The repression of Notch signaling occurs via the destabilization of mastermind-like 1 by Mesp2 and is essential for somitogenesis

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SUMMARY

The rostro-caudal polarity within a somite is primarily determined by the on/off state of Notch signaling, but the mechanism by which Notch is repressed has remained elusive. Here, we present genetic and biochemical evidence that the suppression of Notch signaling is essential for the establishment of rostro-caudal polarity within a somite and that Mesp2 acts as a novel negative regulator of the Notch signaling pathway. We generated a knock-in mouse in which a dominant-negative form of Rbpj is introduced into the Mesp2 locus. Intriguingly, this resulted in an almost complete rescue of the segmental defects in the Mesp2-null mouse. Furthermore, we demonstrate that Mesp2 potently represses Notch signaling by inducing the destabilization of mastermind-like 1, a core regulator of this pathway. Surprisingly, this function of Mesp2 is found to be independent of its function as a transcription factor. Together, these data demonstrate that Mesp2 is a novel component involved in the suppression of Notch target genes.

KEY WORDS: Mastermind-like 1, Mesp2, Notch signaling, Somitogenesis, Mouse

INTRODUCTION

In the developing vertebrate embryo, the somites are the most obviously segmented structure and give rise to metameric structures such as the vertebrae and ribs. The somites are rhythmically produced from the presomite mesoderm (PSM) under the control of the so-called ‘segmentation clock’, which is characterized by the periodic expression of genes involved in the Notch, Wnt and Fgf signaling pathways (reviewed by Dequeant and Pourquie, 2008; Lewis, 2008). In the posterior PSM of the mouse embryo, the transcripts of Notch signaling components such as Hes7, a basic helix-loop-helix (bHLH)-type transcription factor and Lfng (a glycosyltransferase implicated in Notch receptor modification), oscillate and travel in a posterior-to-anterior direction during each segmentation cycle (Bessho et al., 2003). Notch activity also oscillates and travels in the posterior PSM (Morimoto et al., 2005). Once Notch signals reach the anterior PSM, they are arrested at the future segmentation point, where temporal information is translated into the spatial pattern that generates segmented somites (Saga and Takeda, 2001).

Each somite is subdivided into anterior (rostral) and posterior (caudal) compartments and this division is already determined prior to the physiological segregation of the somite (Aoyama and Asamoto, 1988). The repression and activation of Notch signaling are known to be essential for the establishment of the rostral and caudal compartments of a somite, respectively. Hence, many mice that lack the components of the Notch signaling pathway or have activated Notch1 throughout the PSM show defective rostro-caudal (RC) patterning (Bessho et al., 2001; Evrard et al., 1998; Feller et al., 2008; Takahashi et al., 2000; Zhang and Gridley, 1998). In addition, Mesp2, a bHLH-type transcription factor, is known to be required for the establishment of RC patterning within a somite (Morimoto et al., 2005; Saga et al., 1997; Takahashi et al., 2000). Mesp2 expression is induced in the anterior PSM just before segmental border formation. Its initial expression domain of approximately one somite in length becomes quickly restricted to the rostral compartment within a presumptive somite. In the absence of Mesp2, the rostral identity within a somite is lost and the somite is completely caudalized, indicating that Mesp2 is required to establish the rostral compartment (Saga et al., 1997; Takahashi et al., 2000).

