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Feathers and Fins: Non-mammalian models for hair cell regeneration

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Abstract

Death of mechanosensory cells in the inner ear results in two profound disabilities: hearing loss and balance disorders. Although mammals lack the capacity to regenerate hair cells, recent studies in mice and other rodents have offered valuable insight into strategies for stimulating hair cell regeneration in mammals. Investigations of model organisms that retain the ability to form new hair cells after embryogenesis, such as fish and chicks, are equally important and have provided clues as to the cellular and molecular mechanisms that may block hair cell regeneration in mammals. Here, we summarize studies on hair cell regeneration in the chicken and the zebrafish, discuss specific advantages of each model, and propose future directions for the use of non-mammalian models in understanding hair cell regeneration.

Keywords

hair cell regeneration; chick; zebrafish; ear; lateral line

Overview

More than 50% of individuals over the age of 60 suffer hearing loss as the result of aging, genetic predisposition or environmental exposure to noise or ototoxic drugs (Beisel et al., 2008). Most hearing and many balance deficiencies spring from damage or loss of sensory hair cells, which are highly specialized cells with elaborate microvillar arrays called hair bundles. The hair bundle is responsible for transducing sound energy or head movements into neural signals that are the initial input to the auditory and vestibular nervous system.

Two broad strategies can be envisioned to treat hair cell loss: prevention and/or replacement. Pharmacological approaches for preventing hair cell loss have been identified in model systems and in human patients (reviewed in Guthrie, 2008 and Cotanche, 2008). Genes contributing to hair cell protection or susceptibility have also been discovered via genetic screens and may be targets for gene therapy in the future (Lang et al., 2006; Friedman et al., 2008; Owens et al., 2008). These results are promising first steps to the eventual goal of preventing hair cell loss.

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However, to treat individuals already suffering from hair cell loss, strategies for cellular replacement must be investigated. The only currently available treatment is a biomechanical approach to compensating for hair cell loss via cochlear implants. These implants bypass the need for hair cell transduction and directly stimulate the auditory nerve, attempting to replicate the interactions of inner hair cells and their associated nerves (reviewed in Rubinstein, 2004). Despite advances in cochlear implants, they lack the precise tuning and sensitivity of a functioning ear and regeneration of hair cells an appealing alternative for re-establishing auditory function.

Mammals, in general, lack the ability to regenerate hair cells (reviewed in Matsui and Cotanche, 2004). In contrast, new hair cell production is common among cold-blooded vertebrates following amputation (Stone, 1933, 1937), as a normal part of body growth (Corwin, 1981; Popper and Hoxter, 1984; Corwin, 1985), and after hair cell lesion (Balak et al., 1990; Lombarte et al., 1993). It was the unexpected discovery of hair cell regeneration in the auditory system of birds following experimental damage that spurred scientific investigation in this area (Corwin and Cotanche, 1988; Ryals and Rubel, 1988). As discussed below, studies in avian models over the last 20 years have revealed the progenitor cell identity, the time-course of regeneration, and the cellular processes involved. So far, however, they have provided modest information about how hair cell regeneration is controlled. The principal obstacle is the identification of genes and signaling pathways that direct progenitor cell behavior.

Genetic analyses are needed to reveal which regulatory pathways have been conserved and lost across evolution. This information may unveil molecular strategies for re-activating hair cell regeneration in mammals. Indeed, several studies of the mature mammalian inner ear suggest non-sensory cells can be induced to give rise to hair cells. For example, a small number of purified supporting cells from the adult mouse can differentiate into hair cells *in vitro* (White et al., 2006), and non-sensory cells from the mature end organs may have this capacity (Li et al., 2003; Oshima et al., 2007). Further, misexpression of the transcription factor *Atoh1* is sufficient to induce ectopic hair cell formation in the adult Guinea pig organ of Corti or rat utricle (Zheng and Gao, 2000; Kawamoto et al., 2003; Shou et al., 2003; Izumikawa et al., 2005). However, activation of *Atoh1* does not induce proliferation of supporting cells necessary to maintain hair cell function (Shou et al., 2003). Nonetheless, these experiments highlight the potential for activating hair cell regeneration in mammals, and they underscore the importance of characterizing the molecules that direct and integrate the cellular processes associated with new hair cell production in birds and other animals capable of hair cell regeneration. These processes include re-initiation and termination of cell proliferation, differentiation of precursor cells into hair cells and supporting cells, and innervation of new hair cells.

One powerful strategy for identifying proteins that are critical regulators of hair cell regeneration is to analyze regeneration in animals subjected to unbiased mutagenesis. Historically, such forward genetic screens have provided breakthrough information for understanding control of cellular processes in other tissues. For example, several genes regulating programmed cell death, and now known to have human orthologs, were first identified during forward genetic screens of the invertebrate nematode, *C. elegans* (Putchá and Johnson, 2004). Among vertebrates, mice have been used extensively for genetic analysis. However, mice do not spontaneously form new hair cells, and therefore they are only useful for identifying genes that single-handedly trigger hair cell regeneration, a formidable task! Zebrafish, another genetically tractable model, has recently emerged as a powerful tool with the potential to identify molecular regulators of hair cell regeneration.

In this review, we will address recent studies of hair cell regeneration in chickens and zebrafish, and discuss how these animal models are likely to make substantial contributions to our

comprehension of hair cell regeneration in non-mammals and to open up avenues for new study in mammals.

