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ORIGINAL ARTICLE

Mutation of IFNLR1, an interferon lambda receptor 1, is associated with autosomal-dominant nonsyndromic hearing loss

Xue Gao,¹,² Yong-Yi Yuan,¹ Qiong-Fen Lin,³,⁴ Jin-Cao Xu,² Wei-Qian Wang,² Yue-Hua Qiao,⁵ Dong-Yang Kang,¹ Dan Bai,⁶ Feng Xin,⁷ Sha-Sha Huang,¹ Shi-Wei Qiu,¹,⁵ Li-Ping Guan,³,⁴ Yu Su,¹ Guo-Jian Wang,¹ Ming-Yu Han,¹ Yi Jiang,¹,⁸ Han-Kui Liu,³,⁴ Pu Dai¹

ABSTRACT

Background Hereditary sensorineural hearing loss is a genetically heterogeneous disorder.

Objectives This study was designed to explore the genetic etiology of deafness in a large Chinese family with autosomal dominant, nonsyndromic, progressive sensorineural hearing loss (ADNSHL).

Methods Whole exome sequencing and linkage analysis were performed to identify pathogenic mutations. Inner ear expression of Ifnrl1 was investigated by immunostaining in mice. Ifnlr1 Morpholino knockdown Zebrafish were constructed to explore the deafness mechanism.

Results We identified a cosegregating heterozygous missense mutation, c.296G>A (p.Arg99His) in the gene encoding interferon lambda receptor 1 (IFNLR1) – a protein that functions in the Jak/STAT pathway - which is associated with ADNSHL. Morpholino knockdown of ifnrl1 leads to a significant decrease in hair cells and non-inflation of the swim bladder in late-stage zebrafish, which can be reversed by injection with normal Zebrafish ifnlr1 mRNA. Knockdown of ifnrl1 in zebrafish causes significant upregulation of cytokine receptor family member b4 (interleukin-10r2), jak1, tyrosine kinase 2, stat3, and stat5b in the Jak1/STAT3 pathway at the mRNA level.

Conclusion IFNLR1 function is required in the auditory system and that IFNLR1 mutations are associated with ADNSHL. To the best of our knowledge, this is the first study implicating an interferon lambda receptor in auditory function.

INTRODUCTION

Hereditary hearing loss is characterised by a high degree of genetic heterogeneity with mutations in several hundreds of genes encoding a variety of proteins. Individuals with autosomal-dominant non-syndromic hearing loss (ADNSHL), comprising ~20% of those with inherited hearing loss, typically display postlingual progressive hearing impairment that initially involves hearing loss of high frequencies. To date, ~59 ADNSHL genetic loci have been mapped, and ~36 causative genes have been identified (http://hereditaryhearingloss.org). Based on the type of gene product, these genes can be categorised into several groups of encoded proteins such as those involved in the structure and function of hair cells, the auditory nerve and virtually every structural element of the inner ear. The pace of gene discovery has accelerated with the increased availability of high throughput sequencing techniques.

Interferon (IFN) lambda receptor 1 (IFNLR1, MIM 607404) belongs to the class II cytokine receptor family, which is responsible for recognition of cytokines and IFNs in the extracellular environment and initiation of intracellular signalling cascades that lead to an array of responses such as haematopoiesis, regulation of the immune system and cellular growth and development. The functions of IFNLR1 include antiviral activity, antiproliferative effect, anti-tumor activity and the regulation of major histocompatibility complex class I/II molecule expression and immune responses. Three research groups identified IFNLR1, so it has three alternative names: CRF2-12, IL28R and LICE1. However, the function of IFNLR1 in the auditory system has not been described.

Here, we used a combination of genetic linkage analysis and whole-exome sequencing to identify a mutation in IFNLR1 as the cause of an autosomal-dominant hearing impairment. We further evaluated the expression of this gene in mice and verified that its disruption in zebrafish leads to auditory organ impairment and developmental defects.

METHODS

Ethics statement

We obtained fully informed written consent from adult subjects and parents of minor subjects for participation in this study and publication of their clinical data.

