Pax3 Stimulates p53 Ubiquitination and Degradation Independent of Transcription

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Pax3 Stimulates p53 Ubiquitination and Degradation Independent of Transcription

Xiao Dan Wang, Sarah C. Morgan, Mary R. Loeken*

Section on Developmental and Stem Cell Biology, Department of Medicine, Joslin Diabetes Center, Harvard Medical School, Boston, Massachusetts, United States of America

Abstract

**Background:** Pax3 is a developmental transcription factor that is required for neural tube and neural crest development. We previously showed that inactivating the p53 tumor suppressor protein prevents neural tube and cardiac neural crest defects in Pax3-mutant mouse embryos. This demonstrates that Pax3 regulates these processes by blocking p53 function. Here we investigated the mechanism by which Pax3 blocks p53 function.

**Methodology/Principal Findings:** We employed murine embryonic stem cell (ESC)-derived neuronal precursors as a cell culture model of embryonic neuroepithelium or neural crest. Pax3 reduced p53 protein stability, but had no effect on p53 mRNA levels or the rate of p53 synthesis. Full length Pax3 as well as fragments that contained either the DNA-binding paired box or the homeodomain, expressed as GST or FLAG fusion proteins, physically associated with p53 and Mdm2 both in vitro and in vivo. In contrast, Splotch Pax3, which causes neural tube and neural crest defects in homozygous embryos, bound weakly, or not at all, to p53 or Mdm2. The paired domain and homeodomain each stimulated Mdm2-mediated ubiquitination of p53 and p53 degradation in the absence of the Pax3 transcription regulatory domains, whereas Splotch Pax3 did not stimulate p53 ubiquitination or degradation.

**Conclusions/Significance:** Pax3 inactivates p53 function by stimulating its ubiquitination and degradation. This process utilizes the Pax3 paired domain and homeodomain but is independent of DNA-binding and transcription regulation. Because inactivating p53 is the only required Pax3 function during neural tube closure and cardiac neural crest development, and inactivating p53 does not require Pax3-dependent transcription regulation, this indicates that Pax3 is not required to function as a transcription factor during neural tube closure and cardiac neural crest development. These findings further suggest novel explanations for PAX3 functions in human diseases, such as in neural crest-derived cancers and Waardenburg syndrome types 1 and 3.

Introduction

Understanding how regulators of embryonic development function on a molecular level is a major objective of developmental biology. Pax3, a member of the mammalian Pax family of developmental regulators, is expressed in the neuroepithelium, neural crest, and somitic mesoderm [1,2,3]. One hundred percent of mouse embryos that are homozygous for the mutant Pax3 allele, Splotch (Pax3<sup>Sp/Sp</sup>) develop neural tube defects (NTD), cardiac outflow tract defects (COTD), and fail to form skeletal muscle, indicating that Pax3 is essential for formation of these structures [4,5,6]. In humans, Waardenburg syndrome (WS) types 1 and 3 is an autosomal dominant condition that is caused by Pax3 mutations and affects neural crest-derived structures, [7]. Pax proteins are characterized by the presence of a paired box DNA-binding element [1]. Some of the Pax proteins, including Pax3, contain a paired-type homeodomain that also binds to DNA, and a conserved octapeptide [1]. It has traditionally been accepted that Pax3 regulates developmental processes by operating as a transcriptional regulator because: (i) Pax3 contains sequence-specific DNA-binding domains that are capable of directing trans-activation [8,9,10]; (ii) the protein product of the mutant Splotch Pax3 allele is trans-activation defective [11]; and (iii) several genes have been identified that are directly or indirectly regulated by Pax3 [12,13,14,15,16,17,18,19,20,21,22,23]. However, exactly how Pax3 regulates formation of the neural tube and neural crest-dependent structures has not yet been determined.

Apoptotic cells are observed in embryos expressing nonfunctional Pax3 alleles at sites where normal Pax3-expressing neuroepithelial and cardiac neural crest cells are located in w.t. embryos [24,25,26]. This suggests that the ensuing NTD and COTD result from depletion of progenitor cells that are necessary to populate these structures. We showed that inactivation of p53 through germ-line mutation or chemical inhibition prevented the NTD, exencephaly and spina bifida, and COTD that are characteristic of Pax3<sup>Sp/Sp</sup> embryos, as well as associated apoptosis, in embryos expressing nonfunctional Pax3 alleles [25,27]. This indicates that Pax3 is not required in neuroepithelium and neural
cortex to regulate genes that direct morphogenesis or migration, but that it is required to block p53-dependent processes that lead to apoptosis. This contrasts with the role of Pax3 in skeletal muscle development where it serves as an upstream regulator of myogenic gene expression [16,17]. Pax3 protein, but not mRNA, was increased in Pax3<sup>Spp/Sp</sup> embryos, suggesting that Pax3 blocks p53 function by inhibiting p53 protein synthesis, stability, or both [27]. However, the precise mechanism by which Pax3 regulates steady state levels of p53 protein, and whether it involved Pax3 functioning as a transcription factor, has not been determined.