Lessons from the feathered

Birds offer great opportunities to examine hair cell regeneration in its different forms. By far, most studies have been conducted in chickens. In the chicken vestibular epithelia (utricle, saccule, lagena, and cristae), there is continuous and asynchronous low-level cell proliferation (Jorgensen and Mathiesen, 1988; Roberson et al., 1992; Kil et al., 1997). This proliferation is driven by periodic hair cell apoptosis which appears to occur after hair cells reach 3 months of age (Kil et al., 1997; Stone et al., 1999; Matsui et al., 2002). Rates of supporting cell division in chicken utricles are increased when hair cell death is experimentally increased (Weisleder and Rubel, 1993). In contrast, no ongoing hair cell production occurs in the chicken auditory epithelium (Oesterle and Rubel, 1993). Rather, progenitor cells are mitotically quiescent by mid-embryogenesis and cellular differentiation is completed by hatching (Cohen and Fermin, 1978; Cotanche and Sulik, 1984; Tilney et al., 1986). Production of new hair cells is only triggered by hair cell damage (Cruz et al., 1987; Corwin and Cotanche, 1988; Ryals and Rubel, 1988; Oesterle and Rubel, 1993), and the replacement of hair cells leads to near-complete recovery of auditory and vestibular function within 1–2 months (reviewed in Bermingham-McDonogh and Rubel, 2003). Hair cell regeneration even occurs in the inner ears of senescent birds (Ryals and Rubel, 1988). The remarkable ability of the avian auditory epithelium to jump-start cellular growth despite long periods of quiescence places it in stark contrast to the mammalian organ of Corti, in which no signs of spontaneous regeneration have been noted (Roberson and Rubel, 1994; Forge et al., 1998).

In both auditory and vestibular epithelia, regenerated hair cells emerge during the first week after damage (Cotanche, 1987; Janas et al., 1995; Stone et al., 1996). At this time, some new hair cells already possess well differentiated cytoplasm and hair bundles, and they form synapses with afferent and efferent terminals that remained nearby after damage (Ryals and Westbrook, 1994; Hennig and Cotanche, 1998). By 3–4 weeks after damage, auditory and vestibular function has recovered substantially, and by 2 months, recovery is near-complete (reviewed in Bermingham-McDonogh and Rubel, 1999), although some small deficits in epithelial structure and sensory function can persist for longer periods (Marean et al., 1993).

Studies looking at regeneration in avian models use several methods for damaging hair cells. In the earliest studies, investigators used acoustic overstimulation (Cotanche, 1987), which kills hair cells in different regions of the cochlea, depending on the frequency of the stimulus and often has high levels of variability in the extent of cell death. Ototoxic drugs, including aminoglycoside antibiotics, such as gentamicin, also damage the chicken inner ear epithelia (Cruz et al., 1987). The primary advantage of aminoglycosides is that they produce a broader, more homogeneous field of hair cell damage than noise damage. Other ototoxins, such as cisplatin or heavy metals, have been poorly studied in birds.

Difficulty in accessing structures of the inner ear *in situ* has led investigators to develop other techniques for analyzing hair cell regeneration after damage and understanding how regeneration is altered by modifying the cellular environment. These techniques include cell culture methods to isolate supporting cells from auditory (Stone et al., 1996) and vestibular epithelia (Warchol, 1995). Organotypic cultures of cochlear ducts (Oesterle et al., 1993; Navaratnam et al., 1996; Warchol and Corwin, 1996; Frenz et al., 1998; Chen et al., 2003; Daudet et al., 2009) or of the utricle or the saccule (Oesterle et al., 1993; Warchol and Corwin, 1993) provide a method for easier access to a cells in the intact organ. These *in vitro* preparations make it feasible to do studies using pharmaceutical inhibition or activation of signaling pathways by adding drugs directly to culture media. In addition, these preparations

provide opportunities for gene misexpression analyses by electroporating DNA into the sensory epithelium. To date, only small numbers of supporting cells have been transfected using this approach (Daudet et al., 2009). For future studies, it will be important to develop methods for broader conditional transgene activation/inhibition in chicken sensory epithelia.

Techniques have also been developed to alter the environment of the inner ear by *in ovo* manipulation. Wide-spread misexpression of genes can be achieved by transfecting progenitor cells in the embryonic inner ear *in ovo* (Morgan and Fekete, 1996) using either viral transduction (Fekete et al., 1998) or plasmid electroporation (Daudet and Lewis, 2005). Alternatively, very young embryos can be broadly transfected *in ovo*, and embryo mosaics can be hatched out and studied. Data generated as a result of many of these approaches are discussed below and has been vital to progress in understanding the process of avian hair cell regeneration.