Family ascertainment and clinical evaluation

Participating subjects were evaluated by medical history interviews, and a physical examination was performed on index patient from family JS4842. The degree of hearing loss was assessed using pure-tone audiometry, auditory brainstem response (ABR) and distortion product otoacoustic emission (DPOAE). CT scans of temporal bones were performed. Vestibular functions were evaluated using the tandem gait, Romberg test and caloric
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The index patient was further subjected to an ophthalmological examination with funduscopy and other tests including serum chemistry analysis, blood count, urinalysis and an ECG. Genomic DNA was extracted from peripheral blood using a blood DNA extraction kit according to the manufacturer’s instructions (TianGen, Beijing, China).

Whole-exome sequencing

Whole-exome capture and sequencing was performed (II:1, II:4, III:4, III:5, III:6, III:7, figure 1A). DNA was sheared, ligated to adaptors, extracted, amplified by ligation-mediated PCR and then hybridised to the Nimblegen SeqCap EZ Exome Kit V.3.0 (Roche, Basel, Switzerland) for enrichment. Each captured library was loaded onto the Illumina Hiseq2000 platform. After filtering out low-quality and duplicate reads, clean data were aligned to the human reference genome hg19 using the Burrows-Wheeler Aligner. After alignment, variants were called using four types of software (SOAPspn, GATK, Samtools and Platypus), merged into variant call format files and annotated using a variant effect predictor, including those with minor allele frequencies (MAF), in public databases and the Beijing Genomics Institute (BGI) in-house databases. We used ExomeDepth software to detect the CNVs of this pedigree. Under the assumption of autosomal-dominant pattern of inheritance, only variants that were heterozygous in the four affected siblings and absent in the two unaffected individuals were selected as candidates and verified using PCR-Sanger sequencing.

Linkage analysis and haplotype analysis

We performed a genome-wide linkage analysis of 15 family members (marked with asterisks in figure 1A) using the Human Omni ZhongHua-8 Bead chips (Illumina, San Diego, California, USA) containing 900015 SNP markers. A total of 10 566 Tag SNPs distributed every 0.3 cM of genomic DNA were chosen to calculate the logarithm (based 10) of odds (LOD) scores using the Merlin (V.1.1.2) parametric linkage analysis package. The complete penetrance autosomal-dominant model was used with a rare disease frequency of 0.0001. Critical recombination thresholds reveal the presence of moderate to severe sensorineural hearing loss, which occurred at a late onset in all affected individuals. For clarity, thresholds are shown for one ear from each individual. No differences in hearing were detected when the two ears were compared in an affected individual. Younger individuals had less severe hearing loss compared with the older affected individuals, suggesting that hearing loss in this family is progressive in nature. ADNSHL, autosomal-dominant, non-syndromic, progressive sensorineural hearing loss; IFNLR1, interferon lambda receptor 1; SNV, single nucleotide variant.

Figure 1

Identification of a mutation in IFNLR1 causing ADNSHL. (A) The pedigree of a three-generational family with segregating progressive ADNSHL. DNA samples were obtained from six unaffected and nine affected individuals (denoted by asterisks). Individuals who underwent whole-exome sequencing and linkage analysis are marked with W. Black symbols represent affected individuals. The haplotype created with SNP markers shows complete cosegregation of a locus at 1p34.1–1p36.12 (red) in family JS4842. (B) Distribution of variants in the chromosome. Blue represents the distribution of somatic SNVs, orange indicates the distribution of somatic Indel mutations and grey represents the distribution of somatic CNVs. (C) Schematic diagram of IFNLR1 and protein alignment showing IFNLR1 Arg99His occurred at evolutionarily conserved amino acids (in red box) within the tissue_fac domain across nine species. (D) Electropherograms showing that the IFNLR1 c.296G>A mutation cosegregated with hearing loss. (E) Audiograms from selected individuals of family JS4842. Thesholds reveal the presence of moderate to severe sensorineural hearing loss, which occurred at a late onset in all affected individuals. For clarity, thresholds are shown for one ear from each individual. No differences in hearing were detected when the two ears were compared in an affected individual. Younger individuals had less severe hearing loss compared with the older affected individuals, suggesting that hearing loss in this family is progressive in nature. ADNSHL, autosomal-dominant, non-syndromic, progressive sensorineural hearing loss; IFNLR1, interferon lambda receptor 1; SNV, single nucleotide variant.
events of the pedigree were also determined through haplotype construction using the Merlin (V.1.1.2) software.

