

Grhl1 deficiency affects inner ear development in zebrafish

FEI LIU^{1, #}, FAN YANG^{1, #}, DANPING WEN¹, WENJUN XIA¹, LILI HAO¹, JIONGJIONG HU², JIE ZONG³,
XIAOFANG SHEN¹, JING MA¹, NAN JIANG¹, SHAOYANG SUN¹, JIN ZHANG¹, HUIJUN WANG⁴, XU WANG¹,
ZHAOXIN MA^{*, 2} and DUAN MA^{*, 1, 4}

¹Key Laboratory of Metabolism and Molecular Medicine, Ministry of Education, Department of Biochemistry and Molecular Biology, Institute of Biomedical Sciences, School of Basic Medical Sciences, Fudan University, ²Department of Otorhinolaryngology, Shanghai East Hospital, Tongji University, ³Novel bioinformatics Co., Ltd and ⁴Children's Hospital of Fudan University, Fudan University, Shanghai, China

ABSTRACT Many genes that have been found to contribute to deafness are currently being studied. Some 87 non-syndromic hereditary deafness genes have been confirmed. Proteins associated with cochlear development have also been confirmed. Some of these proteins have important relationships with gap junctions (GJ) and tight junctions (TJ). However, the desmosome junction has received little attention due to controversy over whether it could be detected in the inner ear. *GRHL1* is a conserved transcriptional regulator, and it is key to vertebrate desmosome formation. *GRHL2* has been confirmed as a deafness gene at the DFNA28 locus. These two homologous proteins have similar sequences and functions. Here, a *grhl1* down-regulated zebrafish model exhibited inner ear developmental malformations, including missing otoliths, disordered and abnormal numbers of hair cells in the inner ear and lateral line, and sound insensitivity. The mutant zebrafish swam in circles. Hair cell apoptosis was evident. Under electron microscopy, desmosomes in the otic sensory epithelium were found to be damaged. These defects were partially rescued by treatment with either *GRHL1* or its target gene, *DSG1*. Collectively, these data are the first to indicate that *grhl1* is important to the developing inner ear epithelia in zebrafish and that it acts via desmosome junction regulation.

KEY WORDS: *GRHL1*, zebrafish, desmosom, hair cell, *DSG1*

Introduction

Federal surveys estimate that up to 36 million Americans have hearing loss, and these numbers are expected to increase worldwide over time. Approximately 50% of hearing impairments are attributable to genetic causes (Ganapathy *et al.*, 2014), and 80% of hereditary hearing loss is non-syndromic (lacking other clinical symptoms). Up to Jan 2015, approximately 87 NSHL deafness genes have been identified (<http://hereditaryhearingloss.org/main>) and previously unknown genes that contribute to deafness are under investigation. As more genes are identified and confirmed to be associated with hearing loss, gene distribution patterns suggest that they cluster in one family (Table 1). This paper concerns the function of genes in the same families as known deafness genes. *GRHL1* was chosen as the target gene and its role in the inner ear

of zebrafish was studied in depth. The grainy head (GRH) family of transcription factors is one of the most conserved genes found in vertebrates. It is critical to various types of system development (Cenci and Gould, 2005, Gao *et al.*, 2013, Han *et al.*, 2011, Janicke *et al.*, 2010, Sanchez-Calderon *et al.*, 2007). For example,

Abbreviations used in this paper: DAPI, 4',6-diamidino-2-phenylindole; DEPC, diethyl pyrocarbonate; DFNA, autosomal dominant non-syndromic sensorineural hearing loss; dpf/hpf, days/hours post-fertilization; DSG1, desmoglein 1, *Homo sapiens*; GJ, gap junctions; *grhl1*, grainyhead-like 1 (*Drosophila*); HC, hair cell; Mcon, mismatch morpholino oligonucleotides; MO, morpholino oligonucleotide; PBST, phosphate buffer; PTU, Propylthiouracil; SC, supporting cell; SE, sensory epithelium; TEM, transmission electron microscopy; TJ, tight junction; TUNEL, terminal deoxynucleotidyl transferase (TdT)-mediated dUTP nick end labeling; WISH, whole mount *in situ* hybridization.

***Address correspondence to:** Duan Ma. Key Laboratory of Metabolism and Molecular Medicine, Ministry of Education, Department of Biochemistry and Molecular Biology, School of Basic Medical Sciences, Institutes of Biomedical Science, Shanghai Medical College, Fudan University, Shanghai 200032, China. Tel/Fax: +86-21-5423-7441. E-mail: duanma@fudan.edu.cn or Zhaoxin Ma. Department of Otorhinolaryngology, Shanghai East Hospital, Tongji University, Shanghai, 200120, China. Tel/Fax: +86-21-5882.2171. E-mail: mzhx114@163.com

[#]These authors contributed equally to this work.