Previous functional studies have shown that Mesp2 plays valuable roles during somitogenesis via its regulation of several target genes as a transcription factor, including the upregulation of Lfng, Epha4 and Ripply1/2 (Morimoto et al., 2007; Morimoto et al., 2005; Nakajima et al., 2006; Takahashi et al., 2010). Mesp2 has also been shown to have suppressive effects on Notch activity, in part by activating Lfng expression in the rostral somite compartment (Morimoto et al., 2005). Lfng has been further implicated as a suppressor of the Notch signaling pathway by preventing the formation of cleaved Notch1 (active Notch1, Notch1 intracellular domain, referred to as NICD). Lfng expression cycles in the posterior PSM are under the control of Notch signaling, whereas its expression in the anterior PSM is under the control of Mesp2 (Evrard et al., 1998; Hicks et al., 2000; Zhang and Gridley, 1998). To elucidate the functional significance of Lfng acting downstream of Mesp2, we previously generated a knock-in mouse that reproduces the expression pattern of Lfng DNA at the Mesp2 locus (Mesp2Lfng+/−) and analyzed Mesp2Lfng+/− embryos. However, the activation of Lfng instead of Mesp2 fails to rescue the phenotype of Mesp2-null mice and the somites are still caudalized, indicating that Lfng is not responsible for Mesp2 function as a suppressor of Notch signaling (Oginuma et al., 2010). Therefore,
although there appears to be a requirement for Mesp2 in the suppression of Notch signaling, the action point in this mechanism has remained largely unknown.

**MATERIALS AND METHODS**

**Generation of knock-in and transgenic mice**

The knock-in strategy we used to target the Mesp2 locus is largely similar to our previously described approaches (Takahashi et al., 2000) except that an Rbpj R218H or VP16 Rbpj cassette was inserted, and these mice do not express Mesp2 (see Fig. S1 in the supplementary material). The targeting vectors were introduced into embryonic stem (ES) cells (TT2) and the chimeric mice were then crossed with MCH female mice to establish each mouse line. The CAG mouse lines were established by crossing with the CAG-Cre mouse line. Mouse tail or embryo yolk sac genomic DNA was used for genotyping by PCR using the allele-specific primers

**Western blotting analysis in cultured cells**

The expression vectors, modified-HA human MAML1 (Kitagawa et al., 2001), 3×Flag-Mesp2 or the deletion forms of Mesp2, and 3×HA-Mesp1 were constructed using pcDNA3-1 (Invitrogen). NIH3T3 cells were then transfected with these plasmids using Lipofectamine 2000 (Invitrogen). After 24 hours, cellular proteins were extracted as previously described (Kitagawa et al., 2001) and, after separation by SDS-PAGE, were transferred onto Immobilon-P Membranes (Millipore). The membranes were incubated with the primary antibodies anti-Flag (1:8000; Sigma-F3165), anti-HA (1:1000; 12CA5), anti-Myc (1:1000; 9E10; sc-40; Santa Cruz) and anti-tubulin (1:2000; D66; T0198; Sigma). Positive signals were visualized by incubation with an appropriate secondary antibody conjugated with horseradish peroxidase followed by detection using an ECL Western Blotting Analysis System (GE Healthcare). In some cases, the membranes were stripped and reblocked.

**Skeletal preparations and gene expression**

Skeletal preparations via Alcian Blue or Alizarin Red staining have been described previously (Saga et al., 1997; Takahashi et al., 2000). Whole-mount in situ hybridization was performed using an InsituPro robot (Intavis), also as described previously (Takahashi et al., 2000). The probes forDll1 and Uncx4.1 were kindly provided by A. Gessler (MH-Hannover, Germany) and P. Gruss (Max-Planck Institute, Germany), respectively.

**Analysis of mutant embryos**

Embryos were collected, fixed with 4% paraformaldehyde and processed for whole-mount in situ hybridization, cryosectioning or paraffin sectioning (Saga et al., 1997; Takahashi et al., 2000). Immunohistochemistry was performed on frozen sections after antigen retrieval as previously described (Oginuma et al., 2008). Immunostaining using the TSA system (PerkinElmer) was performed with 7 μm frozen sections of embryonic day (E) 10.5 embryos as previously described, with minor modifications (Oginuma et al., 2008). Antibodies against Mesp2 (1:800) (Morimoto et al., 2005), the cleaved NICD (1:400, Cell Signaling Technology) and mastermind-like 1 (Maml1; 1:800; Millipore) were used for immunohistochemistry. The specificity of the anti-Maml1 antibody was confirmed using a Maml1-null embryo (Oyama et al., 2007). For the whole-mount detection of TP1-Venus, fixed embryos were incubated with rabbit anti-GFP antibody (1:500; MBL), followed by an Alexa-488 conjugated goat anti-rabbit IgG secondary antibody. Whole-mount immunohistochemistry was performed using rabbit anti-Tbx6 antibodies (1:800; kindly provided by D. L. Chapman, University of Pittsburgh, PA, USA) as described previously, and detected using the Vectastain ABC kit (Vectorstain) and 3,3′-diaminobenzidine (DAB) substrate (White and Chapman, 2005). Whole-mount embryos and sections thereof were observed using a confocal microscope (Carl Zeiss 510) or stereomicroscope (Leica MZ16F).