**Mutation analysis**

Direct sequencing was used for mutation screening. Primers were designed to amplify all IFNL1 exons and −100 bp of adjacent intronic sequence flanking the exons (primer sequences available on request). A total of 500 negative control samples with normal hearing and 97 individuals from ADNSHL cohorts with sloping audiograms were sequenced for mutations in IFNL1.

**Model building and multiple sequence alignment**

Three-dimensional modelling of p.Arg99His was performed using SWISS-MODEL, an automated homology modelling program (http://swissmodel.expasy.org/workspace). Data obtained by the homology models were visualised using Swiss-PdbViewer 4.1. Multiple sequence alignment was performed according to a Homologene program.

**Immunostaining**

Slides spanning the entire inner ear from three different mice were stained, and the observed expression patterns were considered reliable if present in all three samples. For cryosections, the ears of C57 mice were fixed with 4% paraformaldehyde, decalcified, dehydrated with a graded series of ethanol; serial sections were cut at 8 µm thickness. An anti-Ifnlr1 antibody was diluted (1:200 rabbit polyclonal antibody; Bioss, Beijing, China), and Phalloidin-iFluor 555 (1:400, Abcam, Cambridge, UK) was diluted (1:200 rabbit polyclonal antibody; Bioss, Beijing, China), and the primary antibody was omitted as a control. Sections were examined using confocal microscopy. For immunostaining of whole-mount organ of Corti, mouse cochlea ducts were dissected, fixed and incubated with anti-Ifnlr1 (1:200) and DAPI and analysed using a confocal microscope (Zeiss).

**Zebrafish husbandry and ifnlr1 Morpholino (MO) knockdown**

AB line zebrafish were used and maintained at the PLA general hospital Zebrafish Breeding Centre. Tg (Brn3:GFP) 5'35S'T transgenic zebrafish expressing GFP in hair cells under control of the POU4F3 promoter that is targeted to the plasma membrane by a GFP-43 membrane targeting sequence (provided by Professor Hua-Wei Li, Fudan University) were used. Antisense MO (Gene Tools, Philomath, Oregon, USA) was microinjected into fertilised one-cell-stage embryos according to standard protocols. The sequence of the exon 4-intron 4 splice region of ifnlr1 MO (ifnlr1-e4i4-MO) was 5'-AGAGATGATACTAAGCCTGCGGCCTGC-3' and the sequence for the standard control MO was 5'-CCTCTACCTCAGTATAATTTA-3' (Gene Tools). For the ifnlr1 gene knockdown experiment, 4ng of control-MO or ifnlr1-e4i4-MO (E4I4-MO) were used per injection. Total RNA was extracted from 30 to 50 embryos per group using the PrimeScript RT reagent Kit with gDNA Eraser (Takara, Otsu, Japan). RNA was reverse transcribed using the PrimeScript RT reagent Kit with gDNA Eraser (Takara, Otsu, Japan). Primers spanning ifnlr1 exon 3 (forward primer: 5'-ACAGTTCTGGGTGAAGTG-3' and exon 3 (reverse primer: 5'-AAGGAGACCTGGATGCCTCAAA-3') were used for RT-PCR analysis to confirm the efficacy of the E4I4-MO. The ef1a primer sequences used as the internal control were 5'-GGAAATTTCCAAGCCTCAACC-3' (forward) and 5'-GATACCGCTCAAACTCACC-3' (reverse).

