A morphogenetic wave of \( p27^{\text{Kip1}} \) transcription directs cell cycle exit during organ of Corti development

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The molecular mechanisms coordinating cell cycle exit with cell differentiation and organogenesis are a crucial, yet poorly understood, aspect of normal development. The mammalian cyclin-dependent kinase inhibitor \( p27^{\text{Kip1}} \) is required for the correct timing of cell cycle exit in developing tissues, and thus plays a crucial role in this process. Although studies of \( p27^{\text{Kip1}} \) regulation have revealed important posttranscriptional mechanisms regulating \( p27^{\text{Kip1}} \) abundance, little is known about how developmental patterns of \( p27^{\text{Kip1}} \) expression, and thus cell cycle exit, are achieved. Here, we show that during inner ear development, transcriptional regulation of \( p27^{\text{Kip1}} \) is the primary determinant of a wave of cell cycle exit that dictates the number of postmitotic progenitors destined to give rise to the hair cells and supporting cells of the organ of Corti. Interestingly, transcriptional induction from the \( p27^{\text{Kip1}} \) gene occurs normally in \( p27^{\text{Kip1}} \)-null mice, indicating that developmental regulation of \( p27^{\text{Kip1}} \) transcription is independent of the timing of cell cycle exit. In addition, cell-type-specific patterns of \( p27^{\text{Kip1}} \) transcriptional regulation are observed in the mature organ of Corti and retina, suggesting that this mechanism is important in differential regulation of the postmitotic state. This report establishes a link between the spatial and temporal pattern of \( p27^{\text{Kip1}} \) transcription and the control of cell number during sensory organ morphogenesis.

KEY WORDS: \( p27^{\text{Kip1}} \), Cell cycle, Development, Morphogenesis, Inner ear, Cochlea, Organ of Corti, Mouse

INTRODUCTION

Cell proliferation and differentiation are coordinated during the normal development of tissues and organs, although our knowledge of the molecular mechanisms underlying this coordination remains incomplete (Cremini et al., 2003; Pagano and Jackson, 2004; Zhu and Skoulitchi, 2001). During development, cell cycle exit is regulated by a family of cyclin-dependent kinases (CDKs), which, together with their positively acting co-factors, the cyclins, mediate the progression through the cell cycle (Sherr and Roberts, 1999). Regulation of the activity of the cyclin/CDK complexes occurs at several levels, including transcriptional and posttranscriptional control of cyclin genes. Posttranslational modifications of the CDK molecule itself, and regulation by two families of CDK inhibitor proteins (CKIs): the Ink4 family, which includes p16\(^{\text{Ink4a}}\), p15\(^{\text{Ink4b}}\), p18\(^{\text{Ink4c}}\), and p19\(^{\text{Ink4d}}\), and the Cip/Kip family which includes p21\(^{\text{Cip1}}\), p27\(^{\text{Kip1}}\), and p57\(^{\text{Kip2}}\). In particular, the developmental role of \( p27^{\text{Kip1}} \) has received some attention since it was shown that the loss of \( p27^{\text{Kip1}} \) leads to overall growth defects, multiorgan hyperplasia and other tissue-specific defects caused by a lack of timely cell cycle exit (Ellledge et al., 1996; Fero et al., 1996; Kiyokawa et al., 1996; Nakayama et al., 1996). Examples include developmental abnormalities in the inner ear (Chen and Segil, 1999; Lowenheim et al., 1999), retina (Dyer and Cepko, 2001a; Dyer and Cepko, 2001b; Levine et al., 2000; Nakayama et al., 1996), hematopoietic system (Ezoe et al., 2004), ovary (Tong et al., 1998) and nervous system (Casaccia-Bonnefil et al., 1999; Cunningham and Roussel, 2001; Doetsch et al., 2002; Durand et al., 1998; Zindy et al., 1999). The appearance of tissue-specific defects suggests that the timing of \( p27^{\text{Kip1}} \) expression during development is critical, not only for the generation of the correct relative numbers of constituent cell types in any given tissue, but also for the proper timing of cell cycle exit relative to other developmental events such as differentiation.

Development of the organ of Corti, the auditory sensory epithelium, provides an example of the need for the precise control of cell number during development, and the importance of \( p27^{\text{Kip1}} \) in coordinating cell cycle exit with differentiation and patterning. In \( p27^{\text{Kip1}} \)-null animals, the timing of cell cycle exit of auditory sensory progenitors is delayed, and supernumerary hair cells and supporting cells are produced (Chen and Segil, 1999; Lowenheim et al., 1999). Although hair cells and supporting cells in the \( p27^{\text{Kip1}} \)-null organ of Corti appear normal, and also appear to connect normally to neurons of the spiral ganglion, the animals are deaf, as assayed by a number of physiological parameters, including auditory brainstem responses and otoacoustic emissions (Chen and Segil, 1999; Lowenheim et al., 1999). While not ruling out the possibility that defects in other elements of the auditory system are responsible for the deafness of these mice, one possible explanation is that the delicate micromechanics of the organ of Corti (Nilsen and Russell, 2000) are disrupted by the presence of the supernumerary cells present in the mutant, and that the precise control of cell number by \( p27^{\text{Kip1}} \) during the formation of the organ of Corti is crucial to normal cochlear function.