**RESULTS**

**Rescue of Mesp2-null defects in dominant-negative Rbpj knock-in mice**

To determine whether the suppression of Notch signaling underlies the mechanism by which Mesp2 confers the rostral identity to a somite in vivo, we established two mouse lines that express the dominant-negative form (Rbpj R218H; abbreviated as R218H) and constitutively active form (VP16 Rbpj; abbreviated as VP16) of the Rbpj gene (also referred to as CBFI or CSL) in the place of Mesp2 (see Fig. S1 in the supplementary material). The rationale for this approach was that Rbpj is a potent downstream effector of Notch signaling (Chung et al., 1994; Kato et al., 1997). It has also been reported that the R218H mutant lacks DNA binding ability but still competes with endogenous Rbpj for binding to the NICD or an unknown cofactor (Kato et al., 1997).

We first evaluated the expression pattern of several marker genes to confirm that our knock-out and knock-in strategies had been successful (Fig. 1A-P). Mesp2 expression was lost as expected (Fig. 1A-D), whereas Mesp1 (a homolog of Mesp2) expression was upregulated in these knock-in mice (Fig. 1E-H), probably owing to the upregulation of Tbx6 in the absence of Mesp2 (Fig. 1I-L) (Oginuma et al., 2008; Saga, 1998; Takahashi et al., 2010). The
expression of Hes5, a target of Notch signaling, normally observed as a single band in the anterior PSM in wild type (Fig. 1M), was slightly expanded in Mesp2MCM/MCM mice (Fig. 1N) (Takahashi et al., 2007), downregulated in Mesp2R218HR218H mice (Fig. 1O) and upregulated as two striped bands in Mesp2VP16/VP16 mice (Fig. 1P). These gene expression data confirmed that Mesp2 expression was lost from Mesp2R218HR218H and Mesp2VP16/VP16 mice and suggested that Notch signaling activity might be repressed and activated by R218H and VP16, respectively.

Next, we examined the resulting skeletal phenotypes of these knock-in mice as the RC patterning of vertebrae is known to correlate with Notch signaling activity in the Mesp2-expressing domain. In the absence of Mesp2 (Mesp2–/–), the pedicles of the neural arches and the proximal region of the ribs fused with their neighbors owing to the upregulation of Notch activity, and the mice died shortly after birth as previously reported (Fig. 2B,F,J) (Saga et al., 1997; Takahashi et al., 2007). Intriguingly however, we found that the Mesp2R218HR218H knock-in mice showed a marked rescue of this vertebral phenotype (Fig. 2C,G,K). Although we found some variation in the degree of rescue among these animals, some showed an almost identical morphology to the wild-type littermates. The degree of pedicle fusion in Mesp2VP16/VP16 mice was more severe than those of the Mesp2MCM/MCM mice and the vertebrae were completely caudalized (Fig. 2D,H,L). These results also indicate that Notch activity is actually repressed by R218H and activated by VP16. However, the heterozygous knock-in mice, Mesp2VP16/+, showed no abnormalities (Fig. 3A-C). We expected that a half dose of Mesp2 would be sufficient to antagonize VP16. This idea was supported by further comparative analyses among Mesp2VP16/+, Mesp2MCM/MCM, Mesp2VP16/MCM and Mesp2VP16/VP16 littermates. The degree of pedicle fusion in Mesp2VP16/VP16 mice that contains a single copy of VP16 in a Mesp2-null background was found to be slightly more severe compared with that of Mesp2MCM/MCM mice, but milder than that in Mesp2VP16/VP16 mice (Fig. 3D-F). These results indicate that VP16 can activate the Notch target gene but that this activity is repressed by a single copy of Mesp2, in addition to the endogenous Rbpj (repressor-type) in Mesp2VP16/VP16 mice and by Rbpj alone in Mesp2VP16/MCM (see model in Fig. S2 in the supplementary material).