**Immunofluorescence staining and cell proliferation assays**

Four days postfertilisation (dpf) MO and WT larvae were incubated in EM (Embryomedium) containing 15 mM bromodeoxyuridine (BrdU; Sigma-Aldrich) for 48 hours at 28.5°C. The larvae were then fixed in 4% PFA (Paraformaldehyde) for 4 hours at room temperature (RT) or overnight at 4°C and washed three times in PBST with 0.1% TritonX100 (PBST). All larvae were placed into 2 n M HCl for 1 hour at RT. Larvae were washed again in PBST and blocked in 10% normal goat serum in PBST for 1 hour at RT. The larvae were incubated in the primary antibody, including the Chicken anti-GFP (1:200, Abcam, ab13970), rabbit monoclonal anti-sox2 (1:200, Abcam, ab137385), mouse anti-BrdU IgG (1:200, Santa Cruz Biotechnology, Dallas, Texas, USA) overnight at 4°C, and the secondary antibody including Alexa Fluor 488 anti-Chicken (1:200, Life technologies, A11008), Cy3 anti-Mouse (1:200, Jackson Immunoresearch Laboratories, West Grove, PA, USA), Alexa Fluor 647 anti-Rabbit (1:200, Abcam, ab150075) was used at 4°C overnight. DAPI were used at R for 20 min. Cells were counted under a confocal microscope.

**Acridine orange staining for apoptosis**

Control MO-injected embryos and embryos injected with 4 ng ifnlr1-e4i4-MO were immersed in 5 µg/ml acridine orange hemi-(zinc chloride) (AO; Sigma-Aldrich, St. Louis, Missouri, USA) in fish water for 60 min at 3 dpf. Zebrafish were then oriented on their lateral side and mounted with methylcellulose in a depression slide for observation by fluorescence microscopy.

**In vivo macrophage migration assays in zebrafish**

To evaluate macrophage migration in zebrafish, fertilised one-cell (zlyz:EGFP) transgenic (TG) line embryos were injected with 4 ng ifnlr1-e4i4-MO or control-MO. At 6 dpf, the number of macrophages recruited to the body trunk was counted.

**DASPEI staining of lateral line hair cells**

After microinjection, larvae (6 and 7 dpf) were immersed in 1 mM 2-(4-(dimethylamino)styryl)-N-ethylpyridinium iodide (DASPEI; Sigma-Aldrich, Oakville, Ontario, Canada) in fish water for 1 hour. Larvae were then orientated on their lateral side (anterior, left; posterior, right; dorsal, top) and mounted with methylcellulose in a depression slide for observation by fluorescence microscopy.

**Quantitative real-time PCR**

Total RNA was extracted from 80 to 100 embryos per group in Trizol (Roche, Indiana, USA) according to the manufacturer’s instructions. RNA was reverse transcribed using the PrimeScript RT reagent Kit with gDNA Eraser (Takara, Otsu, Japan). Quantification of gene expression was performed in triplicate using Bio-Rad iQ SYBR Green Supermix (Bio-Rad, Hercules, California, USA) with detection on the Realplex system (Eppendorf). Relative gene expression quantification was based on the comparative threshold cycle method (2 − ΔΔCt) using e1fa as an endogenous control gene. Primer sequences are available on request.

**pcDNA3-ifnlr1 recombinant vector construction**

The ifnlr1 cDNA was reverse transcribed from mRNA from zebrafish embryos. The complete ifnlr1 cDNA was subcloned into pcDNA3 to construct the recombinant vector pcDNA3-Ifnlr1.
Image acquisition and statistical analysis
Embryos and larvae were analysed using a Nikon SMZ 1500 fluorescence microscope and subsequently photographed with a digital camera.

All data are presented as mean±SEM. Statistical analysis and graphical representation of the data were performed using GraphPad Prism 5.0 (GraphPad Software, San Diego, California, USA). Statistical significance was calculated using Student’s t-test, one-way analysis of variance (ANOVA) or $\chi^2$ test, as appropriate. Statistical significance is indicated as *P<0.05 and **P<0.0001.