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TABLE 1

MANY GENES RELATED TO DEAFNESS ARE FROM THE SAME FAMILY

GJB2	GJB3	GJB6		
MYO1A	MYO6	MYO7A	MYO15A	MYO3A
SLC17A8	SLC26A4	SLC26A5		
DIAPH1	DIAPH3			
MYH9	MYH14			
POU3F4	POU4F3			
COL4A6	COL11A2			
.....				

the GRH family is important to epithelial barrier development and post-wounding barrier repair via regulation of junction protein expression and to epithelial adhesion, which is essential to organ development (Hama) (Forge *et al.*, 2013, Zhu *et al.*, 2013). Within this family, *GRHL2* has been confirmed to be related to DFNA28. Two genes in the same family, *GRHL1* and *GRHL3*, have yet to be characterized (Vona *et al.*, 2013). *GRHL1* was studied here because it is evolutionarily more similar to *GRHL2* than to *GRHL3* (Fig. 1).

Zebrafish have an integrated inner ear consisting of HCs, supporting cells, and cilia and principles of inner ear development in the zebrafish seem to be the same as in other vertebrates desmosomal (Bok *et al.*, 2007, Haddon and Lewis, 1996, Mogass *et al.*, 2000, Waterman and Bell, 1984). During embryogenesis, special neuromasts within HCs form along the embryo head and lateral line. Zebrafish share 84.87% gene homology with humans, making them excellent models for genetic and molecular analyses (Wu *et al.*, 2010). Here, zebrafish were used to verify the influence of *grhl1* in hearing and to identify the mechanism underlying this process.

Morpholino-modified antisense oligonucleotides were used in this study to down-regulate *grhl1* in zebrafish. Zebrafish lacking *grhl1* exhibited abnormal phenotypes consisting of small and eliminated otoliths, disordered and abnormal numbers of HCs in the inner ear and lateral line, and insensitivity to sound stimulation. Injection of morpholino oligonucleotides (MO) can also cause apoptosis of HCs. At the subcellular level, desmosomes in the sensory epithelium were

seriously damaged. These abnormal defects could be rescued by coinjecting the mRNA of either *GRHL1* or its target gene *DSG1*.

Results

Multi members associated with hearing loss in one protein family

To discover the candidate deafness genes, stocks of known genes in genome were scanned for regularity. As shown (Table 1), some genes were found to cluster in one family.

Grhl1 is expressed in the inner ear and is important for auditory development in zebrafish

During auditory development, the embryonic zebrafish inner ear appears as a solid otic placode near the hindbrain by 13.5 hpf (Colantonio *et al.*, 2009). RT-PCR (0–96 hpf) and WISH were used to investigate the timing of *grhl1* mRNA emergence. The *grhl1* gene was expressed at the 6th hour onward (Fig. 1B). WISH was performed in 12 and 24 h samples (Fig. 1D). Results showed that *grhl1* expressed in inner ear and is important for auditory development in zebrafish. This pattern of *grhl1* expression suggests that the gene may place a role in inner ear development.

MO was designed with Gene Tools as described previously to block the splice site between the 3rd exon and the 3rd intron (Janicke *et al.*, 2010). This produced mature mRNA with a terminator codon (Sup. Fig. 1). RT-PCR was performed to evaluate MO knock-down efficiency and specific cDNA products were amplified. MO zebrafish had 400 bp products and morphants had no product. These assays confirm that *grhl1*-MO is highly efficient (Fig. 1C, Sup. Fig. 2).

Phenotypes of otoliths, hair cells, and neuromasts in the antisense morpholino oligonucleotide (MO) group

To determine whether *grhl1* is essential to otic development in zebrafish, the MO zebrafish phenotype was examined and compared to that of wild-type embryos. The overall morphology of wild-type embryos, mismatch control MO (Mcon MO), and *grhl1* MO at 60 hpf were used to exclude nonspecific phenotypes. Zebrafish in the MO group had abnormal otoliths with respect to size, number, and location, and a malformed semicircular canal was observed