Little is known about the mechanism by which the complex patterns of \( p27^{\text{Kip1}} \) abundance are regulated during embryonic development in vertebrates. Studies of \( p27^{\text{Kip1}} \) regulation have been conducted primarily in cell culture and have emphasized the importance of posttranscriptional (Agrawal et al., 1996; Hengst and Reed, 1996; Millard et al., 1997) and posttranslational (Muller et al., 1997a; Nakayama et al., 2001; Pagano et al., 1995; Sheaff et al., 1997; Tam et al., 1997; Vlach et al., 1997) mechanisms for cell cycle...
regulation. Nonetheless, a growing number of reports, particularly in cancer cells, indicate a role for transcriptional regulation in response to specific physiological conditions and in a variety of isolated cell types (Servant et al., 2000; Chandramohan et al., 2004; Gizard et al., 2005; Inoue et al., 1999; Laub et al., 2005; Li et al., 2002; Medema et al., 2000; Murata et al., 2005; Stahl et al., 2002; Wang et al., 2005; Williamson et al., 2002). In addition, expression of the Drosophila p27Kip1 homolog Dacapo (DAP) (de Nooij et al., 1996; Lane et al., 1996) has been shown to be regulated transcriptionally by a complex array of tissue-specific and developmentally regulated enhancer/promoter elements (Liu et al., 2002; Meyer et al., 2002).

Thus, in spite of the emphasis on posttranscriptional mechanisms of p27Kip1 regulation during the cell cycle, the long-term transcriptional regulation of p27Kip1 during development may play a role in the tissue-specific pattern of cell cycle exit in mammals. Here, we report that a developmentally regulated wave of p27Kip1-protein expression controls the spatial and temporal pattern of cell cycle exit in the embryonic cochlear duct. With the aid of a BAC transgenic reporter in which GFP is expressed under the control of the p27Kip1 locus, we show that this wave of p27Kip1 expression is regulated at the transcriptional level, and that this pattern of transcriptional regulation of p27Kip1 expression is independent of the cell cycle events in this tissue. In addition, tissue- and cell-type-specific patterns of p27Kip1 expression at later stages in the development of the inner ear and the retina suggest that the transcriptional control of p27Kip1 may be important for the ongoing control of the postmitotic state of a number of cell populations. Thus, the precise spatial and temporal control of p27Kip1 transcription is crucial for the normal development and homeostasis of the organ of Corti, and probably many other developing organ systems.

**MATERIALS AND METHODS**

**Animals, cell birth dating and quantification of BrdU incorporation**

Animal care was in accordance with institutional (AALARAC) guidelines and was approved by the Animal Care and Use Committee of the House Ear Institute. Animals for timed matings were put together in the evening and the next morning litters of those females that were discovered to have plugs were designated E0.5.

To analyze cell cycle events in the developing inner ear, timed pregnant female mice were injected with BrdU to label mitotic cells in the embryos. BrdU (5 mg/ml) was prepared in 7 mM NaOH buffer (pH 7.0) and injected intraperitoneally into pregnant mice at 50 mg of body weight. Two different injection regimens were used:

1. To quantify cell cycle exit of hair cells, timed pregnant females (CD-1) were injected three times (at 10.00, 12.00 and 14.00 h) on specific embryonic days and the embryos were allowed to survive until birth, at which time newborns were decapitated, and organ of Corti dissected, prepared as whole-mount surface preparations, and double-labeled with anti-BrdU and anti-Myosin VIIa to identify hair cells whose progenitors were still dividing at the time of BrdU injection. Double-labeled surface preparations were photographed along their entire length and computer reconstructed using Adobe Photoshop. For quantification of BrdU+ hair cells, the photographed organ of Corti was divided into seven segments of equal length, and the number of BrdU+ hair cells, and the total number of Myosin VIIa+ hair cells were counted for each segment. The percentage of BrdU-positive hair cells versus total hair cells was used to determine the percentage of hair cell progenitors still actively in the cell cycle at the time of BrdU injection (Fig. 2B).