Further study of the molecular mechanism by which Pax3 regulates p53 may be facilitated by a cell culture model of developing neuroepithelium and neural crest. Murine embryonic stem cells (ESC) can be induced to form neuronal precursors that express genes that are characteristic of neuroepithelium, including Pax3 [28]. Thus, if expression of Pax3 causes a reduction in steady-state levels of p53 protein, differentiating ESC would be a valid cell culture model to study the mechanism by which Pax3 blocks p53 function in embryonic neuroepithelium and neural crest.

Results

p53 protein is negatively regulated by Pax3 in ESC

We first investigated whether abundance of p53 protein, but not mRNA, was inversely related to abundance of Pax3 in ESC as in mouse embryos. Murine ESC were grown as undifferentiated cultures (stage 1), or were induced to form neuroepithelial-like neuronal precursors (stage 3) using established methods [29]. There was no difference in abundance of p53 mRNA between stage 1 and stage 3 (Figure 1 A). In contrast, Pax3 mRNA was undetectable in stage 1 ESC but was significantly increased during stage 3. Nestin mRNA, which is expressed in neuroepithelium in vivo and in mESC-derived neuronal precursors [29,30] increased in stage 3 ESC. In contrast to p53 mRNA, p53 protein significantly decreased during ESC differentiation, while Pax3 protein increased in parallel to Pax3 mRNA (Figure 1 B). Nestin protein levels also significantly increased in stage 3 ESC. Immunofluorescence using antibodies against p53 or Pax3 further supported that p53 and Pax3 protein abundance are inversely related in undifferentiated and differentiating ESC (Figure 1 C, D).

Thus, in ESC, just as in mouse embryos, p53 protein, but not mRNA, is inversely related to production of Pax3.

To test whether Pax3 was responsible for the decrease in p53 protein in differentiating ESC the effects of expressing Pax3 in stage 1 ESC, and of knocking down expression of Pax3 in stage 3 ESC, on p53 were examined. Transfecting ESC with a Pax3 expression vector showed that constitutive expression of Pax3 had no effect on p53 mRNA (Figure 1 E) but was sufficient to suppress p53 protein in stage 1 ESC (Figure 1 F). Conversely, knocking down Pax3 using an inducible shRNA in stage 3 ESC increased

Figure 1. Pax3 negatively regulates p53 protein, but not mRNA levels in ESC just as in mouse embryos. (A) Real time RT-PCR of p53, Pax3, and Nestin mRNA in stage 1 (open bars) and stage 3, days 2–8 (solid bars) ESC. Nestin mRNA is expressed in neuroepithelium and in ESC-derived neuronal precursors [29,30] and served as a control for a marker of neuroepithelial neuronal precursors. Each mRNA was normalized to rRNA. In (A), (B), and (D) values represent the mean ± SEM (n = 3 culture dishes). *p<0.01 vs. stage 1. (B) Quantification (band intensity in arbitrary units) of immunoblots of p53, Pax3, and Nestin normalized to β-actin in stage 1 and stage 3 ESC harvested on days as indicated in (A). (C) Indirect immunofluorescence of p53 (green) and Pax3 (red) in stage 1 and stage 3 ESC. Cells were counterstained with DAPI (blue) to visualize nuclei. Cells incubated with secondary antibodies alone generated no detectable signals (not shown). (D) Percent Pax3 or p53 positive cells in stage 1 and stage 3 ESC. Values represent the mean ± SEM (n = 10 fields). (E) Real time RT-PCR of Pax3 and p53 mRNA in stage 1 ESC transfected with empty vector (Control), or vector encoding w.t. Pax3. Each mRNA was normalized to rRNA. ***p<0.0001 vs. control cells. (F) Immunoblot of Pax3 or p53 in stage 1 ESC stably transfected with empty pCMV vector or pCMV-Pax3. (G) Immunoblot of Pax3 or p53 in stage 1 or stage 3 ESC. Stage 3 cultures were untransfected, or transfected with empty shRNA vector (pSingle), pSingle expressing a scrambled shRNA sequence (scrambled), and 3 different Pax3 shRNA sequences. Stage 3 cultures were treated or not with doxycycline during days 4–6.