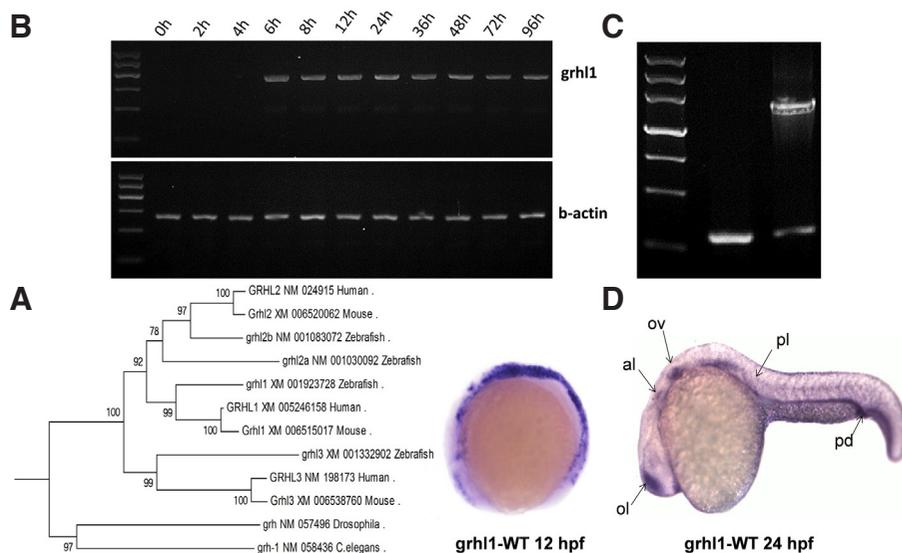


Fig. 1. *grhl1* mRNA expression in embryonic zebrafish. **(A)** Phylogenetic analysis indicates that *GRHL1* is evolutionarily nearer to *GRHL2* than to *GRHL3*. **(B)** *Grhl1* expression persists from 6 hpf onward in zebrafish. **(C)** Reverse-transcription PCR indicates considerable knockdown efficiency in the MO group. Primers were designed to work in intron 3 and exon 3. **(D)** WISH indicates a ubiquity of *grhl1* in embryos at 12 and 24 hpf. The signal was detected in the ear region, al, anterior lateral line primordium; ll, lateral line neuromast; ol, olfactory placode; ov, otic vesicle; pd, pronephric duct; pf, pectoral fin; pl, posterior lateral line primordium.