2. To analyze the ongoing pattern of cell division in embryos, timed pregnant females were injected once at 11:00 h and sacrificed two hours later (as in Fig. 2A,E,F and Fig. 4). Embryos were fixed by immersion in 4% buffered paraformaldehyde for 1-2 hours and the inner ears were then dissected either for whole mounts or for cryostat sectioning and immunohistochemistry as previously described (Chen and Segil, 1999). **Immunohistochemistry**

Embryos or dissected bulla were submerged overnight in 4% paraformaldehyde in phosphate-buffered saline (PBS, pH 7.4) at 4°C. Cryosections were prepared from whole embryos using standard procedures, as before (Chen and Segil, 1999). For whole-mount immunohistochemistry, cochleae were dissected in PBS, the lateral wall of the cochlea and tectorial membrane were first dissected free and the organ of Corti was then removed. For immunostaining, organ of Corti whole-mount preparations and cryosections were permeabilized in 0.2% Triton X-100/PBS for 20 minutes, blocked with 4% donkey serum/PBS for 30 minutes, then incubated with primary antibody (diluted in blocking solution) at 4°C overnight. Secondary antibodies conjugated with fluorescent dyes were used to visualize the labeled cells. The primary antibodies used were anti-BrdU antibody (Chemicon, mouse monoclonal, dilution 1:100), anti-p27Kip1 antibody (NeoMarkers, mouse monoclonal, dilution 1:100), anti-Myosin VIIa antibody (rabbit polyclonal, courtesy of Christine Petit and Aziz Ed-Amraoui, Pasteur Institute, dilution 1:10000) and anti-Glutamine Synthetase (rabbit polyclonal, Transduction Laboratories, dilution 1:100). Secondary antibodies were either FITC- or Rhodamine-conjugated (Jackson ImmunoResearch, dilution 1:200).

For BrdU staining, the tissues were pre-treated in 2 N HCl for 1 hour at 37°C, followed by neutralization with 0.1 M boric acid (pH 8.5) for 30 minutes at room temperature. For anti-p27Kip1 staining, antigen retrieval was accomplished by boiling in 10 mM citric acid buffer for 10 minutes before permeabilization (Chen and Segil, 2002). Because the sodium citrate treatment attenuates EGFP reporter signal significantly, micrographs of native EGFP were captured prior to treatment. Confocal imaging of whole-mount cochlea was carried out under the z-sectioning mode at 10-μm intervals followed by 3D projection using a Zeiss LSM410 microscope.

**p27Kip1/BAC transgenic mice**

Bacterial Artificial Chromosome (BAC) #485G10 containing the p27Kip1 locus was identified by screening a mouse BAC library (High density CITB Mouse BAC Colony DNA membranes, Catalog number 96050; Research Genetics, AL). Nucleotide (nt) numbering is based on NCBI contig number NT_039359. BAC end sequencing indicated that clone #485G10 contained a 129-kb insert from nt 4627867 to nt 4756781. This p27Kip1 locus is flanked by ~51 kb 5' and ~78 kb 3' relative to the start site of p27Kip1 transcription (Coleman et al., 2001).

Bacterial homologous recombination was used to modify the BAC (Yang et al., 1997; Yang et al., 1999). An IRES/EGFP reporter cassette (Yang et al., 1999) was targeted to the 3' non-coding region of the p27Kip1 gene using two homology arms of ~500 bp in length. The left homology arm corresponds to nt 4680198-4680727, 5'-GCAATTAAATTAACCCCTATCCGGAGCTTT-GTCTTGGCC-3' and 5'-GCAAGGTATCCTGCTTCGCAGAAGCCGGCCGGTCTTCC-3'; and the right homology arm corresponds to nt 4680728-6468123, 5'-GCAATTAAATTAACCCCTATCCGGAGCTTT-GTCTTGGCC-3' and 5'-GCAACTCTAGGAGCCGCTAATCTCACCCTTACATC-3'. The first exon of the p27Kip1 gene was replaced in a second round of bacterial homologous recombination inserting the bacterial neo gene between nt 467950 and 4680024. The neo gene coding sequence was not placed in frame to the translation start site of p27Kip1 gene. Mutations were subsequently verified by the Southern blot and sequence analysis (data not shown). BAC DNA was prepared as described (Yang et al., 1999), and transgenic mice were established using standard techniques by the Transgenic Mouse Core Facility (University of Southern California, Los Angeles, CA). The transgenic founders were generated in the genetic background B6D2F1 and mated to CD-1 mice to generate mice used for this study. Genotyping was performed using polymerase chain reaction (PCR) with PCR primer pairs: 5'-CGAAGGCTCAAGGGCGCCCA-CCAT-3' and 5'-GCACGGGGCCGTGCAGGTTGGGTCTCAGTGT-3', producing a 314 bp EGFP band; and 5'-ATGATTTGAAAGCTTGGG-3' and 5'-TCAAGAAGACTCTGGTACAAGAGGG-3', producing a 794 bp neo band.