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p53 protein (Figure 1 G). These results demonstrate that Pax3, and not the process of differentiation per se, is responsible for the decrease in p53 in stage 3 ESC.

**Pax3 stimulates p53 ubiquitination and degradation**

Treatment of lung carcinoma cells transfected with a Pax3 expression plasmid with cycloheximide suggested that Pax3 stimulates p53 degradation [31], however, whether synthesis of p53 or synthesis of a regulator of p53 turnover was also inhibited by cycloheximide was not determined. To examine whether the decrease in p53 protein in ESC-derived neuronal precursors was due to a reduction in protein synthesis, stability, or both, newly synthesized p53 was pulse labeled with [35S]-methionine. The rate of incorporation of [35S]-meth into p53 demonstrated that p53 protein synthesis was not reduced in stage 3 ESC (Figure 2 A). However, assay of [35S]-meth-labeled p53 followed by a chase with unlabeled meth demonstrated that the t1/2 of p53 is reduced approximately 3-fold in stage 3 ESC compared to stage 1 ESC (Figure 2 B), p53 degradation is stimulated by association with Mdm2 and activation of Mdm2 ubiquitin ligase activity [32]. To test whether decreased stability of p53 in stage 3 ESC might be due to increased ubiquitination, ubiquitinated p53 relative to total p53 was assayed by immunoblot. The amount of p53 that was ubiquitinated was significantly increased in stage 3 ESC (Figure 2 C), suggesting that Pax3 stimulates p53 degradation by promoting its ubiquitination.

Although it is possible that Pax3 could regulate expression of genes whose products participate in p53 ubiquitination, we considered that a more rapid modulation of p53 degradation could be effected if Pax3 physically associates in a complex containing p53 and Mdm2. To study this, we immunoprecipitated p53, Pax3, or Mdm2 and examined protein associations by immunoblot. As shown in Figure 2 D, Pax3 and p53 associated with each other, particularly using extracts from stage 3 ESC, and Pax3 also associated with Mdm2. As expected, Mdm2 co-immunoprecipitated with p53, although more of p53 and Mdm2 were associated with each other using extracts from stage 3 ESC than from stage 1 ESC. Inasmuch as p53 is less abundant in stage 3 than in stage 1 ESC, it is possible that Pax3 promotes association of p53 with Mdm2.

We next investigated which structural domains of Pax3 are responsible for association with p53 or Mdm2. As diagrammed in Figure 2 E, the structural domains of Pax3 that have been previously identified include an N-terminal transcription inhibitory domain (ID), the paired domain (PD), a conserved octapeptide (OCT), the paired-type homeodomain (HD), and a C-terminal trans-activation domain (TAD). The PD and HD are each independent DNA-binding domains [9,10] that bind to DNA with higher affinity together than when only one of the domains is bound together [8], the OCT is necessary for homodimerization [11], and the ID and TAD possess transcription inhibition and transcription activation activities, respectively [33]. We constructed plasmids to express glutathione-S-transferase- (GST) and FLAG-tagged proteins fused with full-length w.t. Pax3, or fragments containing various Pax3 structural domains. Additionally, we constructed plasmids to express GST or FLAG fused with the least defective of the proteins encoded by the mutant Pax3 allele, Splotch. The Splotch mutation disrupts the splice acceptor site of exon 4, resulting in four aberrantly spliced transcripts [11,34,35]. Three of the predicted protein products cause frame-shifts beginning in the PD, but the least defective deletes 45 amino acids that include part of the ID and the OCT (Figure 2 E).

GST fusion proteins were incubated with extracts from stage 1 ESC to determine which Pax3 structures can associate with p53 or Mdm2 in vitro (Figure 2 F), and plasmids encoding FLAG fusion proteins were transiently transfected into stage 1 ESC to determine which Pax3 structures can associate with p53 or Mdm2 in intact cells in vivo (Figure 2 G). All fusion proteins containing either the PD or HD associated with p53 and Mdm2 both in vitro and in vivo. Notably, the PD and HD were each able to associate with p53 and Mdm2 in the absence of the other DNA-binding domain. p53 associated with Splotch Pax3 at levels comparable to that of w.t. Pax3 in vitro, but only weakly in vivo. The weak association of Splotch Pax3 in vivo, despite the presence of the HD, which can associate with p53 in the absence of other Pax3 structural domains, suggests that the part of the PD and OCT that are deleted in Splotch Pax3 are necessary to prevent interference by the N-terminal transcription inhibitory domain or the C-terminal trans-activation domain for association of the HD with p53. Mdm2 only weakly associated with Splotch Pax3 both in vitro and in vivo.