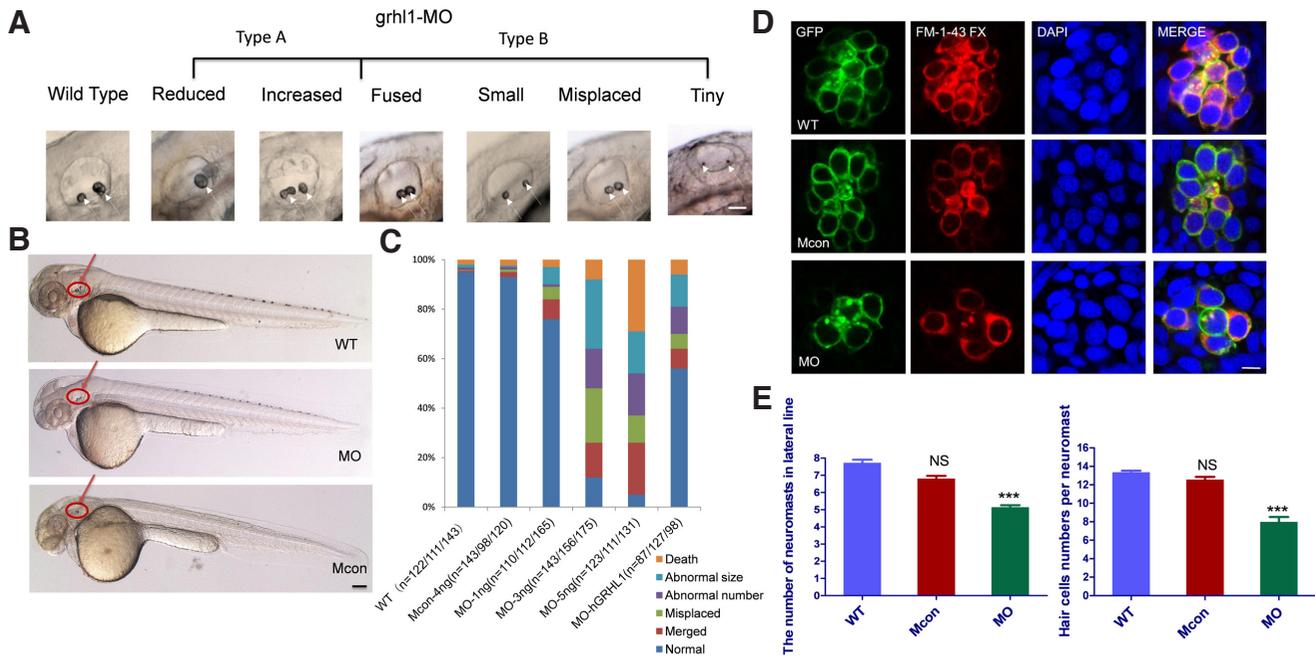


Fig. 2. Knockdown of *grhl1* induces otolith and neuromast defects in larval zebrafish. (A) Different types of malformed otoliths in the MO group. (B) No significant exterior differences among wide-type embryo and zebrafish injected with MO or mismatch control MO. (C) Statistical results of different types of malformed otoliths over all MO concentrations (3 ng was the optimal concentration). (D-F) Lack of *grhl1* led to decreased HCs/neuromasts. Bar: 200 μ m in (A,B); 10 μ m in (D).

to stain and image cilia.

Zebrafish have a lateral line system composed of neuromasts within HCs and supporting cells. Neuromasts, originating from a primordium near the head, are neatly arranged from L1 to L8 (Sup. Fig. 5). However, the primordium is homologous to the neuromasts

of the inner ear. A transgenic zebrafish model in which the *pou4f3* promoter drives GFP expression specifically in HCs was used to quantify neuromasts in the lateral line and HCs in a single neuromast (Sup. Fig. 5) (He *et al.*, 2013).

As shown, *grhl1* MO decreased the number of neuromasts in

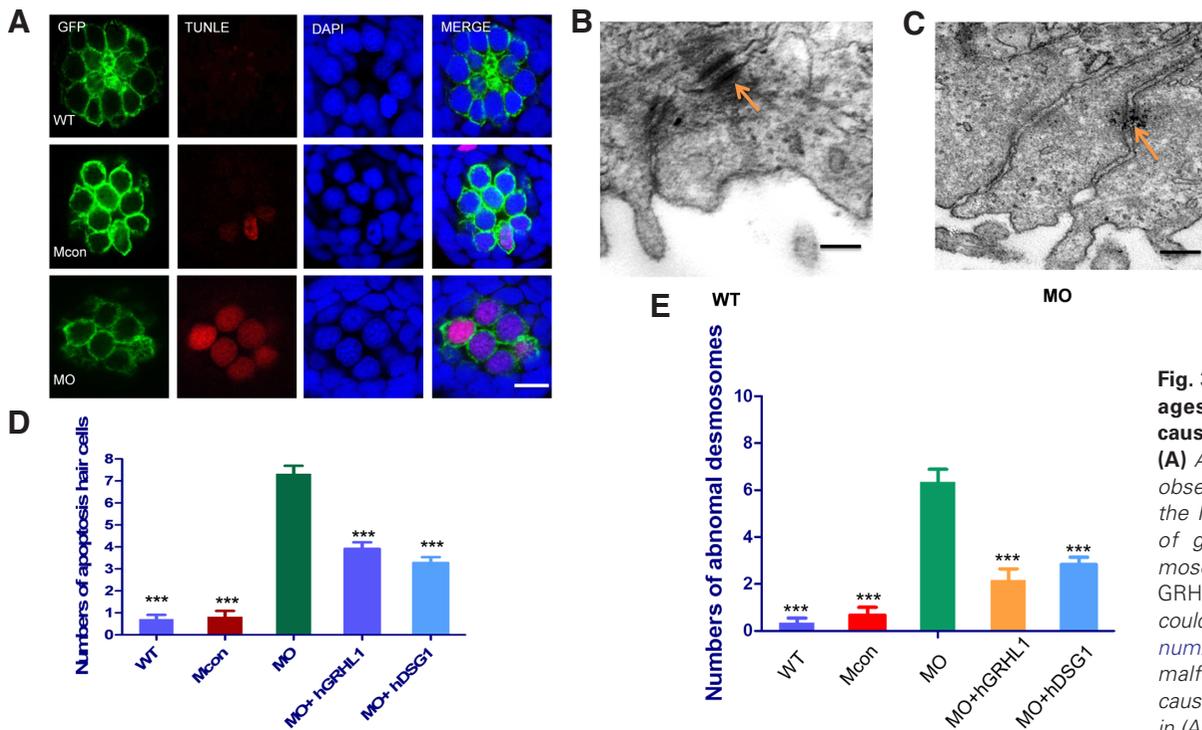


Fig. 3. Lack of *grhl1* damages desmosomes and causes hair cell apoptosis (A) Apoptotic signals were observed in hair cells in the MO group. (B,C) Lack of *grhl1* damages desmosomes (arrows). (D,E) GRHL1 and DSG1 mRNA could rescue the decreased number of hair cells and malformed desmosomes caused by MO. Bar: 15 μ m in (A); 1 μ m in (C,D).

the lateral line and disturbed their order (Fig. 2E). The neuromasts were also brighter in the WT group (Sup. Fig. 4). Changes in the numbers of HCs numbers in a single neuromasts were studied using confocal microscopy (Fig. 2 D,F).