**RESULTS**

The mouse inner ear develops from the otic placode between embryonic day 8.0 (E8) and E8.5 (Kelley and Bianchi, 2001; Kiernan et al., 2002). Starting on E9 the placodal epithelium
begins to invaginate to form the otic pit and by E9.5 an otic vesicle has formed. Starting around E10.5, the ventral portion of the otocyst begins to elongate and by E11.5 this elongating portion forms a rudimentary cochlear duct. In Fig. 1, a collection of dissected embryonic cochlear epithelial whole mounts illustrates the growth of the cochlear duct between E12.5 and E17.5. Coiling of the cochlear duct begins around E12, and the duct continues to grow and coil until it has reached a full 1.5 turns by around E18. Cellular differentiation within the cochlear duct requires the upregulation of the atonal homolog Atoh1 (Math1) (Bermingham et al., 1999). The different varieties of hair cells and supporting cells are labeled: I, inner hair cell; O1-O3, outer hair cell-row 1-3; IP, inner phalangeal.

Transcription of p27kip1 in development

The onset of p27kip1 protein expression occurs in an apical to basal wave that precedes the wave of cell cycle exit

Previous studies have shown that by E14.5, the time when hair cell and supporting cell differentiation is beginning in the base of the cochlear duct, the cells that will form the entire organ of Corti have largely exited the cell cycle (Ruben, 1967). These cells form a zone of non-proliferating cells (ZNPC) whose borders represent the borders of the nascent organ of Corti (Chen et al., 2002; Chen and Segil, 1999). Based on analysis of [3H]-thymidine labeling, Ruben (Ruben, 1967) suggested that cell cycle exit occurred in an apical to basal pattern starting around E12.5 and ending around E14.5. BrdU injections at E12.5, E13.5 and E14.5 confirm that, starting at E12.5, cells in the apical region fail to incorporate BrdU, and at E13.5 and E14.5 the region of BrdU-negative staining increases in area, which is indicative of a wave of cell cycle exit that is responsible for establishing the ZNPC (Fig. 2A). This wave of cell cycle exit was quantified in a second experiment in which BrdU was injected at E12.5, E13.5 and E14.5 and the embryos were allowed to survive until birth. At that time, whole mounts were stained with antibody to both Myosin VIIa and BrdU. Double-labeled hair cells (BrdU+/Myosin VIIα+) are indicative of hair cells that were still in the cell cycle at the time of BrdU injection. The percentage of double-labeled cells was compared with the total number of hair cells (Myosin VIIα+) along the length of the cochlea (Fig. 2B). The progression of cell cycle exit is apparent from the rapid decrease in double-labeled cells that occurs from cochlear apex to base between E12.5 and E14.5.

To compare the wave of cell cycle exit with p27kip1 expression, whole-mount cochlea were dissected and stained with antibody to p27kip1. A steep wave of p27kip1 expression between E12.5 and E14.5 (Fig. 2C) parallels or slightly precedes the wave of cell cycle exit (compare Fig. 2A with 2C). A correlation between the wave of cell cycle exit and the expression of p27kip1 can also be seen in a tissue section double labeled for BrdU incorporation and p27kip1 expression, which is taken from an E14.5 embryo whose mother was injected with BrdU 2 hours earlier (Fig. 2E,F). The section was taken so that apical, middle and basal turns of the cochlear duct are simultaneously visible (the angle of cross-section is shown in Fig. 2D). The ZNPC is present in both the apical and middle turns of the cochlea and correlates with the presence of p27kip1 staining (compare brackets Apex with Middle, Fig. 2E with 2F). By contrast, BrdU-stained cells are present in the region at the base of the cochlea, where the ZNPC has yet to form at this time on E14.5, and this correlates with the absence of p27kip1 staining (compare Fig. 2E with 2F, Base).

Thus, formation of the postmitotic, prosensory domain of the cochlear duct is largely complete shortly after E14.5, the time of onset of hair cell differentiation. This means that unlike most other regions of the nervous system, where ongoing cell cycle exit is temporally correlated with cell differentiation, in the developing organ of Corti, a pool of postmitotic progenitors is established in toto.
prior to the onset of terminal differentiation. Indeed, the pool of sensory progenitors in the apical regions of the cochlear duct is maintained in an undifferentiated, but postmitotic state for 4-5 days before differentiation occurs.