The Pax3 paired domain and homeodomain stimulate Mdm2-mediated ubiquitination of p53 and p53 degradation

The physical association of Pax3 with p53 and Mdm2 suggested that Pax3 might regulate p53 ubiquitination. To test this, ubiquitination of GST-p53 by GST-Mdm2 in the presence or absence of GST-Pax3 was assayed in vitro. Ubiquitination of GST-p53 was stimulated by GST-Pax3 in a dose-dependent fashion (Figure 3 A). This activity was dependent on Pax3 structures, as GST alone did not stimulate p53 ubiquitination (Figure 3 B). GST-Pax3 did not stimulate p53 ubiquitination in the absence of GST-Mdm2 (Figure 3 C), demonstrating that Pax3 was not itself an ubiquitin ligase, but that it stimulated ubiquitin ligase activity of Mdm2.

To determine which structural domain(s) of Pax3 are responsible for stimulation of p53 ubiquitination, in vitro ubiquitination of GST-p53 by GST-Mdm2 with the addition of each of the GST fusion proteins containing Pax3 structural domains was examined. Each of the structural domains that are capable of complex formation with p53 and Mdm2 stimulated ubiquitination of GST-p53, although the PD appeared to be more potent than the HD (Figure 3 D). Notably, GST-Splotch Pax3 did not increase ubiquitination of GST-p53.

To test whether the same Pax3 structural domains that can stimulate Mdm2-mediated p53 ubiquitination in vitro can stimulate p53 ubiquitination and degradation upon expression in ESC, plasmids encoding FLAG fusion proteins were transiently transfected into stage 1 ESC. As shown in Figure 4 A, the Pax3 structures that contain the PD or the HD, except for Splotch Pax3, stimulated p53 ubiquitination in vivo, just as they did in vitro. Transfecting increasing concentrations of plasmids encoding FLAG fusion proteins caused a dose-dependent decrease in steady state levels of p53 only if they encoded Pax3 structures that were capable of stimulating p53 ubiquitination (Figure 4 B, C). Because each of the PD and HD were capable of stimulating p53 ubiquitination and down regulation when they were expressed in the absence of the C-terminal trans-activation domain or the N-terminal transcription inhibitory domain, this indicates that down regulation of p53 does not require Pax3 to function as a transcriptional regulator. There was no effect of increasing concentrations of FLAG-Splotch Pax3 on p53 steady state levels. This is not due to decreased stability of the Splotch Pax3 protein, because steady-state levels of FLAG-Splotch Pax3 were similar to those of FLAG-w.t. Pax3 (Figure 4 B, C). Instead, the failure of Splotch Pax3 to decrease p53 levels appears to be due to defective association of Splotch Pax3 with p53 and Mdm2, and failure to stimulate Mdm2 ubiquitin ligase activity.
Figure 2. Pax3 stimulates p53 degradation and ubiquitination and physically associates with p53 and Mdm2. (A) Pulse labeling with \(^{35}\)S-met to determine the rate of p53 synthesis in stage 1 and stage 3 ESC. Quantitation of \(^{35}\)S-p53 is described in the supporting online material. (B) Pulse-chase labeling to determine the t1/2 of p53 in stage 1 and stage 3 ESC. (C) Quantitation of ubiquitinated p53/total p53 in stage 1 and stage 3 ESC following immunoprecipitation of p53 and immunoblotting using anti-ubiquitin or anti-p53 antibodies. *p < 0.05 vs. stage 1. (D) Whole cell extracts of stage 1 or stage 3 ESC were immunoprecipitated using antibodies against p53, Pax3 or Mdm2, and then immunoblotted using antibodies against p53, Pax3, and Mdm2. (E) Schematic diagram of full-length w.t. Pax3, Pax3 structural domains, and a Splotch Pax3 (Sp) protein product that were expressed as GST and FLAG fusion proteins. N-term, amino-terminus of Pax3 through the homeodomain; C-term, carboxy-terminus distal to the homeodomain (including the trans-activation domain); DBD, DNA-binding domain (PD through HD); ID, the trans-activation inhibitory domain (amino-terminal to the PD); PD, paired domain; OCT, octapeptide (carboxy-terminal of the PD to amino-terminal of the HD); and HD, homeodomain. The Splotch cDNA deletes exon 4 and lacks coding sequence for part of the PD and the OCT but retains the HD. Numbers refer to amino acid positions of w.t. Pax3. (F) Immunoblot using antibodies against p53 (upper panel), Mdm2 (middle panel), or GST following incubation of whole cell lysates from stage 1 ESC with GST-Pax3 fusion proteins linked to glutathione-sepharose beads. (G) Immunoblot using antibodies against p53 (upper panel), Mdm2 (middle panel), or FLAG following incubation of whole cell lysates from stage 1 ESC that had been transiently transfected with plasmids encoding FLAG-tagged Pax3 fusion proteins with antibody against FLAG linked to M2 beads.