Hair cell progenitors

In birds and cold-blooded animals, the predecessors to new hair cells during normal turnover and during damage-induced regeneration are supporting cells, the non-sensory cells that surround hair cells and serve structural and physiological auxiliary functions in the tissue. Although regeneration of hair cells in birds was first described as a process requiring supporting cell division (Corwin and Cotanche, 1988; Jorgensen and Mathiesen, 1988; Ryals and Rubel, 1988), the earliest phase of hair cell regeneration in fact involves a very different cellular process: the phenotypic conversion of supporting cells into hair cells without cell division called *direct transdifferentiation* (Fig. 1a), (Adler and Raphael, 1996; Baird et al., 1996; Roberson et al., 1996; Roberson et al., 2004). During this rather unusual process, supporting cells undergo a dramatic set of morphological and molecular changes to acquire all of the properties of sensory hair cells. The conversion begins as early as 15 hours after gentamicin administration, and converting cells have acquired several hair cell characteristics two days later (Roberson et al., 2004; Cafaro et al., 2007). Studies in the chicken auditory epithelium, in which nucleotide analogs were provided to track all cells that divided over the course of regeneration, showed that a substantial proportion of new hair cells were not labeled for the nucleotide and were therefore not derived from mitotically active progenitor cells (Roberson et al., 1996; Roberson et al., 2004). Short systemic treatments with the mitotic inhibitor, AraC, did not prevent the formation of new hair cells in chickens after noise damage, and further support the dispensability of cell division for new hair cell formation in the ear (Adler and Raphael, 1996). Similar results were found using a different mitotic inhibitor, aphidicolin, in drug-damaged saccules of frog ears (Baird et al., 1996; Baird et al.,) and newt ears (Taylor and Forge, 2005). However, it is not established that direct transdifferentiation occurs in the vestibular epithelium of chickens, primarily due to the difficulty of ruling out normal maturation of undifferentiated precursor cells since this epithelium has continual cellular turnover.

It is important to stress that there is no evidence for latent, undifferentiated hair cell precursors in the chicken auditory epithelium and therefore, this process is likely triggered in fully differentiated supporting cells. Further, although approximately 30–50% of new hair cells are formed by direct transdifferentiation in the chicken basilar papilla (Roberson et al., 1996; Roberson et al., 2004) it is not clear when directly transdifferentiated hair cells become functional or the degree to which their production contributes to the early phases of functional recovery.

Later phases of hair cell regeneration are driven by supporting cell division. Supporting cells first re-enter the cell cycle between 2 and 3 days after damage and they continue to proliferate until the second week after damage (Corwin and Cotanche, 1988; Ryals and Rubel, 1988). It has been suggested that supporting cell proliferation may only be needed when significant

supporting cell depletion has occurred due to direct transdifferentiation (Roberson et al., 2004). However, since both new hair cells and supporting cells differentiate from supporting cell progeny (Corwin and Cotanche, 1988; Ryals and Rubel, 1988); this proliferative phase clearly serves more purpose than to simply replace supporting cells that have converted (irreversibly) into hair cells.

During cell division, supporting cell nuclei, which normally reside near the basal lamina, migrate toward the lumen, where they undergo mitosis (Raphael, 1992; Tsue et al., 1994). Cell progeny then differentiate into either hair cells or supporting cells. Statistical analysis of mitotic events shows a strong propensity for asymmetric differentiation in the chicken utricle during ongoing hair cell regeneration (Roberson et al., 1992; Stone et al., 1999) but considerably less predictability for cell fate outcomes of sibling cells in the damaged chicken basilar papilla (Stone and Rubel, 2000). These observations suggest there are no separate cell lineages for hair cells and supporting cells in either epithelium but rather, that cell fate is determined by signals in the microenvironment, such as numbers or patterning of existing hair cells.

Regulation of supporting cell behaviors after hair cell damage

One looming challenge is to identify the intrinsic and extrinsic factors that direct supporting cell behavior in animals capable of regeneration and then make comparisons with mammals to determine why supporting cells in their inner ears lie dormant after hair cell damage. Mechanisms that direct supporting cells to undergo mitotic or non-mitotic production of hair cells, or to remain quiescent, remain largely unknown. Supporting cells may be a heterogeneous population: subpopulations of supporting cells may be pre-programmed to regenerate hair cells via either mechanism while other supporting cells are incapable of changing their phenotype and do not contribute to hair cell replacement. It is clear that cells across the sensory epithelia are not identical, in quiescence or after damage. Expression of transcription factors such as Gata3 and Prox1 define subpopulations of supporting cells in the undamaged utricular and auditory epithelia, respectively (Stone et al., 2004; Warchol and Speck, 2007). The expression of Prox1, limited to hair cells in the quiescent (undamaged) basilar papilla, is strongly upregulated in ~50% of supporting cells following hair cell damage (Stone et al., 2004). In the regenerating auditory epithelia, those cells with high levels of nuclear Prox1 expression differentiate as hair cells rather than supporting cells, suggesting a role for Prox1 in the hair cell fate specification or differentiation. Gata3 is a second example of a marker for subpopulations of supporting cells (Warchol and Speck, 2007). In the avian utricle, Gata3-positive supporting cells are localized to the striolar reversal zone, a central stripe where hair cell bundle polarity is 180° to hair cells on either side. Unlike Prox1, Gata3 is strongly expressed in both quiescent and regenerating tissues. The specific expression pattern of Gata3 is not downregulated after damage, in contrast to other, more ubiquitous transcription factors in the same tissue. This suggests a role for the Gata3 positive subset of supporting cells in defining the orientation of hair cell polarity in both development and regeneration. Both Gata3 and Prox1 expression provide support for the idea that there are specializations in supporting cells that regulate their behavior during regeneration.