The wave of p27^Kip1 expression is regulated at the transcriptional level

In order to assay the mechanism of p27^Kip1 regulation in the developing organ of Corti, we constructed a reporter using a Bacterial Artificial Chromosome containing 129 kb of genomic DNA surrounding the mouse p27^Kip1 locus (Fig. 3A). An IRES-GFP cassette was inserted into the 3’ non-coding region of the p27^Kip1 gene in the BAC to monitor gene transcription, and the coding region of p27^Kip1 was deleted to avoid artifacts of overexpression (see Materials and methods). Two independent lines of transgenic mice were analyzed and the two lines expressed the transgene in the same region. The percentage of BrdU+ hair cells per segment is shown (error bars indicate s.d.). (C) Whole-mount preparations of embryonic cochlea at E12.5, E13.5 and E14.5 stained with anti-p27^Kip1. Antibody staining appears as a gradient with the highest intensity in the apical third of the nascent organ of Corti at E12.5. The gradient increases in length with the growing cochlear duct and the gradient of expression appears in approximately two-thirds of the length of the cochlea at E13.5. By E14.5 the p27^Kip1 gradient of expression has nearly reached the base of the cochlea, coincident with the termination of cell division within the presumptive organ of Corti at this time. (D) Reconstruction of cochlear and vestibular components of the inner ear at E14.5 depicting the level of cross-section shown in E,F. (E,F) Cross-section through an E13.5-E14.5 cochlea stained for BrdU (E) and p27^Kip1 (F). BrdU was injected three times at 2-hour intervals into a timed pregnant female mouse starting 6 hours prior to removing and fixing the embryos. The section was double-labeled to reveal both BrdU incorporation and p27^Kip1 expression. The absence of BrdU staining in the apical and middle turns indicates the presence of a zone of non-proliferating cells in the apical and middle turns (E, apex and mid bracket). BrdU-labeled cells are seen in the basal turn, indicating that the ZNPC has not yet formed in this region. p27^Kip1 staining is present in the apical and middle turns, but absent from the base (F), coincident with the apical to basal progression of cell cycle exit as revealed by the BrdU labeling (E). Scale bar: 100 μm.

Analysis of GFP expression showed that a gradient of p27^Kip1/GFP transcription (Fig. 3B) coincides with the temporal and spatial pattern of p27^Kip1 protein expression (Fig. 3C). At E12.5, expression of p27^Kip1 protein is detected in a small region in the apex of the organ of Corti and this is coincident with the expression of the GFP transgene. This is also the site where cell cycle exit is first observed (Fig. 2A,B). On E13.5, p27^Kip1 protein expression has spread in a stripe through the apical third of the cochlear duct, paralleled by the expression of GFP (Fig. 3B,C). At this time quantitative differences in p27^Kip1 levels are visible along the length of the cochlear duct at both the transcription (GFP) and protein (antibody) level, suggesting that a graded increase in the accumulation of p27^Kip1 mRNA is driving a similar increase in protein levels. Because p27^Kip1 acts quantitatively to bring about cell cycle exit, the leading edge of p27^Kip1 expression is likely to slightly precede the leading edge of the wave of cell cycle exit. At E14.5, p27^Kip1 protein and GFP transgene expression within the stripe of cells that will become the organ of Corti encompasses greater than three-quarters of the length of the cochlear duct (Fig. 3B,C). Alternate sections through the middle region of the cochlear duct reveal the spatial overlap of p27^Kip1 protein expression (Fig. 3D) and that of the GFP transgene (Fig. 3E). Thus, the developmental regulation of p27^Kip1 transcription correlates with both the increase in p27^Kip1 protein levels, and the wave of cell cycle exit, suggesting that transcriptional control of p27^Kip1 expression is responsible for limiting the number of postmitotic progenitor cells that will go on to form the mature organ of Corti.
Transcriptional control of p27Kip1 is independent of cell cycle exit

Theoretically, p27Kip1 transcriptional induction could be dependent on cell autonomous developmental signals regulating its abundance, or, alternatively, on non-cell autonomous feedback mechanisms that react to the onset of cell cycle exit stimulated by alternate mechanisms. To test whether developmental regulation of p27Kip1 expression is independent of cell cycle exit, we studied the expression of the p27Kip1/GFP transgene in the cochlear prosensory domain of p27Kip1-null mice, where cell cycle exit is delayed and the prosensory progenitors of the organ of Corti continue to divide (Chen and Segil, 1999) (Fig. 4). Pregnant p27Kip1/GFP reporter mice carrying p27Kip1-null embryos were injected with BrdU at E13.5 (Fig. 4A-F) or 14.5 (Fig. 4G,H), and two hours later p27Kip1-null embryos were dissected and cholecleae were stained for BrdU incorporation indicative of continued presence in the cell cycle. BrdU labeling was present throughout the length of the E13.5 cochlear duct (Fig. 4A, BrdU), in contrast to the situation previously
described in wild-type embryos (Fig. 2A,B). Nonetheless, the p27Kip1/GFP reporter is expressed in a pattern identical to wild-type cochlea (compare Fig. 4B with Fig. 3C) at E13.5, and overlaps with the region of BrdU incorporation (Fig. 4C, merge), indicating that transcription of the p27Kip1/GFP transgene is regulated normally, even in the absence of p27Kip1 protein and in the presence of abnormal cell proliferation. Normal expression of the p27Kip1 transgene is also observed overlapping with BrdU-labeled cells in cross-sections through the developing E13.5 cochlea of p27Kip1-null mice (Fig. 4D-F), as well as in cross-sections from p27Kip1-null mice injected with BrdU on E14.5 (Fig. 4G,H). These results indicate that the apical to basal wave of p27Kip1 transcription is regulated cell autonomously and independent of the cell cycle state.