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Discussion

It has long been recognized that Pax3 is essential for formation of the neural tube and neural crest-dependent structures. Until now, it has been believed that the activity of Pax3 as a DNA-binding transcription factor is responsible for these functions, and that the phenotype of \( \text{Pax3}^{\text{Sp}}/\text{Sp} \) embryos is due to loss of transcription factor activity of \( \text{Splotch} \) Pax3 [11,35]. Our previous studies demonstrated that neural tube closure, cardiac neural crest migration, and cardiac outflow tract septation proceeds normally in \( \text{Pax3}^{\text{Sp}}/\text{Sp} \) and \( \text{Pax3} \)-null embryos as long as p53 is inactivated [25,27], demonstrating that Pax3 is required for these processes only to inactivate p53. The results presented here demonstrate that Pax3 inactivates p53 by stimulating its degradation and that stimulation of p53 degradation occurs independent of Pax3 binding to DNA and regulation of transcription. Therefore, while Pax3 may, in addition, regulate gene expression during neural tube closure, cardiac neural crest migration, and cardiac outflow tract septation proceeds normally in \( \text{Pax3}^{\text{Sp}}/\text{Sp} \) and Pax3-null embryos as long as p53 is inactivated [25,27], demonstrating that Pax3 is required for these processes only to inactivate p53. The results presented here demonstrate that Pax3 inactivates p53 by stimulating its degradation and that stimulation of p53 degradation occurs independent of Pax3 binding to DNA and regulation of transcription. Therefore, while Pax3 may, in addition, regulate gene expression during neural tube closure, cardiac neural crest migration, and cardiac outflow tract septation only to stimulate p53 ubiquitination and degradation independent of transcription. Moreover, these findings show that the mutant \( \text{Splotch} \) Pax3 allele is defective in associating with p53 and Mdm2 and fails to stimulate p53 ubiquitination and down regulation. Because stimulation of p53 degradation by w.t. Pax3 occurs independent of its activity as a transcription factor, this indicates that \( \text{Splotch} \) Pax3 is functionally null, not because it is defective as a transcription factor, but because it fails to effectively complex with p53 and Mdm2 and to stimulate Mdm2-mediated ubiquitination of p53.

Associations of the Pax3 PD and HD with other proteins, including the retinoblastoma tumor suppressor protein (Rb), Msx1, Mox1 and Mox2, and Ets have been reported [36,37,38,39]. However, each of these associations functioned to block Pax3 binding to DNA and activating transcription. In contrast, the association of the Pax3 DNA-binding domains with p53 and Mdm2 that are reported here confers an activity on these domains separate from gene regulation.

Additionally, our findings suggest that human diseases associated with \( \text{PAX3} \) may be explained by insufficient or excessive p53 degradation. For example, almost all of the 76 different \( \text{PAX3} \) mutations that have been identified in WS type 1 and type 3 are localized to the PD, the OCT, or the HD (Figure S1 and Table S6). Because these mutations interfere with the transcription factor activity of \( \text{PAX3} \), it has been widely accepted that altered expression of \( \text{PAX3} \) target genes is responsible for the WS phenotype. However, our results predict that mutation of these \( \text{PAX3} \) domains ought to also impair stimulation of HDM2-mediated ubiquitination of p53. Thus, failure to block p53-dependent processes, rather than altered expression of \( \text{PAX3} \) target genes, may be responsible for the WS phenotype. Further research will be necessary in order to determine whether this is the case. On the flip side, \( \text{PAX3} \) over expression occurs in many neural crest or neuroectodermal tumors.
such as melanoma, neuroblastoma, and Ewing’s sarcoma [40,41,42,43,44]. The p53 gene is rarely deleted or mutated in these tumors [45,46]. Thus, p53 loss of function may be accomplished by physical interaction with PAX3, and this may be crucial to the oncogenesis of these tumors. Other Pax proteins have oncogenic potential, as indicated by fibroblast transformation [47]. However, only Pax5 has been shown to regulate p53, and this was by direct transcription inhibition [48]. Whether downregulation of p53 by either transcriptional or post-transcriptional mechanisms is a general property of the Pax family remains to be determined.