It should be noted that normal segmental borders were generated in Mesp2R218HR218H embryos (Fig. 2O), which were similar to those in wild-type embryos (Fig. 2M). It was necessary to then determine whether this rescue event is also caused by the suppression of Notch activity. We speculate that this apparent rescue event might be due to the upregulation of Mesp1 (Fig. 1G) as we reported previously that the Mesp2-null embryo, which lacks the function of both Mesp1 and Mesp2, fails to form epithelial somites (Takahashi et al., 2005), whereas Mesp2MCM/MCM embryos show a milder epithelialization defect (Fig. 2N, arrowheads) owing to the upregulation of Mesp1 (Takahashi et al., 2007). However, it is noteworthy that, in our current experiments, the somite and skeletal phenotypes of Mesp2VP16/VP16 mice were not rescued (Fig. 2L,P), even though Mesp1 is also upregulated in this genetic background (Fig. 1H). We therefore conclude that the rescue event observed in Mesp2R218HR218H mice cannot be only ascribed to the upregulation of Mesp1, but is in fact due to the suppression of the canonical Notch signaling pathway.

### Rostro-caudal polarity is normally established in Mesp2R218HR218H knock-in mice

To further understand the molecular mechanisms underlying this rescue event, we examined the expression of several genes implicated in the downstream activities of Mesp2 or Notch signaling in the anterior PSM. The expression of Tbx18 (Fig. 2Q) was found to be almost completely absent in both the Mesp2MCM/MCM (Fig. 2R) and Mesp2VP16/VP16 (Fig. 2T) embryos. However, it was noted that a normal expression pattern of Tbx18 was observed in Mesp2R218HR218H (Fig. 2S), although at weaker levels than in wild type (Fig. 2Q). The result is consistent with the idea that Tbx18 is required for the maintenance of the rostral properties of the somite (Bussen et al., 2004; Kraus et al., 2001). We also examined the expression ofDll1 and Uncc4.1, caudal markers known to be regulated by Notch signaling (Barrantes et al., 1999; Bettenhausen et al., 1995). In the wild-type embryo, the expression ofDll1 is persistently strong in the posterior PSM but is downregulated just before the segmental border and is localized in the caudal part of somite number 0 (SO, the prospective somite in the most anterior PSM) and in the segmented somites (Fig. 2U). However, Dll1 expression is expanded in the rostral compartment of a somite in Mesp2MCM/MCM embryos (Fig. 2V). By contrast,
Mesp2R218H embryos showed a completely normal expression pattern of Dll1 (Fig. 2W), indicating that Notch signaling is well suppressed in the rostral compartment of a somite in Mesp2R218H embryos. We concluded from these data that the dominant-negative form of Rbpj efficiently competes with endogenous Rbpj, as a result of which Notch signaling is suppressed in the R218H-expressing cells. We also confirmed that the constitutively active form of Rbpj in the Mesp2R218H embryo had the reverse effect upon Dll1, the expression of which was suppressed in the rostral half within a somite (Fig. 4D,H). By contrast, the rostral expansion of Venus signals was significant in Mesp2VP16/VP16, a marker for the rostral half of the somites, Dll1 (U, n=14; V, n=4; W, n=6; X, n=4), a marker of the PSM and the caudal half of the somites, and Uncx4.1 (Y, n=22; Z, n=8; Za, n=8; Zb, n=4), a marker of the caudal half of the somites at E11.5. The genotypes are indicated above the panels.