Cell-type specific regulation of p27Kip1 transcription in postnatal organ of Corti and retina

Mature p27Kip1-null mice display cell-type-specific patterns of abnormal cell division (Fero et al., 1998; Kiyokawa et al., 1996; Nakayama et al., 1996), suggesting that p27Kip1 is involved in the cell-type specific regulation of the postmitotic state. In the inner ear, p27Kip1 protein is rapidly downregulated during hair cell differentiation, while being maintained at high levels in supporting cells (Chen and Segil, 1999). Transcriptional control of p27Kip1 might extend to this and other examples of cell-type-specific expression, or alternatively, posttranscriptional mechanisms could be entirely responsible. To test whether transcriptional regulation plays a role in cell-type-specific expression in the differentiated organ of Corti, we studied expression of the p27Kip1-GFP reporter at P1 (Fig. 5). GFP disappears from differentiating hair cells embryonically within 24 hours of the appearance of Math1 (data not shown), and then remains absent from hair cells postnatally (Fig. 5), indicating that transcriptional downregulation has occurred. By contrast, p27Kip1 protein continues to be expressed at a high level in P1 supporting cells, as is the p27Kip1/GFP reporter (Fig. 5A-C).

These results indicate that the transcriptional control of p27Kip1 remains in force beyond the embryonic period and may play a role in maintaining the homeostatic state of hair cells and supporting cells.

In order to extend these observations to another sensory organ, we have studied the pattern of expression of the p27Kip1/GFP transgene in the postnatal mouse retina (Fig. 5D-G). During retinal development, a dynamic pattern of p27Kip1 expression is involved in regulating cell cycle exit in several differentiating cell types (Dyer and Cepko, 2000; Dyer and Cepko, 2001a; Levine et al., 2000). However, in the mature retina, p27Kip1 expression has been downregulated in all cell types except for Muller glia (Dyer and Cepko, 2000; Dyer and Cepko, 2001a; Levine et al., 2000). We observed that in P21 retinas, the p27Kip1/GFP reporter (Fig. 5E) is expressed in Muller glia, which are marked by expression of glutamine synthetase (Fig. 5D), as previously described (Vardimon et al., 1991). This pattern of p27Kip1/GFP reporter expression (Fig. 5G) parallels the pattern of p27Kip1 protein expression (Fig. 5F). These observations indicate the importance of transcriptional control of postnatal patterns of p27Kip1 expression, and the importance of cell-type-specific regulation of the postmitotic state.

DISCUSSION

We have investigated the means by which p27Kip1 achieves the timely and ordered cell cycle withdrawal of organ of Corti precursors, and we now show that regulated transcription of p27Kip1 is largely responsible for driving the precise pattern of cell cycle exit required for normal development. Transcription of p27Kip1 is shown to follow a temporal progression from apex to base within the cochlear duct that prefigures a wave of cell cycle exit in each of the postmitotic prosensory domains of the cochlea. In p27Kip1-null mice, cell cycle exit is delayed and the wave of cell cycle exit does not form, leading to patterning abnormalities during subsequent differentiation (Chen and Segil, 1999; Lowenheim et al., 1999). Using a p27Kip1/GFP reporter transgene, we show that p27Kip1

![Fig. 5. Cell-type-specific transcriptional regulation of p27Kip1 in the postnatal organ of Corti and retina.](https://example.com/fig5.png)

(A-C) Sections through the postnatal day 1 (P1) organ of Corti triple-labeled with antibody to p27Kip1 (A), the native p27Kip1/GFP transgene (B) and the hair cell marker Myosin Vila (C). Note high levels of p27Kip1 expression in postnatal supporting cells and the lack of staining of differentiated hair cells, indicating that p27Kip1 is downregulated in hair cells at the transcriptional level. (D-G) Cross-sections through the P21 mouse retina. D and E are the same section double-labeled with antibody to glutamine synthetase, a marker of Muller glia in the retina (D), and the native p27Kip1/GFP transgene (E). F and G are the same section double-labeled with antibody to p27Kip1 (F) and the native p27Kip1/GFP transgene (G). Note the co-linearity of staining between glutamine synthetase, the p27Kip1 protein and p27Kip1/GFP in the inner nuclear layer (INL), which is indicative of cell-type-specific transcriptional control in the postnatal retina. ONL, outer nuclear layer; INL, inner nuclear layer; GCL, ganglion cell layer. Scale bar: 100 μm.
transcriptional regulation is unaffected in the p27Kip1-null mouse, indicating that transcriptional timing of p27Kip1 is controlled independently of cell cycle events. Transcriptional control of p27Kip1 is also independent of differentiation within the organ of Corti, as the wave of cell cycle exit occurs prior to the onset of Math1-dependent differentiation (Bermingham et al., 1999; Chen et al., 2002). Finally, we show that the subsequent cell type-specific expression of p27Kip1 in the mature organ of Corti and retina is also regulated at the transcriptional level, suggesting that differential regulation of p27Kip1 transcription is important for maintaining cellular homeostasis in adult tissues (Fig. 5).