RESULTS
Clinical findings
We examined a three-generation Chinese family (No. JS4842; figure 1A) with segregating autosomal-dominant, non-syndromic, bilateral, symmetric, sensorineural hearing loss that begins in the second decade of life, generally accompanied by high-frequency tinnitus. The youngest affected family member, III:6, was diagnosed at 21 years of age with hearing loss involving mid-high frequency, while his previous audiogram was normal at 19 years of age; therefore, the age at onset of hearing loss could be determined. The affected individuals reported a progressive nature of hearing loss, which was verified with audiograms. While affected family members initially had normal low-frequency hearing, their hearing loss became progressive and ultimately deteriorated at all frequencies by the fourth or fifth decade (figure 1E). There were no indications of a relationship between hearing loss and infections or noise. Result of ABR and DPOAE excludes auditory neuropathy spectrum disorders.

All affected individuals did not complain of imbalance, and no abnormalities were found in a detailed vestibular analysis. The affected individuals had no obvious delay in gross motor development and no indications of visual problems or morphological abnormalities were found in a detailed vestibular analysis. All affected individuals did not complain of imbalance, and no abnormalities were found in a detailed vestibular analysis. All affected individuals did not complain of imbalance, and no abnormalities were found in a detailed vestibular analysis.

Linkage analysis, whole-exome sequencing and in silico analysis
DNA samples were obtained from six unaffected and nine affected individuals of family JS4842. One affected individual (III:5) was prescreened and found to be negative for mutations in GJB2, SLC26A4 and mtDNA12SrRNA via direct sequencing.

Linkage and haplotype analysis mapped the pathogenic gene to a genomic region chr1:22,986,610–22,997,110 Mb (1D) and CDC20 (IHCs) and outer hair cells (OHCs), displaying partial colocalisation with phalloidin (figure 2G). Ifnlr1 was enriched in the stereocilia of both inner hair cells (IHCs) and outer hair cells (OHCs), displaying partial colocalisation with phalloidin (figure 2G). An antibody directed against the heavy chain of neurofilament (NF200), which was used to specifically stain nerve fibres and neurons, revealed colocalisation of NF200 with Ifnlr1 in the cochlear nerve fibres and spiral ganglion neurons (figure 2D,E). A magnified image of Ifnlr1 expression in the organ of Corti revealed high expression of Ifnlr1 in the cytoplasm and nucleoplasm of most cells, although their distributions in these cells were somewhat variable. In contrast to the expression of Ifnlr1 in cytoplasm and nucleoplasm of IHCs, Ifnlr1 was negative in the nucleoplasm in OHCs (figure 2C,H–J). We observed a similar colocalisation pattern of Ifnlr1 and phalloidin in the crista ampullaris of vestibular epithelium (figure 2F).

Aberrant ifnlr1 function causes late-stage developmental defects
The ifnlr1 knockdown MO exerted no significant change in the early development of zebrafish from 32-hpf to 4-dpf (online supplementary figure 2). Circulation in the intersegmental vessels (ISV) appeared normal in both the control and ifnlr1-e44-MO-injected fish (online supplementary movie 1). Knockdown of ifnlr1 did not induce organ-specific apoptosis (online supplementary figure 3) or macrophage migration (online supplementary figure 4), indicating that apoptosis and inflammation might not be the cause of reduced hair cell numbers.
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In late stages of development, ifnrl1 knockdown caused non-inflation of the swim bladder and expanded the gut lumen area. The effectiveness of ifnrl1 knockdown was confirmed by RT-PCR.