**Mesp2 represses the activation of Notch signaling both in vivo and ex vivo**

To dissect the molecular mechanisms underlying the suppression of Notch signaling activation by Mesp2, we established a reporter assay system using NIH3T3 cultured cells, in which Rbpj-mediated transcription can be monitored by TP1 luciferase activity (Kato et al., 1997; Kohyama et al., 2005). The forced expression of a constitutively active form of Notch1 (N1ΔECD) resulted in the upregulation of luciferase activity by up to 80 fold (Fig. 4A). This reporter activity was specifically blocked by both Mesp2 and Mesp1 in a dose-dependent manner but not by the other bHLH-type transcription factor paraxis (Fig. 4A). Subsequently, we examined whether Mesp2 could repress Notch signaling activity in vivo. To monitor Notch activation in the mouse PSM, we generated a TP1-Venus transgenic mouse line and confirmed that the Venus signal could be observed in the caudal half within a somite as expected, although we could not detect oscillating Notch activity (Fig. 2Y-Zb). Whole-mount in situ hybridization analysis using Tbx18 (Q, n=12; R, n=7; S, n=8; T, n=6), a marker for the rostral half of the somites, Dll1 (U, n=14; V, n=4; W, n=6; X, n=4), a marker of the PSM and the caudal half of the somites, and Uncx4.1 (Y, n=22; Z, n=8; Za, n=8; Zb, n=4), a marker of the caudal half of the somites at E11.5. The genotypes are indicated above the panels.

**Mesp2 represses Maml1 expression independently of its transactivation activity**

We next examined the precise mechanism by which Mesp2 represses Notch signaling activity. We first speculated that Mesp2 might target Rbpj to inhibit Notch signaling as an R218H mutant...
effectively rescued Mesp2 function. We initially examined the possibility of physical interaction between Mesp2 and Rbpj ex vivo, but found no evidence of this association or of interactions with other components involved in the Notch signaling pathway (data not shown). We did notice, however, that the protein expression of mastermind-like 1 (Maml1) was almost completely diminished when co-transfected with either Mesp2 or Mesp1 in NIH3T3 cells (Fig. 5A). Moreover, this effect appeared to be specific to Maml1 and was not observed for NICD, Rbpj or paraxis (see Fig. S3A,B in the supplementary material).

We first examined whether this apparent lack of Maml1 protein is caused by the reduced stability of Maml1 transcripts. However, RT-PCR analysis ex vivo showed that the expression level of Maml1 was not affected by Mesp1 nor Mesp2 (Fig. 5B). We further examined the pattern of Maml1 expression in vivo. In situ hybridization analysis using wild-type embryos revealed that the expression of Maml1 was ubiquitously observed and not repressed in the anterior PSM where Mesp2 is known to be expressed (Fig. 5C,D). These results indicate that Maml1 protein repression by Mesp1 and Mesp2 does not occur at the transcriptional level or via the instability of mRNA. The other possible mechanism was post-translational destabilization, as it is known that many proteins including Hes7, Mesp2 and Tbx6 are quickly destabilized via proteasome-mediated pathways during somitogenesis (Bessho et al., 2003; Morimoto et al., 2006; Oginuma et al., 2008). To test this possibility, we examined the stability of Maml1 with Mesp2 in the presence of MG132, a potent inhibitor of proteasome pathway. However, we did not observe significant stabilization of Maml1 and its protein levels were rather slightly decreased, which could be partly due to the toxicity of MG132 in NIH3T3 cells (see Fig. S4A in the supplementary material). We tested other protease inhibitors but did not find any that promoted protein stabilization (see Fig. S4B in the supplementary material), indicating that Maml1 is destabilized by Mesp2 via pathways other than the proteasome pathway.