Alternatively, supporting cells may not be specialized in their response to damage and instead may have equal potential for any behavior, with their ultimate responses dependent on cues in the microenvironment. In the drug-damaged chicken auditory epithelium, only one of seven supporting cells divide, and such cells are concentrated in the neural half of the damaged epithelium, despite complete hair cell loss in all regions (Cafaro et al., 2007). While this latter finding suggests the neural region could be enriched in hair cell progenitors or in cells programmed for proliferation, it is also possible that mitogenic signals are stronger in the neural region. Mitogens for supporting cells in the neural region, and their cellular sources, have yet to be identified.

Two general tactics have been used to establish candidate regulators of hair cell regeneration in birds. First, investigators have chosen to study genes or proteins known to be important for cellular production in other tissues, such as those that regulate the developing inner ear, assuming they may have similar functions in the regenerating inner ear (e.g., (Navaratnam et al., 1996). Second, investigators have used genomic queries to identify gene transcripts that are up- or down-regulated after damage. For example, Bermingham-McDonogh et al. (2001) used differential display to analyze transcripts for receptor tyrosine kinases in the chicken auditory epithelium. They determined that, in supporting cells, fibroblast growth factor (FGF) receptor 3 is highly transcribed in normal tissue and is down-regulated after damage. Analysis of FGF in cochlear duct cultures showed that, in fact, FGF inhibits supporting cell division after damage (Oesterle et al., 2000). More recently, Warchol, Lovett, and colleagues have analyzed transcripts in chicken auditory and vestibular epithelia using large microchip gene arrays (Hawkins et al., 2003; Hawkins et al., 2007). This analysis revealed hundreds of genes encoding transcription factors and a limited number of genes encoding other potential regulatory proteins that are transcriptionally up- or down-regulated during the early phases of regeneration in mature chickens. Analyses of gene networks can reveal signaling pathways that are activated or suppressed during regeneration, paving the way for further analyses, such as cellular localization of specific transcripts and functional tests of specific genes or signaling pathways. This important information will undoubtedly help to elucidate the complex molecular regulation of hair cell regeneration in chickens, and perhaps in other animals as well.

The role of specific molecules in regulating supporting cell behavior after hair cell damage has been tested in cultures of explanted sensory organs or epithelia from the chicken inner ear. In the auditory epithelium, stimulation of cAMP promotes supporting cell division (Navaratnam et al., 1996), while application of bFGF inhibits it (Oesterle et al., 2000; Bermingham-McDonogh et al., 2001). In the vestibular epithelium, additional molecules appear to promote supporting cell division, including IGF-1 (Oesterle et al., 1997), PI3-kinase, TOR, MAP Kinase, (Witte et al., 2001), and immune cytokines such as TNF-alpha and TGF-alpha (Warchol, 1999).

Very few studies have addressed the factors that promote avian supporting cells to convert directly into hair cells. The Notch signaling pathway regulates cellular differentiation controlled by cell-cell interactions. A recent study by Daudet et al. (2009) examined the role of Notch signaling in supporting cell behavior in the chicken auditory epithelium. In undamaged conditions, the Notch receptor is transcribed in supporting cells, suggesting Notch signaling could maintain supporting cell quiescence (Stone and Rubel, 1999). However, inhibition of gamma secretase, which blocks all Notch activity, did not cause supporting cells to convert into hair cells. After damage, several genes in the Notch pathway, including ligands Serrate1 and Delta1 and the Notch effector, Hes5, are upregulated. If Notch signaling is inhibited in damaged tissue, via inhibition of gamma secretase activity, substantial overproduction of hair cells via both mitotic and non-mitotic mechanisms occurs. Gamma secretase inhibition has no direct effect on supporting cell division, and overproduction of hair cells occurs at the expense of supporting cell depletion. Further, overexpression of Notch's signaling intracellular domain prevented supporting cells from converting into hair cells. Taken together, these findings demonstrate that Notch activity modulates the number of supporting cells and post-mitotic precursor cells that acquire the hair cell fate, regardless of the mechanism, but only when original hair cells are damaged or absent.

These studies leave open the question of how supporting cells are maintained in their differentiated state prior to damage and suggest a role for Notch-independent pathways. It has recently been shown that pillar cells, a subset of supporting cells in the mouse organ of Corti, display Notch-independent differentiation and maintenance during development (Doetzlhofer et al., 2009). This subset of supporting cells is distinguished by expression of the transcription

factor *Hey2* that, unlike most other *Hes/Hey* transcription factors, is Notch-independent. When *Hey2* is activated by FGF, pillar cells are specifically prevented from differentiating into hair cells, even if Notch signaling is inactivated. Conversely, when *Hey2* activity is disrupted, pillar cells differentiate into hair cells. Although the activity of *Hey2* during hair cell regeneration has not been tested, it is tempting to speculate that it may be similarly important for preventing excessive differentiation of supporting cells into hair cells after damage in mature hair cell epithelia.

Lessons from the finned

Zebrafish, *Danio rerio*, are relative newcomers to the field of hair cell regeneration and an exciting model due to a unique combination of regenerative capacity and genetic tractability. In addition to these traits, small size and high fecundity minimize storage demands while external embryogenesis and transparency as embryos and young larvae facilitate live imaging. The promise of these two features in a single model has led to careful characterization of zebrafish hair cell development, structure and regeneration and comparison to other models. Although the majority of this review is dedicated to regeneration research in zebrafish, there is also a rich history of other (fin-free) non-mammalian vertebrates, in the field. Regeneration studies using salamanders, newts and frogs established the importance of non-mammalian vertebrate models in regeneration (reviewed in Corwin and Oberholtzer, 1997). Together with zebrafish, cold-blooded models of hair cell regeneration are making vital contributions to understanding which regenerative processes are conserved in vertebrates and importantly, which are lost in mammals along with their ability to regenerate hair cells.

