Lhx3, a LIM domain transcription factor, is regulated by Pou4f3 in the auditory but not in the vestibular system

Ronna Hertzano,1,2,4, Amiel A. Dror,1 Mireille Montcouquiol,2,3 Zubair M. Ahmed,4 Buffy Ellsworth,5 Sally Camper,5 Thomas B. Friedman,4 Matthew W. Kelley2 and Karen B. Avraham1

1Department of Human Molecular Genetics and Biochemistry, Sackler School of Medicine, Tel Aviv University, Tel Aviv 69978, Israel
2Section on Developmental Neuroscience, National Institute on Deafness and Other Communication Disorders, National Institutes of Health, Bethesda, MD 20892, USA
3Laboratory of Development Neurosciences - Avenir Team, Centre de Recherche INSERM Francois Magendie, Universite Bordeaux II, 33077 Bordeaux Cedex, France
4Section on Human Genetics, Laboratory of Molecular Genetics, National Institute on Deafness and Other Communication Disorders, National Institutes of Health, Rockville, MD 20850, USA
5Department of Human Genetics, University of Michigan Medical School, Ann Arbor, MI, 48109, USA

Keywords: cochlea, inner ear, hair cell, Gfi1, deafness, mouse

Abstract
A dominant mutation of the gene encoding the POU4F3 transcription factor underlies human non-syndromic progressive hearing loss DFNA15. Using oligonucleotide microarrays to generate expression profiles of inner ears of Pou4f3+/―/ddl mutant and wild-type mice, we have identified and validated Lhx3, a LIM domain transcription factor, as an in vivo target gene regulated by Pou4f3. Lhx3 is a hair cell-specific gene expressed in all hair cells of the auditory and vestibular system as early as embryonic day 16. The level of Lhx3 mRNA is greatly reduced in the inner ears of embryonic Pou4f3 mutant mice. Our data also show that the expression of Lhx3 is regulated differently in auditory and vestibular hair cells. This is the first example of a hair cell-specific gene expressed both in auditory and in vestibular hair cells, with differential regulation of expression in these two closely related systems.

Introduction
The mammalian inner ear consists of six sensory organs that contain the sensory epithelia responsible for transducing sound waves and head movements into neuronal impulses, coding for hearing and balance information. The sensory epithelium of the organ of Corti is responsible for auditory processing, while five sensory organs in the vestibular system are responsible for balance. These five sensory epithelia consist of three cristae ampullaris, in the semicircular canals, and two maculae, the macula utriculi and the macula sacculi. All sensory epithelia consist of a mosaic of sensory and supporting cells. The sensory cells are named ‘hair cells’ due to their apical actin-rich projections named stereocilia, which deflect in response to sound or movement. This deflection results in a mechanical opening of an ion channel at the apical tip of each stereocilium. An ion influx through the opened channels results in a depolarization of the hair cells and a release of neurotransmitter at the base of the hair cell. There are at least five different supporting cell types in the cochlea, at least one in the vestibular system, and their function is still poorly understood. It has been shown that the supporting cells can recycle potassium ions and form a sealed barrier between the endolymph- and perilymph-filled spaces, thus maintaining hair cell function. The transcriptional cascades governing these processes are largely unknown. Genetic mutations leading to defects in hearing or balance may help elucidate these transcriptional pathways.

Pou4f3 (Bm3.1, Bm3c) is a class IV POU domain transcription factor that has a central function in the development and survival of all hair cells in the human and mouse inner ear sensory epithelia (Erkman et al., 1996; Xiang et al., 1997). A mutation of POU4F3 underlies human autosomal dominant, non-syndromic progressive hearing loss DFNA15 (Vahava et al., 1998). In the mouse, hair cells initially differentiate in the absence of Pou4f3, but begin to undergo apoptosis at embryonic day 17 (E17), leading to a complete depletion of hair cells from all inner ear sensory epithelia by early postnatal stages (Xiang et al., 1998; Hertzano et al., 2004). We previously used the dreidel allele of Pou4f3 (Pou4f3/ddl/ddl), a functional null-allele that arose on a C57BL/6J genetic background, to search for downstream targets of Pou4f3 by expression profiling of mouse inner ears. We identified Gfi1, Growth factor independence 1, a hair cell-specific gene, as the first bona-fide downstream target gene of Pou4f3. In the Pou4f3/+ or Pou4f3/ddl/ddl mice, Gfi1 mRNA could not be detected. It appears that outer hair cell degeneration in the Pou4f3 mutant mice results from the lack of expression of Gfi1 (Hertzano et al., 2004). We have now extended our analysis to other differentially expressed genes in the ears of the Pou4f3/ddl/ddl mice and identified Lhx3 as a hair cell-specific gene regulated by Pou4f3. Lhx3 is a member of the LIM homeodomain transcription factor family. We studied the developmental expression pattern of Lhx3 in the cochlea, the expression of Lhx3 in the inner ears of the Pou4f3 and Gfi1 mutant mice, and evaluated it as a candidate for a deafness gene in humans.
Materials and methods