**p27Kip1 expression is responsible for enforcing the temporal separation between cell cycle exit and cell differentiation during cochlear development**

During embryonic development, the processes that control cell division, and those that control cell differentiation are frequently difficult to separate experimentally because of tight temporal coordination between these events (see Cremisi et al., 2003; Fichelson et al., 2005; Zhu and Skoultchi, 2001). The temporal separation between cell cycle exit and cell fate decision during organ of Corti development (Chen et al., 2002) appears to be quite different from the normal pattern of development in other parts of the vertebrate nervous system, such as in the retina (Dyer and Cepko, 2001b; Levine et al., 2000) and the cortex (McConnell, 1990), where a kind of ‘just-in-time’ production of postmitotic cells is tightly linked to their differentiation. The reason for establishing a fixed number of postmitotic progenitors within the cochlear duct prior to the onset of differentiation is not clear; however, we hypothesize that it is related to the linear and iterative geometry of development within the confines of the elongating cochlear duct, wherein the same precise number and proportion of hair cells and supporting cells may be needed at each position along the cochlear length in order to support the final bio-mechanical function of the organ of Corti. By contrast, the retina develops circumferentially, and thus requires a continuously increasing number of progenitors as differentiation progresses from the center to the periphery (Dyer and Cepko, 2001b).

**How is the temporal and spatial gradient of p27Kip1 transcription achieved?**

The molecular mechanisms governing p27Kip1 gene transcription during development are unknown. We have used a 129-kb BAC containing the p27Kip1 locus to study the pattern of transcriptional regulation responsible for controlling cell cycle exit in the developing organ of Corti. The p27Kip1 regulatory regions included within this BAC are sufficient to recapitulate both the temporal and spatial pattern of p27Kip1 expression within the cochlear duct (Fig. 3). Although several studies, involving a variety of cells grown in culture, have indicated that p27Kip1 can be transcriptionally regulated in response to hormones, interleukins and other growth modulating conditions through response elements within sequences that lie 1-2 kilobases 5’ to the start site of p27Kip1 transcription (Chen et al., 2005; Gizard et al., 2005; Stahl et al., 2002), preliminary results from our laboratory indicate that developmental regulation of p27Kip1 expression is only partly recapitulated in transgenic reporter mice harboring a region of the p27Kip1 gene including 9 kb of DNA 5’ to the start of transcription (data not shown). This indicates that the more complicated developmental control regions of the p27Kip1 locus are likely to be complex and to span a considerable area around the p27Kip1 gene itself. This is in keeping with the situation in Drosophila, where the p27Kip1 homolog Dacapo has been shown to harbor a complex, tissue-specific and developmentally regulated array of enhancer elements (Liu et al., 2002; Meyer et al., 2002).

During the development of the cochlear duct, p27Kip1 expression is confined to a narrow prosensory domain that represents the nascent organ of Corti (Chen et al., 2002; Chen and Segil, 1999). Although the mechanism by which the transcription of p27Kip1 is confined to this region is unknown, one transcription factor that may prefigure the p27Kip1 domain is Sox2. Sox2 is expressed broadly in the otocyst at E9.5 and comes to be expressed in the same domain as p27Kip1 at E14.5 prior to the onset of hair cell differentiation (Kiernan et al., 2005b). Whether the narrowing of Sox2 expression to the p27Kip1 domain precedes or follows the onset of p27Kip1 expression is not known. In addition, although the exact role of Sox2 within the prosensory domain is unknown, its loss leads to a partial failure of p27Kip1 expression and sensory development (Kiernan et al., 2005b).

The p27Kip1 expression domain does not appear to encompass all regions of the cochlear duct that are competent to form hair cells and supporting cells. This is evident from Math1 transfection studies in which cells medial to the organ of Corti [the greater epithelial ridge (GER)] have been shown to be competent to differentiate as sensory cells (Izumikawa et al., 2005; Kawamoto et al., 2003; Shou et al., 2003; Woods et al., 2004; Zheng and Gao, 2000). Although the precise extent of this sensory-competent region is not known, it is possible that a ‘competence’ domain, including the region of the ZNPC and surrounding cells of the GER (and lesser epithelial ridge), is established prior to the establishment of the definitive prosensory domain that gives rise to the organ of Corti. Thus, the mechanisms responsible for p27Kip1 expression may be part of a process that restricts a region of sensory competence to the exact number of cells needed to form the organ of Corti. Discovering the factors controlling p27Kip1 transcription may lead us to the mechanisms by which this postmitotic prosensory domain is spatially defined.