Hair cell structure, function and development are well conserved from fish to mammals (reviewed in Nicolson, 2005b). Conserved hair cell features include distinctive cellular structure of cilia organized with a specific cell polarity (Lopez-Schier et al., 2004), mechanotransduction (reviewed in Nicolson, 2005a), and development. Furthermore, genetic conservation is also evident in the wide range of fish orthologs identified based on human deafness genes such as those responsible for Usher syndrome (reviewed in Whitfield, 2002). Finally, the cellular response to ototoxic stimuli is also conserved in zebrafish. Hair cells respond to a wide range of toxic stimuli that have been characterized in mammalian models as well as in patients. Aminoglycoside antibiotics, including, neomycin and gentamicin, rapidly cause lateral-line hair cell death in a dose dependent manner (Harris et al., 2003; Murakami et al., 2003; Lopez-Schier and Hudspeth, 2006; Santos et al., 2006; Ma et al., 2008). Platinum-based drugs used to treat cancer (Ton and Parg, 2005; Ou et al., 2007; Owens et al., 2008), and other metals including copper and silver (Hernandez et al., 2006; Linbo et al., 2006; Olivari et al., 2008) also cause dose-dependent hair cell death.

In addition to hair cells in the inner ear, zebrafish have a set of easily accessible hair cells in lateral line neuromasts, similar to that in other cold-blooded vertebrates such as salamanders, newts and tadpoles. The lateral line is located on the surface of the fish where hair cells, clustered into neuromasts, sense water movement (Coombs and Montgomery, 1999; Montgomery et al., 2003). Information about water movement is critical for a range of behaviors such as localization of predators or prey, orientation against currents, and interactions with other fish (Coombs and Montgomery, 1999). The structure and function of lateral line hair cells is very similar to that of the avian inner ear (Coombs et al., 1989). Moreover, genes identified as orthologs of human deafness genes that functioned in the zebrafish ear also disrupt lateral line hair cell function, reinforcing the conservation of functional mechanisms at the cellular level. Due to their location on the surface of the body, and the stereotyped positions of neuromasts, hair cells in the zebrafish lateral line can be rapidly screened for regeneration in live animals and the majority of zebrafish studies on hair cell regeneration have utilized the lateral line system.

Zebrafish hair cell regeneration has been demonstrated following ototoxic treatments in a range similar to those affecting avian, mouse models, and human patients. In nearly all zebrafish studies on hair cell death and regeneration, animals have been analyzed at 3 to 10 days post-fertilization. Despite the young age of these animals, the process of regeneration appears strikingly conserved in comparison to other models. It remains to be established whether regeneration in larval zebrafish relies on lingering developmental plasticity or uses distinct regenerative pathways. One approach to answering this question is to identify genes that alter hair cell regeneration without affecting development.

In all the larval stages analyzed, hair cell regeneration in the zebrafish lateral line is robust and rapid (Williams and Holder, 2000; Harris et al., 2003; Hernandez et al., 2006; Lopez-Schier and Hudspeth, 2006; Ma et al., 2008). Within 48 hours, hair cells have regenerated, reestablished both mechanotransduction, hair cell bundle polarity, and synapses with the auditory nervous system (Hernandez et al., 2006; Lopez-Schier and Hudspeth, 2006). Little is known about hair cell regeneration in terms of fish behavior, although several groups are actively pursuing methods for studying functional recovery of the zebrafish lateral line.

Regeneration in zebrafish has been analyzed using a variety of well established techniques including antibody labeling, RNA *in situ* hybridization labeling and electron microscopy. These techniques have been particularly important for the validation of live imaging approaches, which are a major advantage of the zebrafish over other models for hair cell regeneration. In live animals, the presence or absence of hair cells can be detected by a variety of vital dyes, including DASPEI, Yo-Pro and FM1-43 (Seiler and Nicolson, 1999; Harris et al., 2003; Murakami et al., 2003; Collazo et al., 2005; Santos et al., 2006). Dyes added to fish media are rapidly and specifically taken up by hair cells. Although the precise mechanism of vital dye uptake remains unclear, uptake of FM1-43, for example, depends on functional mechanotransduction and so is a good indicator of hair cell maturity in a live animal.

Hair cells in live zebrafish can also be analyzed using a variety of transgenic lines. Developing animals remain optically clear until the formation of metamorphic pigment cells at ~15–20 days (Budi et al., 2008) and fluorescent proteins expressed in the lateral line can be easily observed during this period. Transgenic strains include markers specific to hair cells, afferent and efferent nerves, and supporting cells (Parinov et al., 2004; Scott et al., 2007). Combining transgenic lines with vital dyes and live imaging provides a powerful tool for dissecting the process of hair cell regeneration.