Because Mesp2 has already been identified as a transcriptional activator, we predicted that the factor(s) involved in Maml1 destabilization would be induced by Mesp2 (Morimoto et al., 2005; Nakajima et al., 2006). To evaluate this possibility, we generated a mutant Mesp2 (Mesp2ΔbHLH) that lacks both DNA binding and dimerization abilities. If Mesp2 functions as a transcription factor, we expected that Maml1 destabilization would not be observed by the addition of Mesp2ΔbHLH. Unexpectedly however, Maml1...
expression was also repressed by this mutant (Fig. 5E, lane 4). To further map the domain required for Maml1 suppression, we generated a series of truncated Mesp2 constructs and tested their ability to destabilize Maml1. Mesp2 proteins lacking the N-terminal domain (Mesp2AA83-370 and AA75-370) did not repress Maml1 expression (Fig. 5E, lanes 7 and 8), whereas AA70-370 retained the capacity to destabilize Maml1 (Fig. 5E, lane 9). Conversely, the N-terminal protein AA1-69 of Mesp2 was sufficient to destabilize Maml1, but a truncated product corresponding to amino acids AA1-60 lacked this repression activity (Fig. 5E, lanes 10 and 11), indicating that there are at least two crucial domains, AA61-69 and AA70-74, in Mesp2 (Fig. 5E). These findings thus strongly suggest that Mesp1 and Mesp2 promote the destabilization of Maml1 independently of their activity as transcription factors.

Maml1 colocalizes with Mesp2 in the nucleus and is repressed in situ
Another possible mechanism by which the destabilization of Maml1 occurred was translational suppression. To test this, we directly monitored Maml1 localization and stability ex vivo. After a 1-hour transfection with HA-Maml1 alone or Maml1 and either Flag-Mesp2 or a Flag-Mesp2 mutant (AA83-370), we monitored the time-course of cell population changes using antibodies against either HA or Flag. In the case of transfectants with HA-Maml1 only, Maml1 expression was detected as a very weak signal at 1 hour after a medium change (data not shown). The signal level and ratio increased thereafter and reached a saturated level after 4 hours. Maml1 expression was found to be stable because the rate of Maml1-expressing cells was unchanged from 4 to 16 hours (Fig. S5 in the supplementary material). In the case of co-transfection with Maml1 and Mesp2, three types of cells, expressing either Maml1 or Mesp2 or coexpressing both proteins, were observed. Interestingly, we found that Mesp2 completely colocalized with Maml1 as nuclear dots that probably correspond to PML bodies (Wu et al., 2000).

It was noted also that cells showing a lower signal for HA-Maml1 than for Flag-Mesp2 were observed only in the transfectants expressing wild-type Mesp2 (Fig. 6B) but not those harboring mutant-type Mesp2 (Fig. 6C). This indicated that HA-Maml1 is initially translated but might be repressed by Flag-Mesp2. In support of this possibility, the cell expression profile changed quickly and the number of cells showing coexpression of HA-Maml1 and Flag-Mesp2 decreased with time and cells expressing only Flag-Mesp2 became predominant after 16 hours (Fig. 6D, left). By contrast, in the Mesp2 mutant transfectants, the profile was almost unchanged with time (Fig. 6D, right) and HA-Maml1-positive cells were observed at a higher frequency compared with those in wild-type Mesp2 transfectants (Fig. 6). These observations led us to conclude that Mesp2 colocalizes with Maml1 in PML bodies and might facilitate their destabilization.
Mesp2 (anti-Flag, green) and nucleic acids (TOTO-3, blue) were detected.

We finally evaluated whether Maml1 is also downregulated by Mesp2 in vivo, the expression pattern of Maml1 would be expected to depend on the expression pattern of Mesp2, which is regulated by the cyclic changes in Notch signaling. We exhaustively examined the dynamic changes of the Maml1 protein expression that are related to changes in the Mesp2 protein expression profile in different Notch clock cycles in the wild-type PSM (Fig. 7A–F’). We used phases I, II and III as the Notch standard time according to the definition by Oginuma et al., which is assessed by the localization of NICD (Oginuma et al., 2008). As expected from our ex vivo analysis, Maml1 expression was significantly lower only in the Mesp2-expressing cells when compared with cells in other regions where Mesp2 is absent in all phases (Fig. 7A–F’). It was further noted that Maml1 protein was not yet affected in the domain with newly activated Mesp2 (Fig. 7F,F’, arrowheads). The repressive effects of Mesp2 were also supported by the analysis of Mesp2-null embryos in which Maml1 was expressed ubiquitously throughout the PSM (Fig. 7G).