Breeding, phenotyping and genotyping of mice

All procedures involving animals met the guidelines described in the National Institutes of Health Guide for the Care and Use of Laboratory Animals and had been approved by the Animal Care and Use Committees of the National Institutes of Health and Tel Aviv University (M-00-65). Breeding, phenotyping and genotyping of the Pou4f3<sup>ddl/dll</sup>, Pou4f3<sup>−/−</sup>, Gfi1<sup>−/−</sup> and Lhx3<sup>−/−</sup> mice were described previously (Sheng et al., 1996; Karsunky et al., 2002; Hertzano et al., 2004). To study the inner ears of Lhx3<sup>−/−</sup> mice, cochlear cultures of inner ears from E15.5 embryos were made as described (Montcouquiol & Kelley, 2003). Time-mated female mice were killed by cervical dislocation. E18.5 mice were killed by decapitation.

RNA expression analysis

Microarray analyses, RNA extraction, reverse transcription and real time reverse transcriptase PCR (RT-PCR) were performed as described (Hertzano et al., 2004). The following primers and FAM-labeled probes were used: Lhx3 (F) 5'-GCAGAATTGTGACCCGTA-3', (R) 5'-CCACGCTTCCCTCAGTGGAA-3', (probe) 6FAM-CACCTTGCACAACAGACTGTGCTCC-TAMRA; Scinderin (F) 5'-CATGTCCGCGTTTTCTGCTTTG-3', (R) 5'-AAATAGTGGTTTATGTTCAAGGCA-TAMRA; Stat5b (F) 5'-TGGATCCCTCTGCGACCA-3', (R) 5'-TCCACGAGGGCGTATGA-3', (probe) 6FAM-TGAC-CAAGCCCTACCTGCAGC-TAMRA; Calbindin2 (F) 5'-AG-ACTCAGATGAAAAATGAGATG-3', (R) 5'-CAGGAA-TCTCCGTTGCGGACTCTT-TAMRA; Rtkn (F) 5'-TGAGGACTTTGATTGAA-3', (R) 5'-GATGGTGTTCTAGCGGCTCAA-TAMRA; FoxA2 (F) 5'-GCCAAGTACGACCCACCTCA-3', (R) 5'-AGATCAGCTGGCCCCATCTATTAG-3', (probe) 6FAM-CCTCAAGGAGAGCTCTCCAGTGCTCTGTA-MAR; Pou4f3 (F) 5'-GGCCCTTGTGAGGAGATTACC-3', (R) 5'-GATGGTGCGCTCAGCGGCTCAA-TAMRA; Dlg3 (F) 5'-CCACCCCCCATACTGCTCCTT-3', (R) 5'-TGCTCATCTCCCTCCAGTATGA-3', (probe) 6FAM-AAGGCAACGTGCCTCACCTCCTC-TAMRA. The primers and probes for the amplification of Myo6, Myo7a, Pou4f3 and Gfi1 were previously described (Hertzano et al., 2004).

For in situ hybridization, 647 bp from the Lhx3 3' untranslated region (UTR) (L38248, nucleotides 1428-2074) were cloned into pGEM-T Easy (Promega, Madison, WI, USA) for the generation of digoxigenin-labeled sense and antisense probes. In situ hybridization of whole mounts and sections of mouse cochleae were performed as described (Hertzano et al., 2004). For protein detection, samples were incubated with a myosin VI antibody at a dilution of 1:100 (Sigma, St. Louis, MO, USA) or a monoclonal antibody against Lhx3 at a dilution of 1:5 (DSHB, The University of Iowa).