Although we do not know which developmental pathways are responsible either for temporal or spatial aspects of this pattern, recent evidence suggests that Notch signaling may play a role in p27Kip1 regulation at this time. The mutation of either of two Notch ligands, Jagged 1 or Jagged 2, or the Notch 1 receptor, leads to gene-specific patterning defects in the organ of Corti involving supernumerary hair cells, as well as apparent perturbations in p27Kip1 expression (Kiernan et al., 2005a; Kiernan et al., 2006; Brooker et al., 2006), although p27Kip1 expression is not completely eliminated. In addition, another recent report indicates that the Notch-responsive gene Hes1 is able to directly bind the p27Kip1 promoter in HeLa cells (Murata et al., 2005). Hes1 does not appear to be expressed prior to or at the time of onset of p27Kip1 expression in the cochlear duct (Zine et al., 2001) (A. Doetzthofer and N.S., unpublished); however, the existence of a Hes-responsive binding site within the p27Kip1-promoter suggests that different members of the Hes gene family may serve as a link between Notch signaling and p27Kip1 transcription in the cochlea.

Our demonstration of the importance of transcriptional control of p27Kip1 to the developmental timing of cell cycle exit does not preclude the possibility that posttranscriptional mechanisms governing the accumulation of p27Kip1 protein are also partly responsible for the timing of these events. Indeed, our preliminary data indicates that loss of the F-box protein Skp2, which is involved in the posttranscriptional regulation of p27Kip1, causes a subtle change in the timing of cell cycle exit in the organ of Corti (F.L. and N.S., unpublished), indicating that coordination between
transcriptional and posttranscriptional mechanisms regulating p27Kip1-mediated cell cycle exit is likely to be crucial for normal development.

**The importance of p27Kip1 regulation to the maintenance of the postmitotic state of hair cells**

Maintenance of cell-cell interactions (tissue architecture) is believed to be the reason that most cells of the nervous system are maintained in a lifelong postmitotic state. CKIs play a significant role in this process (Chen et al., 2003; Zindy et al., 1999). In CNS neurons, p27Kip1 expression continues in the mature cortex, and along with the CKI p19Ink4d, is part of the mechanism underlying the stability of the postmitotic state of neurons (Zindy et al., 1999). In mice wherein both p19Ink4d and p27Kip1 have been mutated, the postmitotic state of mature neurons is compromised, and many cells re-enter the cell cycle and subsequently undergo apoptosis. However, if either p27Kip1 or p19Ink4d is present, the postmitotic state of differentiated neurons is maintained. By contrast, p19Ink4dnull mice suffer from a progressive hearing loss brought about by an inability of hair cells to maintain the postmitotic state (Chen et al., 2003). We have speculated that the developmentally controlled downregulation of p27Kip1 in hair cells leads to a compromised ability to maintain the postmitotic state (Chen et al., 2003). Here, we show that the downregulation of p27Kip1 in hair cells is controlled at the transcriptional level (Fig. 5). Similarly, p27Kip1 levels are downregulated in all neuronal cell types in the mouse retina following differentiation (Levine et al., 2000), and we have observed that the p27Kip1/GFP reporter is also downregulated in mature neurons of the retina (Fig. 5), indicating that this occurs at the transcriptional level as well. Interestingly, p27Kip1/GFP is expressed exclusively in Muller glia of the mature retina (Dyer and Cepko, 2000; Levine et al., 2000), indicating that, as in the organ of Corti, cell-type-specific expression of p27Kip1 in the retina is regulated transcriptionally (Fig. 5). The reason that p27Kip1 expression is maintained at different levels in different postmitotic cell types is not clear. Recent evidence that p27Kip1 functions outside the context of the cell cycle to regulate the cytoskeleton (Besson et al., 2004) suggests that maintenance of the postmitotic state may not be the only reason for its differential expression in mature cell types.

**Transcriptional regulation of p27Kip1 in supporting cells – relationship to regeneration**

The differential expression of the p27Kip1/GFP transgene in hair cells and supporting cells, as well as in the retina (Fig. 5), indicates that cell-type-specific expression of p27Kip1 in the mature organ of Corti is maintained through transcriptional mechanisms. In non-mammalian vertebrates, the loss of hair cells leads to the proliferation of supporting cells and subsequent regeneration of functional hair cells (Corwin and Cotanche, 1988; Ryals and Rubel, 1988). However, in mammals, the loss of cochlear hair cells does not lead to supporting cell proliferation, and hair cell regeneration does not occur (Chardin and Romand, 1995). The loss of hair cells is the major cause of deafness in the adult human population, making the failure of hair cell regeneration an important clinical problem. Although the generation of new hair cells in adult p27Kip1-null mice is unclear, sub-populations of supporting cells are observed to divide spontaneously at postnatal times, indicating that supporting cells depend, at least partially, on p27Kip1 for the maintenance of the postmitotic state, and that the persistence of high levels of p27Kip1 in supporting cells may be one of the obstacles to regeneration (Chen and Segil, 1999; Lowenheim et al., 1999). Our observation that regulated transcription is at least partially responsible for the high level of p27Kip1 expression in supporting cells provides a new set of potential targets for the transient manipulation of p27Kip1 levels with the aim of stimulating the therapeutic proliferation of supporting cells.

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