Disruption of the developmental processes in the inner ear in ifnrl1-morphant zebrafish

Compared with normal controls, morphants had a reduced number of neuromasts (figure 3I,M). Hair cells and supporting cells per neuromast were counted in 6 dpf Tg (Brn3c:mGFP) transgenic zebrafish larvae using four markers, GFP (hair cells), SOX2 (supporting cells), BrdU (proliferated cells) and DAPI (nucleus). Fewer hair cells and supporting cells per neuromast were detected in the neuromasts of lateral line of MO knockdown larvae than in the wild type (WT) (figure 3O). The average number of hair cells per neuromast in 6 dpf zebrafish was 2.3±0.3 for morphants and 0.6±0.26 for WT. The average number of supporting cells per neuromast was 13±1.36 for morphants, while 26.2±1.43 for WT. The average number of proliferated cells per neuromast was 8.4±0.97 for morphants,
null

while 22.4±0.88 for WT. To determine whether the loss of hair cells and supporting cells were related to decreased cell proliferation, we exposed the 4 dpf larvae to BrdU for 48 hours and assessed BrdU incorporation by immunolabeling to visualise the cell proliferation in WT and morphants. The number of BrdU-positive cells was much lower in morphants than in WT (figure 3O,R).

Rescue experiments indicate linkage of the ifnlr1 mutation to reduced numbers of hair cells and non-inflation of the swim bladder in zebrafish

Zebrafish ifnlr1 mRNA was co-injected with MO into one-cell-stage embryos to rescue abnormalities caused by MO in zebrafish, and the number of lateral line neuromasts and the swim bladder size were analysed. The results revealed that WT mRNA could largely rescue the ifnlr1-e4i4-MO-induced non-inflation of the swim bladder and loss of hair cells and head neuromasts at six dpf, suggesting that the IFNLR1 mutation caused hearing loss in family JS4842 (figure 4).

The ifnlr1 mutation may contribute to hearing loss through the Janus kinase (Jak)/signal transducers and activators of transcription (STAT) 3 signalling pathway

The mRNA expression of cytokine receptor family member b4 (crl7b) or interleukin (IL)10 receptor 2, il10r2, jak1, tyrosine kinase 2 (tyk2), stat1a, stat2, stat3, stat4, stat5 and ifn9, related to the Jak/STAT signalling pathway, was tested by quantitative real-time PCR using cDNA obtained from 4dpf WT and morphants zebrafish. In ifnlr1-morphant zebrafish, Jak1/STAT3 pathway members were upregulated, including stat3, jak1, il10r2 (also called crlyb4), stat5 and tyk2 (figure 5). We postulate that upregulation of Jak1/STAT3 signalling is a characteristic event in ifnlr1-morphant zebrafish.

DISCUSSION

This study identified a mutation in IFNL1R1 as a cause of ADNSHL at the DFNA2 locus, a region in which mutations in GJB3 (MIM 603324) and KCNQ4 (MIM 603537) were discovered previously. We focused on this genomic region because a significant linkage was identified in a genome scan, and we found a missense mutation in IFNL1R1 via whole-exome sequencing. A previous study found that IFNL1R1 is expressed in a highly tissue-specific manner, with primary expression in the epithelial and liver tissues in humans. However, no studies have reported IFNL1R1 expression in the auditory system. In this study, we found broad expression of Ifnlr1 in the inner ear, including sensory and non-sensory epithelia of the organ of Corti, cochlear nerve and spiral ganglion of the cochlea and in the cristae ampullaris of vestibular organ. To exclude the non-specific reaction of polyclonal antibodies, we applied two polyclonal antibodies against mouse Ifnlr1 from different companies (Bioss and Abcam) and the results demonstrated similar Ifnlr1 localisations. In the affected individuals of family JS4842, DPOAE and ABR were absent, excluding the possibility of auditory neuropathy spectrum disorders. Although Ifnlr1 was expressed abundantly in both the cochlea and the vestibulum in mice, the affected individuals of the JS4842 family showed no symptoms of vestibular dysfunction. Despite the wide tissue distribution of IFNL1R1, IFNL1R1 missense mutation identified in this study only influenced hearing, as additional clinical signs outside the auditory system were absent in the affected individuals. Such an observation is not unusual; non-syndromic hearing loss is associated with mutant alleles of several ubiquitously expressed genes such as LDLRI (MIM 609739), TPRN (MIM 613354), MARVELD2 (also known as TRIC, MIM 610572), HGF (MIM 142409) and ACTG1...
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IFNLR1 has seven exons, and its coding protein, IFNLR1, has one functional domain, tissue factor domain (19–111 aa). This domain is similar to the fibronectin type-III domain and is found in cytokine receptors, interleukin and IFN receptors and coagulation factor III proteins. The missense mutation c.296G>A causes an amino acid substitution from arginine to histidine at position 99, and this mutation is predicted to affect the tissue factor domain of IFNLR1 (figure 3C).