For immunofluorescence of paraffin sections, dissected inner ears were fixed in 4% paraformaldehyde overnight at 4 °C, dehydrated in a graded series of ethanol followed by a 1-h and a 2-h incubation in isopropanol and toluene. Samples were then embedded in paraffin using a Leica Histoembedder. Sections (10 μm) were dewaxed with xylene and rehydrated with a decreasing ethanol gradient. Antigen unmasking was performed using a citric acid-based antigen unmasking solution (Vector, Burlingame, CA, USA). Following a 2-h incubation in a PBSTG blocking solution (0.2% Tween 20 and gelatin in PBS), immunofluorescence was carried out as described above. The immunohistochemistry was repeated on 36 slides from eight litters in eight independent experiments.

Family enrolment, genomic DNA isolation and genotyping

Institutional Review Board approval (OH93-N-016) and written informed consent were obtained for all subjects in this study. Peripheral blood samples were obtained from participating subjects. DNA was extracted from peripheral blood or buccal swabs ( BuccalAmp™ DNA Extraction Kit, Epicentre Technologies, Madison, WI, USA). Linkage analyses were performed using markers D9S1826 and D9S158 and the data were analysed using ABI GeneMapper (v.3.7) software.

Results

Lhx3 mRNA levels are decreased in the Pou4f3 mutant ears

In order to identify in vivo target genes of the Pou4f3 transcription factor, we hybridized RNA extracted from whole inner ears of E16.5 Pou4f3<sup>ddl/dll</sup> and their wild-type littermates to the Affymetrix Murine Genome U74Av2 oligonucleotide microarrays. From the 12 000 probes present on the array, Gfi1 (Gilks et al., 1993) was the only gene that was identified as ‘present’ in all samples from the wild-type inner ears while being identified as ‘absent’ in all samples from the mutant inner ears (Hertzano et al., 2004). In order to extend our study for differentially expressed genes, we performed a t-test analysis requiring an absolute t score above 1.8 and a fold change greater than 1.5. Ninety-one genes were detected as down-regulated in the samples from the Pou4f3<sup>ddl/dll</sup> mice, as compared with samples from the wild-type mice, and 122 genes showed the opposite pattern of expression (full data set available as a supplementary table linked to Hertzano et al., 2004). We then selected a total of nine potential target genes for validation based on their function, t-test score and fold change. These genes were Gfi1, Bdnf, Lhx3, Scinderin, Stat5b, Calbindin2 and FoxA2, all of which the microarray detected as down-regulated in the ears of the Pou4f3<sup>−/−</sup> mice, as well as Rtkn and Dlg3, which were detected as up-regulated.

At E16 and E18.5, real-time semi-quantitative RT-PCR confirmed that Gfi1, Bdnf, Lhx3 and Calbindin2 transcript abundance were significantly lower in the samples from the Pou4f3<sup>ddl/dll</sup> inner ears as compared with the wild type. The expression of all four genes declined at least two-fold for one or more of these time points, in contrast to hair cell-specific genes not regulated by Pou4f3 that retained 63–88% of their mRNA abundance in the wild-type mice (Table 1) (Clough et al., 2004; Hertzano et al., 2004). Conversely, the measured decreases in the mRNA levels of Stat5b, FoxA2, Rtkn and Dlg3 were less than two-fold, and the semi-quantification of their RNA showed some variability from the Affymetrix microarray results. When we extended the validation to RNA samples from Pou4f3<sup>−/−</sup> mice, we confirmed the down-regulation of Gfi1, Lhx3, Bdnf and Calbindin2 but not of Scinderin (data not shown).

Lhx3 is a transcription factor previously found to be associated with activation of pituitary hormone genes and, through a combinatorial control, with assignment of subtype identity of motor neurons in the spinal cord (Sheng et al., 1996; Sharma et al., 1998; Sloep et al., 1999). Our results indicate that Lhx3 mRNA is expressed in the wild-type mouse inner ear. Lhx3 mRNA levels appear to increase from E16...© The Authors (2007). Journal Compilation © Federation of European Neuroscience Societies and Blackwell Publishing Ltd European Journal of Neuroscience, 25, 999–1005
Lhx3 is a hair cell-specific gene