Our conclusions may appear audacious given the existing dogma that Pax3 regulates neural tube closure and cardiac neural crest development by virtue of its activity as a transcription factor. However, reexamination of the existing literature in light of our findings can reveal a new paradigm of the mechanism by which Pax3 regulates neural tube and neural crest development. In particular, there are several genes, including two identified by us, whose expression is increased or decreased by Pax3 [12,13,14,15,16,17,18,19,20,21,22,23]. Nonetheless, heretofore there is little functional evidence that Pax3 directly regulates any of these putative target genes and that they are mechanistically involved in neural tube closure or neural crest development. The only gene for which there is functional evidence is Msx2, whose expression is negatively regulated by Pax3 in the neural tube and neural crest [19]. Msx2 loss-of-function (Msx2−/−) rescued COTD and embryonic lethality in Pax3Sp/Sp embryos, although NTD were not rescued [19]. This evidence notwithstanding, the putative Pax3 binding site within the Msx2 promoter is low affinity [8], suggesting that Pax3 might not directly regulate Msx2 under physiological conditions. There is evidence that Msx2 expression is upregulated along with p53 [49], suggesting that Msx2 might be a direct or indirect target of p53. Thus, while Pax3 can directly regulate Msx2 under experimental conditions, effects of Pax3 on Msx2 expression in embryonic cardiac neural crest may be indirect and mediated by altered p53 levels. The failure of Msx2 deletion to rescue NTD in Pax3Sp/Sp embryos indicates that Msx2 is not a functional target of Pax3 in the neural tube, or that its downregulation is not sufficient to mediate effects of Pax3 on neural tube closure.

Interestingly, it was recently reported, using conditional deletion of Pax3 in premigratory and/or migratory neural crest, that Pax3 is only required for expression in early premigratory and migratory cardiac neural crest [50]. This is consistent with our findings, using pifithrin-α, that inhibition of p53 by Pax3 is only required during approximately the first 4 hours after the onset of

![Figure 4. The Pax3 domains that associate with p53 and Mdm2 stimulate p53 ubiquitination and down regulation in vivo.](image-url)
Pax3 expression on E8.5 in order for normal cardiac neural crest migration and outflow tract septation to occur [25]. Thus, while Pax3-linked reporter gene expression can be detected in cardiac neural crest cells at least through the 35 somite stage (approximately E9.5) [25], it is only required to block p53-dependent processes that are required for subsequent outflow tract septation in early premigratory and migratory cardiac neural crest cells. Our findings lead to the overarching question of why it is necessary for Pax3 to functionally inactivate p53 during embryonic development. Studies using ESC or generation of induced pluripotent stem (iPS) cells have indicated that p53 is activated during ESC differentiation, and that activation of p53 inhibits self-renewal and promotes differentiation [31,52,53,34,55]. Thus, it may be necessary for Pax3 to titrate the activity of p53 once embryonic cells start to differentiate along a neural lineage in order to prevent premature loss of proliferative capability and multipotency until a critical cell mass or cellular localization is achieved.

Materials and Methods

Ethics Statement

Mouse embryos used for recovery of RNA for generation of p53 and Mdm2 expression plasmids were obtained from pregnant mice on E10.5 using procedures that are approved by the Joslin Diabetes Center Institutional Animal Care and Use Committee under Protocol #92-06.

Embryonic Stem Cell Culture

Mouse D3 ESC (ATCC) were cultured and induced to form neuronal precursors as described [29], except that 0.5 μM retinoic acid (Sigma) was added to embryoid body cultures. Briefly, cells were grown as undifferentiated, monolayer cultures (referred to as stage 1) on 0.1% gelatin-coated tissue culture dishes (without transferrin, and selenium (Sigma) was added to embryoid body cultures. Briefly, cells were transferred to tissue culture dishes in DMEM:F12 media with 0.5 M retinoic acid, but without LIF, for 4 days, then differentiated to stage 3, then 1 μg/ml of doxycycline (Clontech) was added to media on day 4 of stage 3 ESC cultures. Cultures were harvested 48 h after doxycycline administration.