Finally, we addressed whether Mesp2 generally acts as a repressor for the Notch signaling pathway via the repression of Maml1. To induce Mesp2 at the desired time-point in the entire body, we crossed a mouse line bearing heterozygous CAG-CAT-Mesp2 with homozygous Cre-ERT2 mice that express a tamoxifen-inducible Cre-recombinase from the Rosa26 locus (Fig. 7H) (Nakajima et al., 2006). We examined the Maml1 expression profile of each embryo recovered at E10.5 (one or two days after the administration of tamoxifen; Fig. 7I). In Cre-ERT2::CAG-CAT-Mesp2 embryos treated with tamoxifen both at E8.5 and E9.5, the expression of Mesp2 was ubiquitously upregulated in nearly all cells (Fig. 7K,L). Whole embryo extracts were then used for western blot analyses. We found a clear reduction of Maml1 protein from Mesp2-misexpressing embryos (Cre-ERT2::CAG-CAT-Mesp2) compared with control embryos (Cre-ERT2::--; Fig. 7M). The double-transgenic embryos also showed malformed heart morphology and vascular network defects in the yolk sac, which are similar to phenotypes observed upon the loss of Notch signaling (Fig. 7K,L compared with 7J; data not shown). These observations strongly suggest that Mesp2 negatively regulates the Notch signaling pathway via the downregulation of Maml1 expression and that the rostral identity of a somite is established by this regulation within a rostral somite compartment (see model in Fig. 8A).

**DISCUSSION**

The negative regulation of Notch signaling is required at the anterior PSM where Mesp2 is expressed

From the results of our current study, we concluded that the activation of Notch signaling is precisely controlled by a distinct event downstream of Mesp2 during somitogenesis. We have previously shown that Mesp2 is induced in the anterior PSM via Notch signaling and Tbx6 function (Yasuhiko et al., 2006). However, once Mesp2 is induced, the canonical Notch signaling pathway must be suppressed in the anterior compartment of a somite to establish the RC polarity. We have previously reported that Lfng induced by Mesp2 partly contributes to the suppression of Notch activity in the rostral compartment (Morimoto et al., 2005). However, defects in the Mesp2-null mice were not rescued by Lfng in a previous study (Oginuma et al., 2010), which is in contrast to the findings of our current experiments with R218H. Furthermore, we have shown that the RC patterning is generated without an NICD on/off state as long as Mesp2 is expressed, which suggests that Mesp2 acts as a general repressor of Notch activity in the anterior PSM.
as Mesp2 is expressed at the presumptive rostral compartment (Oginuma et al., 2010). This indicates that the Mesp2 function downstream of NICD formation is crucial. We thus propose from our present data that Mesp2 might act as the final shut off switch for Notch signaling by disrupting the NICD-Maml1-Rbpj complex (Fig. 8A,B). As Maml1 is an essential component of the canonical Notch signaling pathway, its rapid turnover might be an effective way to locally suppress this signaling.