The genomic structure of the mouse Lhx3 gene, a LIM and homeodomain transcription factor, was previously characterized (Zhadanov et al., 1995b). 5′ rapid amplification of cDNA ends revealed that Lhx3 encodes two alternatively spliced first exons (146 and 195 bp long), defining two isoforms, Lhx3a and Lhx3b, encoding unique 5′ UTRs and 29 or 31 unique amino acids in Lhx3a (NM_010711) and Lhx3b (L38248), respectively. Lhx3a and Lhx3b are differentially expressed in specific pituitary cell lines (Zhadanov et al., 1995a), and differ in their DNA binding and transcription activation properties (Sloop et al., 1999; Yaden et al., 2005). A third isoform of Lhx3 is formed from an internal start codon (Sloop et al., 2001). By RT-PCR, using primer pairs specific for Lhx3a and Lhx3b isoforms of the gene, we identified expression of both in the E16.5 mouse inner ear (data not shown). Using an antibody that detects both isoforms of the gene, we showed that Lhx3 is expressed in the nuclei of all hair cells of the auditory and vestibular systems in postnatal day 1 (P1) wild-type mice (Fig. 2). No expression was observed in any other cell type of the inner ear, indicating that in the mouse, Lhx3 is a hair cell-specific protein. Whole-mount and section in situ hybridization using a digoxygenin-labeled probe showed similar results in E16 and P0 wild-type inner ears (data not shown). These data correlate with the results of Sage et al. (2005), who used Lhx3 as a marker for nuclei of differentiated hair cells in a study of hair cell development in a targeted deletion of Rb1.

The expression pattern of Lhx3 follows the expression pattern of Pou4f3 in the developing auditory sensory epithelium

To study the expression pattern of Pou4f3 and Lhx3 in the developing organ of Corti, we extracted RNA at seven time points between E12 and P3 as described (Hertzano et al., 2004). The semi-quantitative mRNA profile of Pou4f3 indicated that Pou4f3 mRNA is detectable at a low level as early as E12, with increasing levels of expression up to P3. Lhx3 mRNA transcripts could be detected slightly before E16, but not before E15, and increased in abundance up to P0 followed by a down-regulation between P0 and P3 (Fig. 3). The onset of expression of Lhx3, as well as its pattern of expression, was very similar to that of Gfi1, a gene that we reported to be regulated by Pou4f3 (Hertzano et al., 2004). By comparison, Myo6 and Myo7a are two hair cell-specific genes whose expression is not dependent on Pou4f3 (Xiang et al., 1998; Hertzano et al., 2004), while Bdnf is a gene that is partially regulated by Pou4f3 (Fig. 3) (Clough et al., 2004). The reduction in Lhx3 expression levels between P0 and P3 in the wild type suggests that other transcription factors are required to down-regulate the expression of Lhx3 postnatally.

Lhx3 is differentially regulated in the mouse auditory and vestibular systems

Although Lhx3 mRNA abundance was significantly reduced in the inner ears of the Pou4f3<sup>ddi/ddi</sup> and Pou4f3<sup>−/−</sup> mice, we could still detect it by semi-quantitative RT-PCR analyses at E16 and E18.5 (Fig. 1). This is in sharp contrast to the complete loss of expression of Gfi1 in the ears of the Pou4f3 mutant mice (Hertzano et al., 2004). Given that in the mouse inner ear Lhx3 is uniquely expressed in the hair cells, we tested the hypothesis that Pou4f3 contributes to the expression of Lhx3 but does not solely regulate its expression in all hair cell types. Figure 4 shows that all the hair cells of E18.5 wild-type mice express Lhx3, in both the auditory and the vestibular epithelia (Fig. 4A and D). By contrast, Lhx3 was not expressed throughout the cochlear duct of Pou4f3 mutant mice (Fig. 4B), but was maintained in all hair cells of the vestibular sensory epithelia (Fig. 4E).

The hair cells of the Pou4f3 mutant mice do not express Gfi1 (Hertzano et al., 2004). We stained inner ears of Gfi1 mutant mice with an antibody that detects Lhx3 in order to rule out the possibility that the loss of expression of Lhx3 in the cochlea of the Pou4f3 mutant mice results from a deficiency in Gfi1. In the E18.5 Gfi1<sup>−/−</sup> mice, the expression of Lhx3 is maintained in both auditory and vestibular hair cells (Fig. 4C and F), indicating that the loss of expression of Lhx3 in