Transfection of ESC

All transient and stable transfections of stage 1 ESC were performed using Lipofectamine 2000 (Invitrogen) at a concentration of 10 μg/ml. Stable transfectants were selected using 400 μg/ml of G418 (Invitrogen). Transient transfection cultures were terminated 48 h after transfection. pCMV-Pax3 [8,47] or empty CMV vector [8] were stably transfected into cells in 35 mm dishes using 1.8 μg plasmid DNA. Recombinant shRNA plasmids targeting Pax3 mRNA, or empty vector were stably transfected into cells in 35 mm dishes using 2 μg plasmid DNA. To induce shRNA expression, ESC were first differentiated to stage 3, then 1 μg/ml of doxycycline (Clontech) was added to media on day 4 of stage 3 ESC cultures. Cultures were harvested 48 h after doxycycline administration.

Association of FLAG-Pax3 and Pax3 domain fusion proteins with endogenous ESC proteins was studied using transient transfection of ESC grown in 10 cm plates with 24 μg plasmid DNA. The effect of increased expression of FLAG-Pax3 and Pax3 domain fusion proteins on p53 protein was tested using transient transfection of ESC in 35 mm dishes with 4 μg plasmid DNA.

Real time RT-PCR

Total RNA was extracted using Ultraspec (Biotecx Laboratories), Real-time RT-PCR was performed in quadruplicate as described using rRNA as the normalization control [57]. Primer and probe sequences for Pax3 and p53 were as previously reported [57,58]. Primers and probes for rRNA and Nestin were obtained from PerkinElmer.

Immunoblot Analyses

Whole cell extracts were prepared and analyzed by immunoblot as described [27,59]. Antibodies and their working dilutions of GST fusion proteins encoding murine Mdm2 and p53 coding were generated using cDNA obtained from E10.5 mouse embryos. All PCR were performed using Taq ready mix (Sigma, St Louis, MO), except the PCR to generate the Splotch Pax3 internal deletion, in which PhuulTR High Fidelity DNA polymerase (Stratagene, La Jolla, CA) was used. The PCR products were inserted into pGEX-3X (GE healthcare, Piscataway, NJ) that had been digested with BamHI and EcoRI (New England Biolabs Inc., Ipswich, MA). To construct GST-Splotch Pax3, a linear PCR product was generated using GST-Pax3 FL as template, and primers that would amplify all of the plasmid except nt 839–973 (exon 4). The methylated template was digested with DpnI (New England Biolabs Inc., Ipswich, MA). To generate GST fusion proteins encoding murine Mdm2 and p53, total RNA from whole mouse embryos was reverse transcribed as described [56], and the resulting cDNA was amplified using primer sequences, above. The p53 PCR product was digested with BamHI and EcoRI and inserted into the BamHI and EcoRI sites of pGEX-3X. The Mdm2 PCR product was digested with BglII and EcoRI and inserted into the BamHI and EcoRI sites of pGEX-3X. All plasmids were grown using competent Rosetta cells (Novagen, Madison, WI). DNA sequencing by the Dana-Farber/Harvard Cancer Center DNA Resource Core confirmed the accuracy of cDNA sequences within all recombinant plasmids.
primary and secondary antibodies are listed in Table S3. Antibodies coupled to horseradish peroxidase (HRP) were detected by chemiluminescence (PerkinElmer) and exposure to x-ray film. Band intensity was quantified using Adobe Photoshop (Version 9.0.1).

Immunoprecipitation

Two hundred μg protein from whole cell extracts were pre-cleared at 4°C for 1 hour with 10 mg non-immune IgG and 10 ml of 50% protein A/G beads (Santa Cruz Biotechnology). The pre-cleared extract was incubated with appropriate antibodies (Table S4) while rocking at 4°C overnight. Protein A/G beads were added for one hour prior to precipitation. The precipitated proteins were analyzed by immunoblot as above.

Immunofluorescence microscopy

ESC were grown on gelatin-coated cover slips. Cells were fixed with 4% paraformaldehyde, permeabilized with 10% Triton X-100-PBS, blocked in 5% BSA-PBS, and washed in 1% BSA-PBS. The cells were then incubated with primary antibodies at 4°C overnight, and secondary antibodies for 1 hour in the dark at room temperature (see Supplementary Table S5 for antibody details). Cells were counterstained for 5 min. with 300 nM DAPI in PBS. Both antibody incubations were followed by three 10 minute washes in PBS. Cells were imaged with a Nikon 80i fluorescence microscope.