Lack of *grhl1* damages desmosomes and causes hair cell apoptosis

We observed red signal (TMR-RED) in most living HCs (Fig. 3A). Prior to TUNEL assays, TEM was used to visualize desmosomes in the auditory sensory epithelium (Sup. Fig. 6). Desmosomes were observed in the inner ear neuromasts and saw few integrated desmosomes in the MO group (Fig. 3C, D).

Down-regulation of *grhl1* was found to cause otic developmental defects in zebrafish. *GRHL1* mRNA was injected with MO to correct these defects. *GRHL1* did rescue the MO phenotype, restoring sound sensitivity (Fig. 3D) and decreased HCs/neuromasts (Fig. 3F). These data confirm the phenotype specificity.

Otic defects could be rescued by *DSG1* mRNA

Desmoglein-1 has been shown to be the downstream mediator of *GRHL1* in previous studies. For this reason, the issue of whether phenotypes in the MO group actually originate from decreased regulation of *grhl1* with respect to desmosome formation was addressed here. The rescue efficiency of *DSG1* in *grhl1* mutant embryos was tested using a rescue assay with human *DSG1* mRNA. Data show that *grhl1* affects desmosomes by regulating *dsg1* in zebrafish (Fig. 4 A–D).

Discussion

This study suggests that down-regulation of *grhl1* affects their hearing. Then different categories of otolith phenotype were established for easy observation. The zebrafish in the MO group showed fewer HCs and neuromasts in the inner ear and lateral line than control zebrafish (Figs. 3 and 4). As expected, TEM revealed that desmosomes, as in the *Grhl1*-deficient mouse model, were

damaged in knock-out zebrafish (Wilanowski et al., 2008).

GRHL1 can affect construction of desmosomes by regulating *DSG1*, so a rescue experiment was performed. Results showed that both the abnormal desmosomes and the apoptotic hair cells could be significantly rescued by either *GRHL1* or its target gene *DSG1*, suggesting that *grhl1* regulates inner ear development by promoting the otic expression of “desmoglein-1” in zebrafish.

Inner ear defects were observed in mutant embryos and the underlying mechanisms were explored. Morphogenesis of the zebrafish inner ear has been described in detail in previous works (Haddon and Lewis, 1996, Kimmel et al., 1995). Precursor dispersal particles in the otic vesicle are attracted to vortices caused by cilia motility. These cilia and particles together facilitate otolith formation (Colantonio et al., 2009, Wu et al., 2011). The formation of otolith requires robust cilia; cilia morphology depends on HCs. In this way, loss of HC function could account for observed abnormalities in otoliths (Fig. 3).

Auditory sensory epithelia are mosaic of HCs and supporting cells wherein mechanical sound vibrations are converted to chemical signals (Hawkins et al., 2007). The procedure is highly reliant on the integrity of the circumferential band of cell junctions in epithelia (Deans, 2013, Groves and Fekete, 2012). Considerable integrity is necessary to allow the structure to withstand mechanical stress and maintenance of homeostasis in the inner ear. Physiologically, the barrier is strong enough to maintain ion exchange equilibrium in the otic lumen and the endolymph, but once the barrier is compromised, auditory signal transduction is paralyzed (Han et al., 2011). A typical barrier complex includes tight junctions, adherens junctions, and desmosomes. Previous studies have suggested that different types of intercellular junctions are important to normal ear function (Forge et al., 2013, Hardison et al., 2005, Zhu et al., 2013). Desmosome function in the organ of Corti is a largely unexplored area. As reported, desmosomes develop at the same time as HCs. They then disappear from HC junctional complexes but remain in the intercellular junctional complexes of other types of cells in the membranous labyrinth (Raphael and Altschuler, 1991, Raphael