### Table 1. Real time RT-PCR results

<table>
<thead>
<tr>
<th>Gene name</th>
<th>Affy ID</th>
<th>Fold change</th>
<th>t-score</th>
<th>E16</th>
<th>E18.5</th>
</tr>
</thead>
<tbody>
<tr>
<td>Myo6</td>
<td>162245_f_at</td>
<td>1.2</td>
<td>1.73</td>
<td>-1.13</td>
<td>-1.134</td>
</tr>
<tr>
<td>Myo7a</td>
<td>94713_at</td>
<td>-1.04</td>
<td>-0.64</td>
<td>-1.58</td>
<td>-1.18</td>
</tr>
<tr>
<td>Pou4f3</td>
<td>Not on array</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Gfi1*</td>
<td>103259_at</td>
<td>-2.07</td>
<td>-12.17</td>
<td>-20.34</td>
<td>-11.9</td>
</tr>
<tr>
<td>Bdnf*</td>
<td>102727_at</td>
<td>-1.48</td>
<td>-4.76</td>
<td>-1.89</td>
<td>-2.01</td>
</tr>
<tr>
<td>Lhx3*</td>
<td>102902_at</td>
<td>-1.4</td>
<td>-2.65</td>
<td>-6.3</td>
<td>-5.1</td>
</tr>
<tr>
<td>Scinderin*</td>
<td>103715_at</td>
<td>-1.43</td>
<td>-2.52</td>
<td>+5.7</td>
<td>-1.32</td>
</tr>
<tr>
<td>Stat3b</td>
<td>92199_at</td>
<td>-1.17</td>
<td>-1.29</td>
<td>-1.5</td>
<td>1.02</td>
</tr>
<tr>
<td>Calbindin2*</td>
<td>95036_at</td>
<td>-1.48</td>
<td>-2.93</td>
<td>-9.8</td>
<td>-1.49</td>
</tr>
<tr>
<td>FoxA2</td>
<td>93950_at</td>
<td>-1.34</td>
<td>-0.97</td>
<td>-1.149</td>
<td>+1.23</td>
</tr>
<tr>
<td>Rtna↓†</td>
<td>162243_f_at</td>
<td>+1.34</td>
<td>1.23</td>
<td>-1.517</td>
<td>+1.11</td>
</tr>
<tr>
<td>Dlg3h</td>
<td>160892_at</td>
<td>+1.38</td>
<td>2.82</td>
<td>+1.61</td>
<td>-1.13</td>
</tr>
</tbody>
</table>

*An asterisk indicates a significant difference between wild-type and mutant mRNA transcript abundance (P < 0.0001). †The expression of Gfi1 in the E16 Pou4f3<sup>ddi/ddi</sup> mice did not reach the detection threshold. ‡Genes having more than one probe on the array.

Fig. 1. Lhx3 mRNA is 5–6-fold down-regulated in the ears of E16 and E18.5 Pou4f3<sup>ddi/ddi</sup> mice. Black bars indicate mRNA levels in wild-type inner ears and grey bars indicate mRNA levels in the Pou4f3<sup>ddi/ddi</sup> inner ears. Ordinate: mRNA levels, arbitrary units; abscissa: developmental time points. Error bars represent one standard error, n = 6. *P < 0.0001.

Fig. 2. Lhx3 expression in E16 and E18.5 wild-type and Pou4f3<sup>−/−</sup> mutant mice. (A) Lhx3 expression in the cochlea and (B) in the vestibulocochlear apparatus. The cochlear duct of Pou4f3<sup>−/−</sup> mutant mice is stained with the antibody detecting Lhx3 (red), indicating that Lhx3 is specifically expressed in the hair cells and not in supporting cells. (C) Lhx3 expression in the inner ear of Pou4f3<sup>−/−</sup> mutant mice. Lhx3 expression is lost in the supporting cells (green) but not in the sensory epithelia (red). (D) Lhx3 expression in the inner ear of Pou4f3<sup>−/−</sup> mutant mice. Lhx3 expression is lost in the supporting cells but not in the sensory epithelia.

