pax7+/GFP+ cells did not take up EdU (Fig. 6A,B; 18.9±1.0% and 75.5±2.1% of Pax7+/EdU+ cells in Myf5Cre-NICD and control, respectively). Consistent with the proliferation profile, examination of the cell cycle inhibitor p57 (Cdkn1c – Mouse Genome Informatics) showed that, whereas at E12.5 the majority of the Myf5Cre-NICD+ cells were p57- and actively proliferating (EdU+), by E18.5 most of the cells expressed robust levels of p57 and were EdU- (Fig. 6C-E). Therefore, sustained expression of activated Notch is compatible with foetal progenitors eventually adopting a Pax7+/Myog-/EdU- state, which is characteristic of satellite cells.

In addition to their quiescence, satellite cells are characterised by the expression of specific markers, including calcitonin receptor (CTR; Calcrl), which is highly expressed in postnatal quiescent satellite cells but not in myogenic cells in proliferation (Fukada et al., 2007). This marker showed high levels of expression in most of the Myf5Cre-NICD cells at E18.5, but not during embryonic stages (Fig. 7A; data not shown). Furthermore, a defined feature of the muscle stem cell niche is the expression of laminin in the basement membrane surrounding muscle fibres, and emerging satellite cells are ensheathed by laminin staining. Remarkably, in the total absence of myofibres, laminin staining was observed surrounding these Myf5Cre-NICD cells at E18.5, but not at E12.5 (Fig. 7B), suggesting that these NICD-expressing cells were capable of constructing a component of the adult stem cell niche. Taken together, our data suggest that, at E18.5, Myf5Cre-NICD cells have both foetal and satellite cell characteristics.

**DISCUSSION**

The capacity of stem cells to generate distinct classes of committed progeny spatiotemporally, although well investigated in the nervous system, remains largely undefined for most tissues and organs. Key to understanding this process is interpreting the relative roles of powerful signalling pathways that impinge on these events. Using different combinations of genetically modified mice, we identify Notch signalling as necessary and sufficient for maintaining muscle stem cells and allowing them to be receptive to specification and differentiation cues throughout development. Remarkably, cell-autonomous expression of the intracellular fragment of Notch in muscle stem/progenitors was sufficient to allow their maintenance, temporal specification and recapitulation of ontology in the absence of committed progeny and differentiation.

We demonstrate that myoblasts with high Notch activity fail to terminally differentiate, both in the embryonic and foetal trunk and head. This property of canonical Notch signalling is unique, as other crucial signalling molecules have been shown to impact differently on the myogenic programme, either temporally (embryo/foetus) (Cusella-De Angelis et al., 1994; Hutcheson et al., 2009) or spatially (trunk/head) (Tzahor et al., 2003). We also show for the first time for skeletal muscle in vivo that Notch signalling occurs via an Rbpj-dependent pathway, and that an Rbpj-independent pathway is either not significant or lacking in the somite. Whether this is also the case for muscle stem/progenitor cells in other contexts requires further investigation.

Interestingly, Notch activity is sufficient to autonomously maintain embryonic Pax7+/Myog stem/progenitor cells throughout development, even in the absence of differentiating cells, which we showed previously to be required for their survival (Kassar-Duchossoy et al., 2005). Therefore, this reinforces the notion that the differentiating cells might signal to and sustain the upstream population by direct cell-cell interactions. We propose that Notch signalling fulfils the requirements as the principal pathway, and we show experimentally that it is sufficient. This notion is supported by the transcriptional signature of upstream (Pax7+δ) and differentiating (Pax7+γ) myogenic cells, which shows high Notch activity in the former, and elevated Dll1 ligand expression in the latter. Hence, in the experimental situation in which the stem/progenitor cells have sustained NICD expression, the downstream population becomes dispensable for their survival.
Although not formally proven, a similar mechanism appears to operate for the maintenance of quiescent satellite cells. Satellite cells have high Notch activity that is required for their maintenance (Bjornson et al., 2012; Mourikis et al., 2012) and are in direct contact with the basement membrane and the myofibre. The myofibre is the most likely source of ligand, which, like the Notch receptor, is a transmembrane molecule. One unexpected finding from our work is the observation that allelic expression of Notch was compatible with Myf5 protein expression, as shown also in the chick (Delfini et al., 2000; Hirsinger et al., 2001). A recent study in the chick reported that transient Notch activation was necessary to prime muscle stem cells in the dorsal DM to enter the myogenic lineage (positive for Myf5 and Myod), but sustained NICD overexpression results in the eventual downregulation of Myf5 and Myod and a failure to enter the myotome region (Rios et al., 2011). By contrast, our present study shows that muscle stem/progenitors with sustained NICD continuously express Myf5 and actively transit into the myotomal region. The differences in these results could be related to the levels of NICD expressed or to the specific location of the stem/progenitors in the somites that were examined.