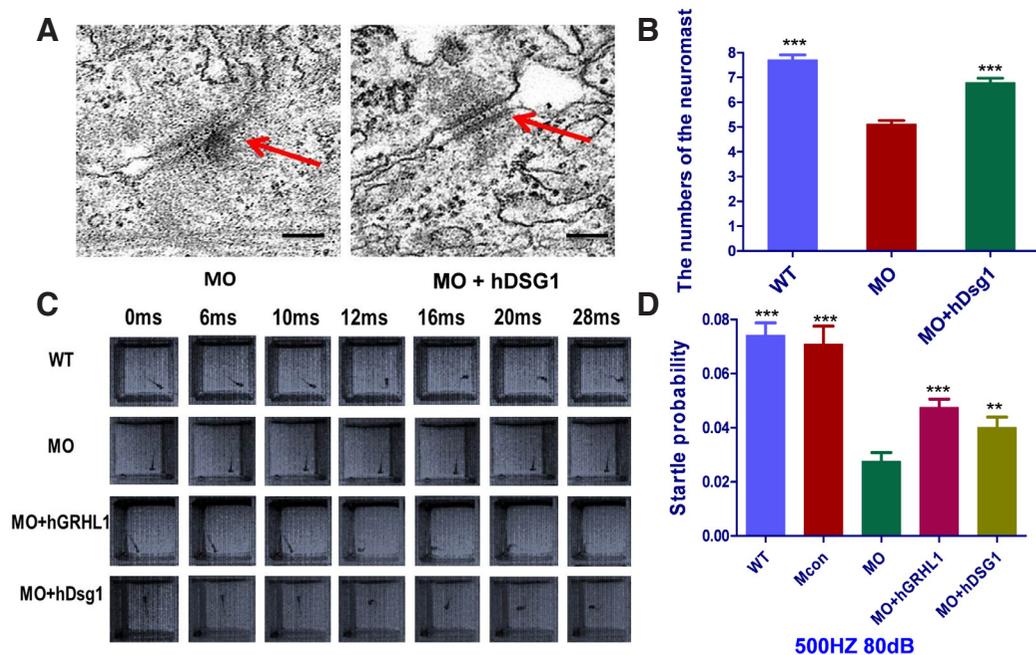


Fig. 4. Hearing disability in *grhl1* knockdown zebrafish which could be rescued by *DSG1* mRNA. (A) Poorly organized desmosomes (arrows) in the MO group could be rescued by *DSG1* mRNA. **(B)** *Dsg1* rescued decreasing numbers of neuromasts in the lateral line. **(C)** Examples of C-shaped startle responses of different larval groups in response to a 500 Hz sound of 10 ms duration. Typical escape response of wild-type larva initiated 10 ms after stimulation. **(D)** Average C-startle response probability after sound stimulation. At least 40 larvae were tested for each group. Bar, 1 μ m.

et al., 1988). Gulley and Reese reported that desmosomes are prominent in junctions between support cells (Gulley and Reese, 1976). Some researchers believe that the specific desmosome distribution pattern is not merely the result of differentiation but may rather regulate tissue morphogenesis and function (Kimura *et al.*, 2012, Wilanowski *et al.*, 2008). Similarly, the current study showed abnormal desmosomes to be correlated with defects in the auditory system.

Desmosome deficiency in sensory epithelium, which was caused by the absence of *grhl1*, led to lesions in the cell junction barrier. Decreased junction barrier integrity compromised membrane permeability, which is important to homeostasis and signal transduction in HCs (Han *et al.*, 2011). Specifically, the barrier maintained membrane tension to permit transmission of mechanical vibration to HCs in the sensory epithelium (Kakehata and Santos-Sacchi, 1995). This renders the MO embryo sound-insensitive (Fig. 4C).

However, the relationship between desmosome defects and HC apoptosis remains poorly understood. As shown in Fig. 3A, apoptotic signals appeared to be restricted to the HCs in the MO group. One possible explanation for this is that HCs may depend on supporting cells for survival within the organ of Corti. HCs may be unable to survive without a supply of nutrients and morphologic-maintenance cells. However, the manner in which SCs are supported requires additional research. Desmosomes may participate in HC development. For this reason, some deficient HCs may be less tolerant to apoptotic-inducing factors.

In this way, the function of *grhl1* was confirmed in the context of hindering normal development of sensory epithelia in zebrafish via desmosome construction. These data offer a foundation for the study and identification of novel deafness genes.

Materials and Methods

Phylogenetic tree mapping

To identify a candidate gene from 2 members of the *GRHL* family, a phylogenetic tree was mapped to determine which genes were closer to *GRHL2*. Clustal X1.83 was used to compare human wild-type *GRHL1* mRNA sequence with the orthologs from mouse, *Drosophila*, Danio, *Caenorhabditis*, and *Xenopus* (sequences obtained from <http://www.ensembl.org/>).