**Mesp2 might affect other signaling pathways or transcriptional factor(s) via its suppression of Maml1 expression**

Based on our present findings, we identified Maml1 as a target molecule of Mesp2. Previous studies in *Drosophila*, mice and human have demonstrated that Maml protein is an essential component of the NICD-Rbpj complex in the nucleus and might regulate Notch signaling at the transcriptional level (Helms et al., 1999; Kitagawa et al., 2001; Oyama et al., 2007; Shen et al., 2006; Smoller et al., 1990; Wu et al., 2000). Maml protein is also required for chromatin-dependent transactivation by the recombinant NICD-Rbpj enhancer complex in vitro and recruits CBP and p300 to promote nucleosome acetylation at Notch enhancers (Fryer et al., 2002). Furthermore, we speculate that Mesp2 acts as a negative regulator for other signaling pathways such as Wnt or p53 signaling as Maml1 is reported to act as a coactivator for β-catenin or p53 at their target sites (Alves-Guerra et al., 2007; Zhao et al., 2007). It is noteworthy in this regard that Wnt signaling has been reported to be involved in somite segmentation (Aulehla et al., 2008; Takada et al., 1994). We also have previously shown that the mRNA expression of Lef1 (a nuclear effector of the Wnt/β-catenin
Mesp2 has three independent functions leading to (1) the induction of Hes7 as a transcription factor.

A novel molecular mechanism by which Mesp2 represses Maml1 expression

We also demonstrate from our present data that Mesp2 represses Maml1 protein independently of its function as a transcription factor. We investigated the step at which Maml1 is suppressed, i.e. the transcriptional, translational or post-translational level. The expression level of Maml1 mRNA is unaffected by Mesp2, and Maml1 is also suppressed by the bHLH-domain-deletion mutant form of Mesp2 that cannot bind DNA directly (Fig. 5B-E), indicating that the repression does not occur at the transcriptional level. Translational suppression was also deemed to be improbable as Mesp2 localizes exclusively in the nucleus. To fully test this possibility, however, we attempted to monitor protein expression using antibodies against specific tags. Completely merged signals for Mesp2 and Maml1 were observed in the PML body, indicating that Maml1 protein could be translated even in the presence of Mesp2 protein. Consequently, we contend that Mesp2 represses Maml1 protein expression at the post-translational level.

It has already been reported that factors involved in mice somitogenesis are degraded by post-translational modification. Hes7, Mesp2 and Tbx6 were found to be quickly destabilized through ubiquitin-dependent proteolysis (Bessho et al., 2003; Morimoto et al., 2006; Oginuma et al., 2008). We therefore speculated that a post-translational process such as ubiquitination regulates Maml1. However, the destabilization of Maml1 by Mesp2 was not rescued by the addition of MG132 (see Fig. S4 in the supplementary material). Rather, the Maml1 protein levels were reduced when the cells were treated with MG132, even in the absence of Mesp2. We subsequently changed the treatment period and the concentration of MG132 but did not see any recovery over prolonged MG132 exposure; instead, this promoted the destabilization of Maml1. We thus now conclude that the proteasome pathway does not mediate the destabilization of Maml1 by Mesp2. An alternative destabilizing pathway might be lysosomal proteolysis but this pathway is primarily involved in endocytotic events, which are unlikely to play a role in the Mesp2 pathways as Mesp2 localizes only in the nucleus. In this regard, it should be noted that Mesp2 was found to colocalize with Maml1 in PML bodies and the suppression of Maml1 occurs as a result.

As we also know that Mesp2 does not directly interact with Maml1 (data not shown), the identification of the mediating factor is a high priority in order to properly elucidate the mechanism underlying the temporal destabilization of Maml1.

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Competing interests statement
The authors declare no competing financial interests.
Supplementary material
Supplementary material for this article is available at http://dev.biologists.org/lookup/suppl/doi:10.1242/dev.055533/-DC1

References

DEVELOPMENT
**Table S1. Primers used to genotype the knock-in/transgenic mice and for the semi-quantitative RT-PCR analysis**

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<thead>
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<th>Primer</th>
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<td>NeoAR2</td>
<td>AAGCCATAGAGCCACGCAATCCAGCCATCC</td>
</tr>
<tr>
<td>RBP-J-3'</td>
<td>CACATGGTTCCAGACCGGTTGCTG</td>
</tr>
<tr>
<td>HLH-R3</td>
<td>GGAAGGTTGGAATGTCGTCGTTGCTCAGACGCTG</td>
</tr>
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<td>NeoAL2</td>
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