Fig. 3. Lhx3 expression in E16 and E18.5 wild-type and Pou4f3<sup>−/−</sup> mutant mice. (A) Lhx3 expression in the cochlea and (B) in the vestibulocochlear apparatus. The cochlear duct of Pou4f3<sup>−/−</sup> mutant mice is stained with the antibody detecting Lhx3 (red), indicating that Lhx3 is specifically expressed in the hair cells and not in supporting cells. (C) Lhx3 expression in the inner ear of Pou4f3<sup>−/−</sup> mutant mice. Lhx3 expression is lost in the supporting cells (green) but not in the sensory epithelia (red). (D) Lhx3 expression in the inner ear of Pou4f3<sup>−/−</sup> mutant mice. Lhx3 expression is lost in the supporting cells but not in the sensory epithelia.
the cochleae of the Pou4f3 mutant mice does not result from the loss of expression of Gfi1. Furthermore, as the outer hair cells of the Pou4f3 and Gfi1 mutant mice have a similar pattern of degeneration, the expression of Lhx3 in the outer hair cells of the Gfi1 mutant mice indicates that a lack of expression of Lhx3 in the cochleae of the Pou4f3 mutant mice is not a consequence of cell death.

Auditory hair cells of the mouse inner ear can develop and differentiate in mice with a targeted deletion of Lhx3
Lhx3 homozygous mutant mice are embryonically lethal or die soon after birth (Sheng et al., 1996). In order to determine whether Lhx3 is necessary for hair cell development and survival, E15.5 embryos were obtained from a time mated intercross of Lhx3+/− mice. Inner ears were dissected and cultured for 4 days in vitro. Cultured ears were then stained with an antibody for myosin VI and for actin using phalloidin. No developmental abnormalities in the inner ear cochlear sensory epithelium were observed (data not shown).

Screening of deaf families for linkage to the LHX3 locus
In humans recessive mutations of LHX3 have been previously reported to underlie combined pituitary hormone deficiency and rigid cervical spine syndrome (Netchine et al., 2000). These mutations included a missense mutation in one of the LIM domains and an intragenic deletion that results in a truncated protein that lacks the DNA binding
Patients with the described mutations were not reported to present with hearing loss. To determine whether \textit{LHX3} could be involved in human hereditary non-syndromic hearing loss, we searched the Hereditary Hearing Loss Homepage (http://webhost.ua.ac.be/hhh/) for deafness loci that map to the region of human chromosome 9q34, the location of \textit{LHX3} gene. We found that \textit{LHX3} localized within the linkage interval for non-syndromic hearing loss DFNB33 (Medlej-Hashim \textit{et al.}, 2002) between short tandem repeat (STR) markers D9S1826 and D9S1838. This region spans roughly two million base pairs. Using D9S158, a marker located 4000 bp upstream of \textit{LHX3}, we screened 452 families segregating recessively inherited non-syndromic deafness, 120 families from India and 332 families from Pakistan (Friedman \textit{et al.}, 2002). We found one consanguineous family, consisting of five affected individuals in two sibships, with homozygosity in affected individuals for DFNB33 markers. We performed a mutation analysis on DNA derived from this family and no mutations were found in the coding region and splice sites of \textit{LHX3} (data not shown; primers available upon request).

**Discussion**

The LIM-homeobox genes encode a family of proteins that consist of a highly conserved homeodomain that functions to bind DNA and two LIM domains, each containing two zinc-fingers, which are necessary for protein–protein interactions (reviewed in Retaux & Bachy, 2002; Gill, 2003). The LIM-homeobox proteins bridge molecules to form multimeric complexes that bind to DNA to activate or repress transcription. This family of proteins is well conserved with homologues in \textit{Drosophila}, \textit{Caenorhabditis elegans}, \textit{Xenopus}, fish and mammals (Hobert & Westphal, 2000).

\textit{Lhx3} plays a pivotal role in the specification of pituitary cell lineages during development (Sheng \textit{et al.}, 1996), activating expression of pituitary hormone genes (Sloop \textit{et al.}, 1999), and in concert with Isl1 determines whether spinal cord motor neurons will differentiate into motor neurons or V2 interneurons (Sharma \textit{et al.}, 1998). \textit{Lhx3} also shares high similarity with mec-3, which is essential for touch neuron differentiation in \textit{C. elegans}. UNC-86 in \textit{C. elegans}, a Pou4f3 homolog (Chalfie \textit{et al.}, 1981; Ninkina \textit{et al.}, 1993), promotes mechanosensory neuron differentiation by first binding to the mec-3 promoter and then activating transcription of mechanosensory neuron-specific genes together with the protein product of mec-3. We have previously described a similar conserved genetic hierarchy with the \textit{C. elegans} homologue of Gfi1 (Hertzano \textit{et al.}, 2004). This suggests a possible role for Lhx3 or another Lhx molecule in the specification of hair cell differentiation in mammals (Lichtsteiner & Tjian, 1995; Duggan \textit{et al.}, 1998; Rohrig \textit{et al.}, 2000).