Zebrafish lines

Wild-type (AB strain) zebrafish were obtained from the International Zebrafish Research Center (University of Oregon, Eugene, OR, U.S.). Embryos were obtained from natural spawning of wild-type adults. Transgenic pou3f4-GFP zebrafish embryos were provided by Dr. Huawei Li. Zebrafish were kept at 28.5°C and 0.003% 1-phenyl-2-thiourea (PTU, Sigma-Aldrich, St. Louis, MO, U.S.) MO was used to suppress pigmentation (Karlsson *et al.*, 2001). Developmental stages were measured by hours after fertilization (hpf) and days after fertilization (dpf). All zebrafish experimental protocols were approved by the Institutional Animal Care and Use Committee of Fudan University.

Morpholino antisense oligonucleotides (MO) and mRNA microinjection

One *grhl1* MO was designed as described in a previous work (Janicke *et al.*, 2010). MO blocked the splice site between the 3rd exon and the 3rd intron, which led to an excrescent 3rd intron with a terminator codon remaining in the mature mRNA. All related MO sequences were obtained from Gene Tools (http://www.gene-tools.com/Oligo_Design) and MO injections were injected into one cell-stage embryos as follows:

```
grhl1 ln3 MO 5'-CTTTGATGAGAGCTTACCTTTTGT-3' 3 ng
Mcon MO 5'- CCTCTTACCTCAGTTACAATTTATA-3' 3 ng
p53-MO 5'- GCGCCATTGCTTTGCAAGAATTG -3' 3 ng
```

Both *GRHL1* and *DSG1* cDNA, obtained from the HeLa cell cDNA library using RT-PCR and amplified with a forward primer that was designed with a consideration for incorporating a T7 forward promoter sequence (5'-GATCAC TAATCGACTCACTATAGGG-3'). The PCR product served as a template after sequence confirmation. Then, capped and polyadenylated RNA of *GRHL1* and *DSG1* were synthesized *in vitro* by transcription with T7 RNA polymerase using the mMessage mMachine T7 Ultra Kit (Ambion, Austin, TX, U.S.) (final concentration of co-injection mixture = 180 ng/μl). All morpholinos and mRNA depicted were diluted to the indicated concentrations with RNase-free water (TaKaRa, Tokyo, Japan).

Reverse-transcription PCR

RNA was extracted from zebrafish embryos at various developmental stages using Trizol (Ambion). First-strand cDNA was then prepared using a SuperScript III First-Strand Synthesis System (Invitrogen, U.S.) with 1 μg RNA as template. cDNA was diluted (1:50) for each PCR reaction. To detect *grhl1* expression in zebrafish, semi-quantitative PCR was performed in triplicate with the primers below:

```
z-beta-actin-F, 5'-ATGCCCTCGTGCTGTTTTC-3';
z-beta-actin-R, 5'-GCCTCATCTCCCACATAGGA-3';
z-grhl1-F, 5'- TCAATGCAGCTAGGGGACAA -3';
z-grhl1-R, 5'-GTTCCGGGACAGTGACAGAGA-3'.
```

To evaluate MO knock down efficiency, one pair of primers was used:

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kd-F, in exon 3, 5'-CTGGAAGTCGTCTCTGGAGA-3';
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kd-R, in intron 3, 5'-AGCCTTTAAACAGCATGAAAAA-3'. The MO group had a 400 bp product, indicating intron 3 was inserted in mature mRNA.

Whole-mount in situ hybridization (WISH)

Whole-mount *in situ* hybridization of *grhl1* was performed as previously described (Janicke *et al.*, 2010). Zebrafish *grhl1* complementary DNA was subcloned into pGEM®-T vector by PCR amplification as follows: forward: 5'-CCC GTTCTCGTACAGGCAATTATAACG-3' and reverse 5'-GCTTCAGTTGGTCATCTCTGGATTTC-3'. After sequence confirmation, pGEM-*grhl1*-T plasmid was linearized using Sall and antisense digoxigenin-UTP-labeled full-length riboprobe was transcribed using T7 RNA polymerase (Promega, Madison, WI, U.S.). Then, *grhl1* mRNA expression was detected 6 h after fertilization by RT-PCR. Embryos (N=30) were collected at 12 and 24 h, washed three times with PBST in DEPC, and fixed in 1 ml 4% paraformaldehyde for 5 min at room temperature. Embryos were then fixed in 1 ml of paraformaldehyde for 12–16 h at 4°C prior to WISH, which was carried out as described previously (Chen and Fishman, 1996, Tassin *et al.*, 1994). Anti-digoxigenin antibody (Roche, Basel, Switzerland) was used to detect *grhl1* mRNA signals.