Hair Cell Progenitors

Several studies in the zebrafish lateral line suggest that the majority of trauma-induced hair cell regeneration is the result of mitotic proliferation (Fig. 1b,c). The proliferation of supporting cells, as measured by BrdU labeling, increases significantly following aminoglycoside- or copper-induced hair cell damage and prior to the appearance of new hair cells (Williams and Holder, 2000; Hernandez et al., 2006; Hernandez et al., 2007; Ma et al., 2008). The majority of regenerated hair cells develop from BrdU labeled precursors (Ma et al., 2008). Furthermore, if supporting cells are damaged, as appears to be the case with high, but not low doses of copper, hair cell regeneration does not occur (Hernandez et al., 2006). Mitotic proliferation is also the major mechanism for hair cell regeneration in the axolotl salamander lateral line (Jones and Corwin, 1996).

These results suggest a predominant role for mitotic regeneration of hair cells in cold-blooded vertebrates. However, it is difficult to draw conclusions from these data alone since there are continuous, low levels of hair cell production in the zebrafish lateral line. It is difficult to distinguish between direct transdifferentiation (Fig. 1a), as observed in avian models, and

differentiation of pre-existing hair cell precursors. The possibility of low levels of direct transdifferentiation in zebrafish and other cold-blooded vertebrates remains an open question.

While these studies clearly establish the importance of mitotic regeneration in the lateral line, significant questions remain about the identity of the proliferating progenitors. In comparison to supporting cells in chick and mammalian models, zebrafish supporting cells are poorly defined and the term often refers to any non-hair cells found in neuromasts. In fact, these cells can be further defined on the basis of morphology and location. The outermost supporting cells in a neuromast, often called mantle cells, are thin, elongated and form the external surface of the neuromast. Beneath the mantle cells and above the basement membrane are a second set of supporting cells with nuclei on the basal side of the neuromast and thin cytoplasmic processes extending apically to intercalate with individual hair cells and prevent hair cell-hair cell contact (Metcalf et al., 1985). As the role of supporting cells during regeneration is better understood, it is likely that the definition of supporting cell in zebrafish will be refined. For example, following hair cell damage, supporting cells closest to the center of a neuromast begin to divide more rapidly than those near the periphery (Ma et al., 2008) hinting at the possibility of functional specialization. Similarly, differentiation of sibling progeny may be symmetric, producing two hair cell precursors (Fig. 1b) or two supporting cells (Fig. 1d) or asymmetric, producing one hair cell precursor and a supporting cell (Fig. 1c). Time-lapse imaging studies have begun to address this question. Following neomycin-induced hair cell death, only symmetric hair cell regeneration was detected during live imaging of zebrafish (Lopez-Schier and Hudspeth, 2006). This is in contrast to studies in salamanders where, following laser ablation, hair cells were replaced by asymmetric divisions resulting in one supporting cell and one hair cell (Fig. 1d), (Jones and Corwin, 1996).

These data provide additional support to the prevailing hypothesis that the majority of hair cell regeneration in the lateral line is proliferative. However, symmetric divisions producing hair cells do not replenish the pool of putative stem-cells (Fig. 1b). This suggests that a second stage of supporting cell division, either symmetric producing two supporting cells (Fig. 1d), asymmetric (Fig. 1c) or by a mechanism, as yet unknown, is responsible for maintaining the population of supporting cells within regenerating neuromasts.

Regulation of hair cell numbers

Not only do hair cells regenerate following aminoglycoside-induced damage, they regenerate just the right number of cells. Regenerating neuromasts maintain their relative sizes suggesting active regulation for termination of hair cell regeneration (Ma et al., 2008). The Notch pathway has recently been implicated in hair cell regeneration (for review see (Collado et al., 2008) although it is best known for its role in fate determination via lateral inhibition during development (reviewed in Lewis, 2008). In the zebrafish lateral line, members of the Notch pathway (*notch3*, *deltaA*, and *atoh1a*) are up-regulated in the 24 hours following aminoglycoside-induced damage, when supporting cell division is most active and new hair cells are being specified (Ma et al., 2008), similar to studies in other systems (Stone and Rubel, 1999; Hori et al., 2007). Pharmacological block of the Notch pathway has no effect on lateral line hair cell number in the absence of injury, but following damage, leads to an excess of regenerated hair cells (Ma et al., 2008), as was later observed in avian cell culture models (Daudet et al., 2009). While the overproduction of regenerating hair cells following inhibition of the Notch pathway occurs in both zebrafish and the chick basilar papilla, their methods differ. In damaged zebrafish neuromasts, both the rate and the duration of supporting cell division are elevated when Notch activity is inhibited. These data suggest that in the zebrafish lateral line, increased Notch signaling during regeneration plays a role in the return to quiescence, ensuring that the right number of hair cells are generated. In avian auditory epithelia recovering from aminoglycoside-induced damage, supporting cell division does not increase

after inhibition of the Notch signaling pathway. Instead, excessive numbers of precursor cells are induced to differentiate into hair cells, regardless of their origin by mitosis or direct transdifferentiation. Therefore, although the exact mechanisms for regulating hair cell numbers are different between the two models, inhibition of Notch signaling results in overproduction of hair cells in both zebrafish and chick, further emphasizing the extent of genetic conservation during hair cell regeneration amongst different species.

Re-innervation

Functional regeneration requires more than replacement of hair cells. It also requires re-establishing afferent and efferent synapses. This is further complicated by hair cell polarity. Within a neuromast, hair cells are oriented with their cilia in parallel with or perpendicular to the lateral line (Flock and Wersall, 1962; Lopez-Schier et al., 2004). A single afferent nerve innervates multiple hair cells and multiple neuromasts, but only hair cells of the same polarity (Nagiel et al., 2008). During regeneration, hair cell polarity is first re-established (Lopez-Schier and Hudspeth, 2006) and then innervation follows; only cells of the same polarity are re-innervated by a given neuron (Nagiel et al., 2008). At this time, little is known about the molecular signals regulating polarity-specific re-innervation of hair cells, nor have any studies explored efferent re-innervation in the zebrafish.