The functional IFN-λs receptor complex is composed of IFNLR1 and IL-10R2 chains. The specific activity of IFN-λs is determined, in part, by the expression level of its receptor chain IFNLR1, which is expressed primarily in epithelial cells and a specific subsets of immune cells. IFN-λs appear to be the major IFN type produced by both murine and human airway epithelial cells in response to various respiratory viruses, and recent studies have suggested the functional importance of IFN-λ beyond innate antiviral protection.

To our knowledge, this is the first report to suggest a role of IFNLR1 in hearing. To mimic the IFNLR1 loss of function, we performed experiments in zebrafish using MO to knockdown ifnlr1. We observed a reduced number of hair cells, supporting cells in the lateral line in morphants compared with WT. Moreover, rescue experiments revealed that WT mRNA could largely rescue MO phenotypes.

At late-stage development in morphant zebrafish (7 dpf), ifnlr1 knockdown caused non-inflation of the swim bladder and expansion of the gut lumen area. The swim bladder in fish is a hydrostatic organ, postulated as a homologue of the tetrapod lung. However, the affected individual of family JS4842 showed no lung disorder symptoms. It is possible that IFNLR1 has a variety of functions depending on the species or tissue distribution. The
mechanism of swim bladder inflation in late-stage development of ifnlr1 morphant zebrafish has yet to be elucidated.

IFN-λ-induced receptor engagement leads to the tyrosine phosphorylation of the IFNLR1 intracellular domain via the activation of receptor-associated Jak kinases, Jak1 and Tyk2, and to the subsequent activation of latent transcription factors of the STAT family: STAT1, STAT2, STAT3, STAT4 and STAT5. Increasing evidence points to a role for the Jak/STAT signalling pathway in the auditory system. Inhibition of the Jak2/STAT3 pathway in zebrafish has yet to be elucidated. Further research is needed to address the specificity of different ethnicities, the various functions of the different IFNLR1 isoforms and possible ligands and interaction partners. 

This study identified IFNLR1 as a gene involved in autosomal-dominant hearing impairment. Several lines of evidence support the hypothesis that the identified IFNLR1 mutation is responsible for autosomal-dominant hearing impairment: (1) IFNLR1 c.296G>A completely cosegregated with hearing loss in an ADNSHL family; (2) the identified mutation influenced the conserved residue of the IFNLR1 protein and in silico analysis suggested that this mutation disturbed protein function; (3) the identified mutation was absent in 3396 ethnically matched controls (2896 in-house controls and 500 controls with normal hearing); (4) Ifnlr1 was expressed in the inner ears of mice and (5) ifnlr1 knockdown induced hair cell and supporting cell loss in zebrafish. Further research is needed to address the spectrum and prevalence of IFNLR1 mutations in ADNSHL families of different ethnicities, the various functions of the different IFNLR1 isoforms and possible ligands and interaction partners. Further characterisation of this novel molecular mechanisms by which genetic defects in IFNLR1 cause non-syndromic hearing loss will contribute to our understanding of the essential processes for normal hearing, which might lead to the development of therapeutic interventions.

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**Contributors** XG, Y-YQ, Q-FL and PD conceived of the study and participated in its design and drafted the manuscript. J-CX, L-PG, S-SH, H-KL and G-JW participated in the data interpretation and analysis. Y-HQ, W-QW, S-WQ, FX, YS, M-YH, YJ, DB and D-YK participated in the experiment in vivo and in vitro. All authors read and approved the final manuscript.

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