Independent studies have shown that the early embryonic Pax7+ cells give rise to foetal and then adult muscle stem cells (Gros et al., 2005; Kassar-Duchossoy et al., 2005; Relaix et al., 2006; Lepper and Fan, 2010). Although these studies have established the embryonic origins of foetal and adult muscle stem cells, it remains unclear if there is a single self-renewing population in the embryo that is sustained to adulthood, or whether intermediate, stage-specific populations are produced that can give rise to the populations of the corresponding developmental stages. The data presented in this study support the former scenario because embryonic myogenic cells with sustained NICD expression are pS7+. Scale bars: 50 µm in A, C; 15 µm in C inset; 20 µm in D.

Fig. 6. Differential effect of NICD on proliferation of myogenic cells. (A) Cell division kinetics of control (Myf5Cre+;R26smEar+GFP+) and Myf5Cre-NICD-expressing cells in E12.5 and E18.5 mouse forelimbs. Cell cycling of the Pax7+ cells was measured by incorporation of EdU. (B) The percentage of total Pax7+/EdU+ cells at E12.5 and E18.5 in control and Myf5Cre-NICD embryos. Error bars indicate s.e.m.; n=3 embryos/stage. **P<0.01, ***P<0.001. (C) Immunostaining of control (top) or Myf5Cre-NICD (bottom) E12.5 and E18.5 embryo forelimbs for Myod and p57 (top) or GFP and p57 (bottom). (D) Immunostaining of Myf5Cre-NICD cells at E12.5 and E18.5 for p57 and EdU. Non-cycling, EdU– cells in Myf5Cre-NICD are pS7+. Scale bars: 50 µm in A, C; 15 µm in C inset; 20 µm in D.
a continuous requirement for Notch, this pathway should not be dominant over other developmental cues, but at the same time it must exert specificity for the cells to assume their appropriate temporal fates. Indeed, we find that foetal myoblasts with sustained activated Notch retain robust myogenic potential in spite of expressing determinant markers of other lineages. Similarly, the dermomyotomal NICD-expressing cells downregulate Pax3 and HeyL when they migrate towards the dermis, whereas they maintain Pax3 and HeyL and also express Pax7 and Myf5 when they enter the myotome (Fig. 1D,E; supplementary material Fig. S1C). Therefore, activated Notch, in combination with tissue-specific factors, specifies and maintains muscle stem cells throughout development.

The outcome of Notch activation is notoriously unpredictable and depends on the spatiotemporal context in which it is acting, i.e. it is influenced by cross-talk with other signalling pathways and/or the cellular state (Hurlbut et al., 2007; Schwanbeck et al., 2011). In the present study, we observe actively dividing NICD-expressing stem/progenitor cells during embryonic stages and cell cycle-arrested cells during late foetal myogenesis, although differentiation is blocked at both stages. Strikingly, late foetal myogenic cells enter cellular quiescence (Pax7+/Myog-/EdU–), indicating that the entire ontological development of muscle stem cells from embryo to reversible cell cycle exit can be recapitulated by constitutive expression of Notch. We and others reported recently the unexpected decrease in Notch activity as soon as satellite cells exit quiescence and enter the cell cycle, and the continued low activity in proliferating myoblasts until they return to quiescence (Bjornson et al., 2012; Mourikis et al., 2012). A recent study confirmed this notion by showing that NICD overexpression in freshly isolated satellite cells decreases their proliferation capacity (Wen et al., 2012). These studies combined point to the importance of Notch signalling in quiescent satellite cells and that downregulation of this pathway is necessary for transit amplification of the satellite cell population after cell cycle re-entry.

Our observation of foetal and satellite cell characteristics in Myf5Cre-NICD foetuses at the single-cell level warrants further investigation. We predict that these cells represent a transition state. Intriguingly, the NICD+/EdU− cells at E18.5 are positive for the cell cycle inhibitor p57, consistent with their non-cycling nature, even though satellite cells do not express p57 (data not shown). This observation supports the notion that these cells are in a transition phase and we speculate that p57 is acting as a brake to the proliferating myoblasts to drive them into a terminal (differentiated) or reversible (quiescent) arrested state.

In summary, we show here that Notch signalling regulates muscle stem cell self-renewal as well as their temporal...
Temporal specification of muscle stem cells

specification. Although Notch activity declines progressively as these myogenic cells differentiate, muscle stem cells can be maintained cell-autonomously with allelic expression of Notch, independently of committed cells. Remarkably, this constitutive expression of NICD does not override environmental signals, thereby allowing the muscle stem cells to integrate cues from the changing environment to progress ontologically.

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The authors declare no competing financial interests.

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