Staining of FM-1-43FX and phalloidin

For 96 hpf embryos, neuromast HCs were labeled by immersing larvae in a solution of FM1-43FX (Invitrogen) for 1–2 min at room temperature. They were washed in PBS. Zebrafish were immobilized in 1% low-melting-point agarose gel and labeled HCs were viewed under a fluorescent microscope.

Before phalloidin staining, 96 hpf embryos were fixed in 4% PFA overnight at 4°C. Larvae were permeated with 2% Triton X-100 (Sigma-Aldrich) in PBS and then washed twice with PBS. Then the embryos were immersed 2.5 mg/ml fluorescein isothiocyanate (FITC)-labeled phalloidin (Sigma-Aldrich) in PBS for 1 h in the dark at room temperature. After incubation, samples were washed with PBST for 2 h and cilia were marked with green fluorescence (Leger and Brand, 2002).

Apoptosis detection by TUNEL and acridine orange staining

A TUNEL assay was performed with a TMR-RED *in situ* cell death detection kit (Roche). Embryos (5 dpf) with HCs marked with GFP were washed

in PBS and fixed in 4% paraformaldehyde overnight at 4°C, immersed in methanol for 1 h at room temperature and then washed twice with PBST. Samples were incubated in acetone at -20°C for 20 min, permeabilized with 0.1% sodium citrate and 0.1% TritonX-100 for 15 min at room temperature and embryos were incubated with the reaction mixture (5 µl enzyme solution + 45 µl labelling solution) for 1 h in the dark at 37°C after washing twice with PBST. Then the reaction was stopped with three washes in PBST. A fluorescent signal was imaged and digitized using a confocal microscope (TCS SP8, Leica, Wetzlar, Germany).

Acridine orange staining was performed at 24 hpf to exclude MO off-target effects. Membranes were stripped from embryos and fish were immersed in 2 mg/l acridine orange. The embryos were washed five times in PBS, and photos were taken.

Startle response tests

The inner ear is important to zebrafish hearing and balance. Developmental defects have been observed in inner ears of *grhl1* MO knockdown zebrafish. Here, swimming behavior and hearing were assessed in MO knockdown zebrafish. For hearing tests, zebrafish were randomly placed in blocks and exposed to a 10 ms audio stimulus at 500 Hz. The C-startle response (named for the embryonic shapes mediated by M-cells in response to sound) was measured using near-field pure tone stimulation at two different intensities. The C-startle response was measured in 96-well plastic plates, and recorded with a high-speed camera. Larvae were considered positive for the C-startle response if this response occurred within 20 ms of the application of stimuli. At least 25 larvae were tested in each group. The probability of the C-startle response for a group of larvae was the average percentage of all C-startle effects (Han et al., 2011).

Transmission electron microscopy (TEM)

A group of 120 hpf embryo types were fixed with 2.5% glutaraldehyde and 1% OsO₄ followed by dehydration with a graded ethanol and acetone solution. Then the embryos were infiltrated with epoxy resin for more than 24 h. The otic sensory epithelium was examined under TEM. The figure in (Sup. Fig. 6) shows a systematic sketch for identifying the sensory epithelium. The anatomy of zebrafish in detail could be found from <http://www.zebrafish.uni-freiburg.de/anatomy/120hrs/120hrs.html>.

Statistical analysis

Data are shown as means ± SEM. All data were processed by SPSS, mono factor analysis of variance was used for analysis. Differences were considered statically significant at $P < 0.01$.

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Author contributions

Conceived and designed the experiments: Duan Ma, Jin Zhang, Huijun Wang, and Xu Wang. Performed the experiments: Fan Yang, Fei Liu, Danping Wen, Jiongjiong Hu, and Nan Jiang. Analyzed the data: Wenjun Xia, Xiaofang Shen, and Jie Zong. Contributed reagents, materials, or analytical tools: Zhaoxin Ma, Xu Wang. Composed the manuscript: Fan Yang and Fei Liu.

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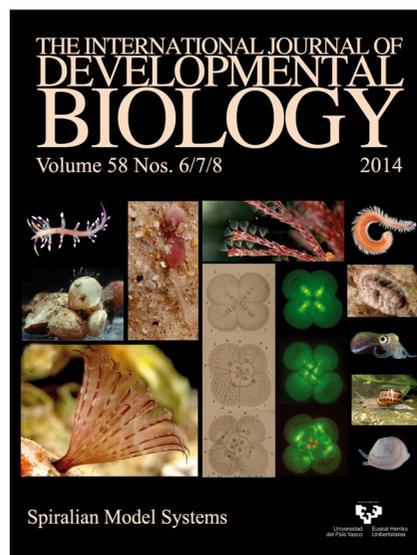
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