Measurement of rates of p53 protein synthesis and decay

p53 synthesis in stage 1 and stage 3 ESC was assayed by pulse labeling with 35S-methionine. Briefly, cultures were incubated in cysteine- and methionine-free DMEM for 15 minutes. The media were replaced with cysteine- and methionine-free media containing 0.17 μCi/μl 35S-methionine ([175 Ci/mmol)] and cultures were incubated for times indicated. p53 was immunoprecipitated from whole cell extracts, electrophoresed, and immunoblotted. p53 bands were cut from nitrocellulose filters and were counted in a scintillation counter (Beckman Coulter). The relative amount of newly synthesized p53 was expressed as 35S-cpm/p53 immunoreactivity (determined by scanning and quantitation of x-ray film). Curves were compared using nonlinear regression.

The rates of p53 decay in stage 1 and stage 3 ESC were assayed by pulse-chase labeling. Briefly, cells were labeled with 35S-methionine-containing media as above for 1 hour. Media were removed, cultures were rinsed two times with PBS, and were then incubated in complete DMEM. The amount of 35S-p53 at each time point was quantitated as above. Nonlinear regression was used to calculate the half-life of p53.

In vitro GST Fusion Protein Association Assay

Expression of GST fusion proteins by Rosetta E. coli was induced as described [60]. GST fusion proteins were isolated as described [8]. Five hundred mg protein from stage 1 whole cell lysates were incubated with glutathione-sepharose beads (GE healthcare, Piscataway, NJ) coupled to GST fusion proteins, according to the manufacturer’s instructions. The ESC proteins that co-precipitated with FLAG fusion proteins were identified by immunoblot using antibodies listed in Table S3.

In vitro Ubiquitination Assay

In vitro ubiquitination reactions were performed as described [60]. The reaction mixture (20 μl) contained 10 ng GST-p53 (murine), 24 ng E1 (Boston Biochem), 20 ng GST-UbcH5C (Boston Biochem), 150 ng GST-Mdm2 (murine), 10 μg His-ubiquitin (Boston Biochem), plus GST fusion proteins containing full length Pax3 or Pax3 domains. After incubation at 37°C for 60 min, the reaction products were terminated with stop buffer (Boston Biochem). Ubiquitinated and unubiquitinated p53 were detected by immunoblot using goat anti-p53 antibodies.

In vivo Ubiquitination Assay

Whole cell lysates were prepared from stage 1 or stage 3 ESC, or from stage 1 ESC transiently transfected for 48 h with 4 μg FLAG-tagged plasmid DNA in 35 mm plates. 500 μg protein were pre-cleared and immunoprecipitated with anti-p53 antibodies (Ab1 and Ab3) and protein A/G beads at 4°C overnight. The precipitated proteins were analyzed by immunoblot with anti-ubiquitin antibodies.

Statistical Analyses

All statistical analyses were performed using GraphPad Prism software v. 4.0. Data shown are mean ± S.E.M.

Supporting Information

Figure S1 Locations of Waardenburg syndrome types 1 and 3 mutations within PAX3. The major structural domains and locations of intron-exon borders are shown. Mutations causing premature termination are shown above the protein structure, and those that do not cause premature termination (frame-shift or deletion) are shown below the protein structure. Mutations associated with WS3 are shown in italics. Mutations caused by nucleotide insertions or deletions are indicated by nt location and number of inserted or deleted nt; mutations caused by point mutations are indicated by amino acid substitutions. Further description of PAX3 mutations associated with WS1 and 3 and references are located in Table S6.

Table S1 Oligonucleotide Sequences for Pax3 shRNA.

Short hairpin RNA (shRNA) sequences targeting Pax3 mRNA were designed and inserted into pSingle-tTS-shRNA (Clontech) as described in Supplementary Materials and Methods. Xho I sites are highlighted in green; short hairpin sequences are highlighted in yellow; Mlu I sites are highlighted in purple; Hind III sites are highlighted in turquoise.

Table S2 Primer sequences and PCR conditions for construction of GST fusion proteins. Key: FL, full length; DBD, DNA-binding domains; ID, inhibitory domain; PD, paired domain; OCT, conserved octapeptide; HD, homeodomain.
References