Genetic screens for novel genes in hair cell regeneration

Reliable regeneration combined with access to hair cells of the lateral line, and the high level of genetic conservation in the processes of hair cell development and regeneration, are all factors that make zebrafish a unique model for discovering new genes specific to regeneration. Furthermore, zebrafish have an established record of successful genetic screens, including screens for mutations that affect development of the inner ear and lateral line (Granato et al., 1996; Malicki et al., 1996; Whitfield et al., 1996; Nicolson et al., 1998; Kappler et al., 2004; Obholzer et al., 2008) and screens for mutations in lateral line hair cells that provide resistance to ototoxic drugs (Owens et al., 2008). Forward genetic screens to identify animals with abnormal regeneration of lateral line hair cells are ongoing in several labs. Identification and characterization of genes regulating zebrafish hair cell regeneration will be followed by studies to determine whether mammalian orthologs can be co-opted to promote regeneration. As with any model system (even mouse), there are caveats about whether mechanisms will directly translate to humans. Some aspects of zebrafish development and regeneration are likely to diverge from other species; for example zebrafish hair cell regeneration shows little of the direct transdifferentiation seen in other systems. However, it is likely that fundamental mechanisms will be conserved and it is also important to determine which mechanisms are not conserved. Comparing the genetics of zebrafish vs. mammalian hair cell development and regeneration may provide critical insights as to why zebrafish regularly regenerate hair cells while mammals cannot.

Other mechanisms requiring hair cell addition

Most zebrafish studies have examined hair cell regeneration after ablation of specific subsets of hair cells with or without supporting cell ablation. However, hair cells need to be replaced in a number of additional situations. Turnover of hair cells is a normal process of aging in fish. In 10 day old zebrafish, low levels of apoptotic cell death, appear to be localized to hair cells within neuromasts (Williams and Holder, 2000). Although hair cell turnover in adult (sexually mature) zebrafish has not been reported, turnover in other fish occurs even at 9 years of age (Popper and Hoxter, 1984; Lombarte and Popper, 1994). We do not yet know whether hair cell replacement as a result of normal turnover following processes distinct from regeneration or shares common mechanisms.

In addition to turnover, neuromasts continue to be added as the fish grows. This requires two additional processes: intercalation and stitch formation. Intercalation is the process of inserting neuromasts into the lateral line in the anterior-posterior axis while stitch formation is the addition of neuromasts dorsoventrally (reviewed in Ghysen and Dambly-Chaudiere, 2007). During intercalation neuromasts are added between existing neuromasts from latent precursors established during the initial development of the lateral line (Grant et al., 2005). Following intercalation the entire lateral line migrates dorsoventrally then expands. The expansion, or addition of stitches, is a dorsoventral addition of neuromasts at each previously established neuromast in the lateral line (Metcalf et al., 1985). Early studies on salamander development describe the addition of neuromasts by budding; existing neuromasts generate additional neuromasts that eventually migrate away (Stone, 1933). Following these studies, performed well before development of live imaging and molecular markers, it was generally assumed that the process of stitch formation was the same in zebrafish. More recently, stitch formation was examined in sexually mature zebrafish (Ledent, 2002; Sapede et al., 2002). When new stitches appear in zebrafish, they are already innervated suggesting that addition does occur by budding (Ledent, 2002). However, stitch formation progresses in anterior to posterior waves, rather than simultaneously, suggesting additional levels of regulation. Revisiting the process of neuromast migration and stitch formation may reveal whether there are significant differences between neuromast addition and regeneration. This question, in combination with genetic screen, will address the question of whether regeneration in the zebrafish is distinct from developmental processes.

Hair cell regeneration also occurs as a part of fin or tail regeneration. In zebrafish, fin regeneration includes regenerating a portion of the lateral line as the fin itself is regenerated. This process differs from regeneration following hair cell-specific ablation since multiple neuromasts, (including hair cells, a variety of supporting cells and neuronal innervation) must be recapitulated in a stereotyped pattern. Following fin amputation in sexually mature zebrafish, mantle cells of the neuromast remaining immediately anterior to the plane of amputation begin to proliferate. These mantle cells essentially recapitulate the process observed during development: they form a small primordium that migrates onto the regenerated fin and deposits new neuromasts. Neuromasts generated during fin regeneration are deposited in the absence of innervation, in contrast to stitch formation where neuromasts migrating dorsoventrally carry along innervating processes (Ledent, 2002; Dufourcq et al., 2006). This two-step process of regeneration, fin before neuromasts, is strikingly similar to that described in other cold-blooded vertebrates including salamanders regenerating their tail tips (Stone, 1933; Stone, 1937; Corwin, 1986; Corwin et al., 1989; Jones and Corwin, 1993), and tadpoles regenerating tails (Speidel, 1947; Wright, 1947). It is worth noting that lateral line regeneration depends on a pool of neuromast-precursors distinct from the fin blastema; the source of regeneration for all other fin structures. While many genes involved in formation and differentiation of the blastema have been identified (reviewed in Akimenko et al., 2003; Iovine, 2007) little is known about the genetics of lateral line regeneration following amputation in the zebrafish. The relationships between precursors that generate new hair cells after damage and those that generate new neuromasts during lateral line growth, stitch formation or during fin regeneration are currently unknown. Establishing whether the replacement of entire neuromasts differs significantly from the replacement of hair cells within an existing neuromast may provide the opportunity to determine the full extent of stem-cell like properties of supporting cells.