We demonstrate that in the ear, Lhx3 is a hair cell-specific protein that in the cochlear hair cells is regulated either directly or indirectly by Pou4f3. However, the role of Lhx3 in the inner ear remains elusive. Cultured cochlear from \textit{Lhx3} \textit{−/−} mice were indistinguishable from those of their wild-type littermate controls, indicating that Lhx3 is not necessary for early hair cell specification, survival or differentiation. Patients with recessive mutations in \textit{LHX3} that cause combined pituitary hormone deficiency and rigid cervical spine syndrome have
not been diagnosed with hearing loss (Netchine et al., 2000). These mutations of LHX3 included a truncating allele that results in a short and inactive form of the protein. It is possible that another LIM-homeodomain protein, such as Isl1-1, a LIM domain protein that is expressed in the inner ear, can compensate for the loss of expression of LHX3/Lhx3 (Meyer, 2003; Radde-Gallwitz et al., 2004). However, Isl1 mRNA levels did not show a statistically significant change in expression levels between the wild-type and the Pou4f3ddl/dd samples in our microarray results (fold of change 1.09, P > 0.3). Moreover, based on a recent microarray experiment performed in our laboratory, only Lhx3 but not Lhx1, 2, 4, 5, 6, 8 or 9 are expressed in the early postnatal auditory or vestibular sensory epithelia (data not shown). Future studies assessing each of these genes individually throughout development might reveal a candidate gene that could compensate for the role of Lhx3. Alternatively, another different molecule might be compensating for the loss of Lhx3, or Lhx3 might not be necessary for the proper function of the auditory epithelium.

Hair cells in the auditory and vestibular systems share common as well as unique morphological features. There are two types of hair cells of the cochlea, inner and outer hair cells (IHCs and OHCs), which differ in their structure, pattern of innervation and function. The IHCs receive most of the afferent innervation of the organ of Corti and very little efferent innervation. In the vestibular system, there are two types of hair cells, type I and type II. Both contain 50–100 stereocilia and a kinocilium that is maintained throughout life. Type I hair cell cell-bodies are pear shaped, similar to the IHCs in the cochlea, and contain a single large calyx engulfing the hair cell body. Type II hair cells have a tubular shape, similar to the OHCs in the cochlea, and multiple nerve endings synapse directly onto the basal end of their cell body. Nevertheless, the same basic mechanism of mechanotransduction operates in all four types and they do share many morphological as well as molecular features.

Although Pou4f3 is a pan-hair cell-specific transcription factor, we show that Lhx3, in contrast to Gfi1, is regulated by Pou4f3 in the auditory but not in vestibular system hair cells. Lhx3 is the first example of a hair cell-specific gene that is expressed in all hair cells of the mouse inner ear, but is regulated differently in auditory and vestibular hair cells. We are clearly just at the beginning of identifying the underlying mechanisms responsible for variation in the regulation of a gene in different hair-cell types, and target genes of Pou4f3 appears to be one such pivotal factor in distinguishing between these two systems.

Acknowledgements

We would like to thank Leonid Mittleman for confocal microscopy, Darcy Butts for animal care and Rani Elkon for the bioinformatic analysis of the microarrays. We thank Tama Hasson for the myosin VIIa antibody, Heiner Westphal for the Lhx3 mice, and Thomas M. Jessell for the Lhx3 monoclonal antibody, obtained from the Developmental Studies Hybridoma Bank developed under the auspices of the NICHD and maintained by The University of Iowa, Department of Biological Sciences, Iowa City, IA. This work was supported by NIH grant R01 DC005641 (K.B.A.), the US–Israel Binational Science Foundation (BSF) Grant 2003335 (K.B.A. and M.W.K.), the European Commission FP6 Integrated Project EUROHEAR LSHG-CT-20054-512063 (K.B.A.), and NIH R01DC041557 (S.C.).

Abbreviations

E, embryonic day; IHCs, inner hair cells; OHCs, outer hair cells; P, postnatal day; PBSTG, PBS with 0.2% Tween and gelatin; RT-PCR, reverse transcription-polymerase chain reaction; STR, short tandem repeat; UTR, untranslated region.

References


© The Authors (2007). Journal Compilation © Federation of European Neuroscience Societies and Blackwell Publishing Ltd