Conclusions and Future directions

The chick is now a classic model for hair cell regeneration with a wealth of studies on a variety of structures, both auditory and vestibular, in the inner ear. In avian models, the time-course of hair cell regeneration, the identity of hair cell precursors and a range of other cellular

processes have been characterized. Studies in birds have generated important questions that will define the direction of future research. The zebrafish, a relative upstart by comparison, is now also established as a hair cell regeneration model, displaying a consistent time-course of regeneration in response to a range of damaging conditions that also function in avian and mammalian models. In zebrafish, work remains to clarify the identity of hair cell progenitors and the processes leading to hair cell and supporting cell replacement. However, this line of examination is significantly aided by the accessibility of lateral line hair cells for manipulation and live imaging. Due to a wide range of existing transgenic lines, mutants and the opportunity for unbiased, forward genetic screens to identify genes involved in regeneration, the zebrafish is an exciting new model for addressing questions that remain about molecular regulation of hair cell regeneration.

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Abbreviations

BrdU	Bromodeoxyuridine
FGF	fibroblast growth factor

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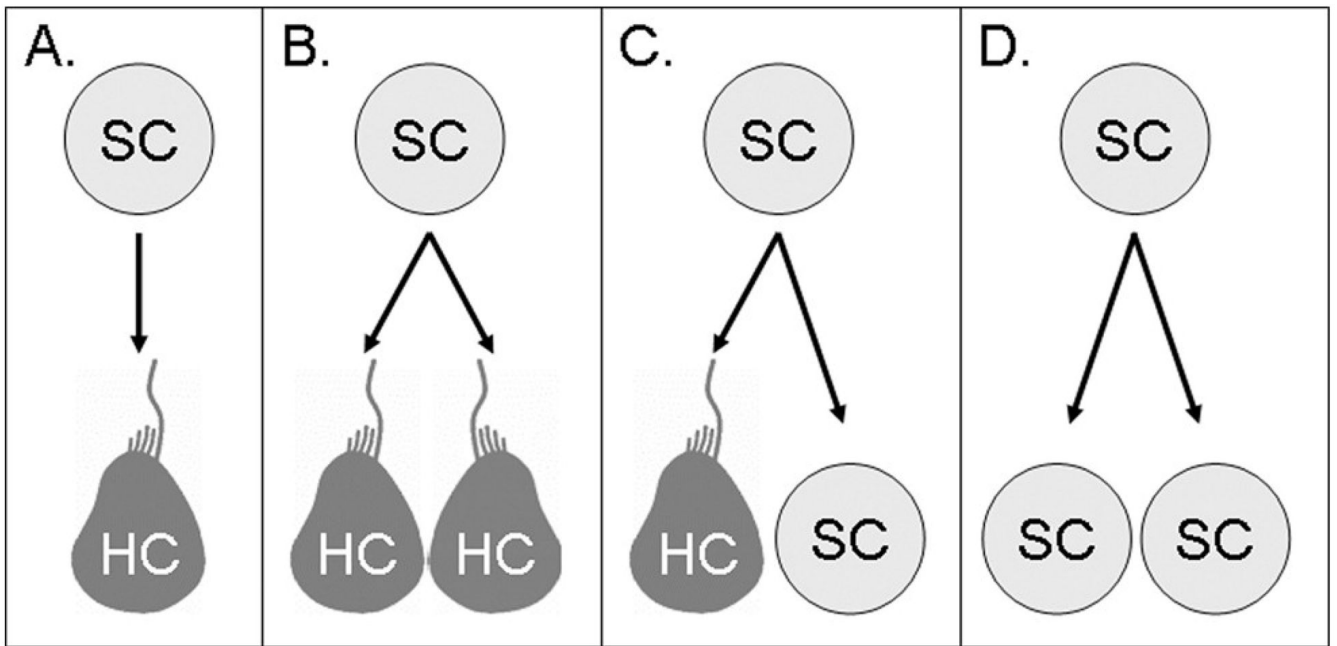


Fig. 1.
Methods of Hair Cell Replacement.

The production of hair cells (depicted here as fish hair cells, which retain kinocillia) may occur by several methods. (A) Supporting Cells (SC) may rapidly produce hair cells by direct transdifferentiation; direct, phenotypic conversion to a hair cell (HC) without the requirement for mitosis. When HC replacement depends on mitosis there are several possible mechanisms. (B) Symmetric division of one SC produces two HCs, rapidly replacing HC but eventually leading to a depletion of SC. (C) Asymmetric SC division produces one HC and one SC, replacing lost HC more slowly but replenishing the SC pool. (D) Symmetric SC division may produce two SC as a method of maintaining the SC population. This symmetric division could occur in tandem with, or following symmetric SC divisions resulting in two hair cells. One final alternative, not depicted, is that SCs produce HC precursors distinct from a fully differentiated HC and thus introduce a middle stage to all of the methods depicted above.