A Novel SLC26A4 (PDS) Deafness Mutation Retained in the Endoplasmic Reticulum

Zippora N. Brownstein, PhD; Amiel A. Dror, BSc; Dror Gilony, MD; Lela Migirov, MD; Koret Hirschberg, PhD; Karen B. Avraham, PhD

Objectives: To identify mutations in the SLC26A4 gene in individuals with nonsyndromic hearing loss and enlarged vestibular aqueduct, to design a predicted model of the pendrin protein, and to characterize novel mutations by means of localization in mammalian cells and effect of the mutation on the predicted model.

Design: Validation of the mutation by its exclusion in more than 300 individuals with normal hearing.

Setting: A laboratory of genetics of hearing loss research, clinical genetics laboratories, an otolaryngology department at Tel Aviv University, and medical centers in Israel.

Patients: A patient with nonsyndromic hearing loss and enlarged vestibular aqueduct, 203 deaf probands, and 310 controls with normal hearing.

Interventions: Sequencing the SLC26A4 gene in the patient with nonsyndromic hearing loss and enlarged vestibular aqueduct. Transfection of yellow fluorescent protein (YFP) constructs into mammalian COS7 cells. Designing a computational model of the human SLC26A4 protein.

Main Outcome Measure: Detection of a novel c.1458_1459insT SLC26A4 mutation.

Results: A computational model of the human pendrin protein suggests that the novel c.1458_1459insT mutation leads to a prematurely truncated protein, p.Ile487TyrfsX39. Mammalian COS7 cells transfected with the YFP-1458_1459insT construct showed mislocalization of the mutant protein.

Conclusions: A novel SLC26A4 mutation was detected in Israel. Because current estimates demonstrate that SLC26A4 mutations are involved in up to 4% of nonsyndromic deafness, our findings emphasize the importance of adding a molecular test for the SLC26A4 gene in the diagnosis of deafness, particularly when bone abnormalities are involved, to the list of genes screened in Israel and elsewhere in the world.


Over 100 mutations in the SLC26A4 (PDS) gene (OMIM 605646) are involved in both Pendred syndrome (PS) (OMIM 274600) and nonsyndromic sensorineural hearing loss (NSHL) (DFNB4) (OMIM 600791) associated with temporal bone abnormalities. The SLC26A4 gene, located on the long arm of chromosome 7, encodes pendrin, a protein expressed in various tissues, including the inner ear, thyroid, and kidney. Pendrin is a transmembrane anion exchanger, with 11 or 12 predicted transmembrane domains, that belongs to the solute carrier 26 family. It functions as a transporter exchanging chloride, iodine, bicarbonate, and formate.

Mutations in SLC26A4 are associated with congenital NSHL beginning at high frequencies, with fluctuating and sometimes progressive hearing loss (HL) with malformations of the temporal bone. The temporal bone abnormalities vary, ranging from isolated enlarged vestibular aqueduct (EVA) to Mondini dysplasia, an abnormality in which the normal cochlear spiral of 2.5 turns is replaced by a hypoplastic coil of 1.5 turns. In many populations, mutations in the SLC26A4 gene are the major genetic cause of these temporal bone inner ear malformations, accounting for up to 90% of the typical population with PS, 80% of individuals with EVA, and the same rate among patients with Mondini dysplasia. The same combination of mutations resulting in variable phenotypic expression, ranging from isolated nonsyndromic EVA to Mondini dysplasia to PS, have been described, suggesting that the same etiology underlies all conditions. In contrast, Pryor et al
ported 2 mutant SLC26A4 alleles in all patients with PS in their study, whereas the nonsyndromic patients with EVA had either 1 or no SLC26A4 mutant alleles. They concluded that PS and nonsyndromic EVA are distinct clinical and genetic phenomena, with PS being caused by biallelic SLC26A4 mutations, and at least some cases of nonsyndromic EVA being associated with a single SLC26A4 mutation. In an additional study among white French families with NSHL and EVA,3 patients with biallelic mutations had more severe deafness, an earlier age at onset, and a more fluctuating course of hearing levels than patients in whom no mutation was identified.

Current estimates demonstrate that SLC26A4 mutations are involved in up to 4% of NSHL,3 which emphasizes the importance of the molecular confirmation of the SLC26A4 gene in the diagnosis of deafness, particularly when bone abnormalities are involved.

**METHODS**

**PATIENTS**

The project was approved by the Helsinki (institutional review board) Committees of the Israel Ministry of Health, Tel Aviv University, Tel Aviv; the Rabin Medical Center, Petach Tikva; and the Haim Sheba Medical Center, Tel Hashomer. Blood samples were obtained following informed consent from each individual and, in case of individuals younger than 18 years, from their parents.

One deaf individual residing in Israel (who was of Iranian ethnic origin) was referred to the study because he was diagnosed as having NSHL and EVA. Palpation of the thyroid gland did not reveal any enlargement or mass. His HL began at age 6 years and progressed to profound deafness. In his mid 20s he underwent cochlear implantation. In his preoperative computed tomographic scan, EVA was observed, suggesting involvement of the SLC26A4 gene. Therefore, the SLC26A4 gene was sequenced.

On detecting the c.1458_1459insT mutation (p.Ile487TyrfsX39) (Figure 1), 203 Jewish deaf probands of mixed ethnic origin, including 3 with Mondini dysplasia, were screened for the mutation by the restriction enzyme assay described in the subsection titled "Detection of the SLC26A4 gene. Therefore, the SLC26A4 gene was sequenced.

On detecting the c.1458_1459insT mutation (p.Ile487TyrfsX39) (Figure 1), 203 Jewish deaf probands of mixed ethnic origin, including 3 with Mondini dysplasia, were screened for the mutation by the restriction enzyme assay described in the subsection titled “Detection of the SLC26A4 gene. Therefore, the SLC26A4 gene was sequenced.

**MUTATION EXCLUSION OF CONNEXIN 26**

The open reading frame of connexin 26 (GJB2) (OMIM 121011) was sequenced for mutations as described previously.4 Briefly, primers GJB2-2F, 5′-TCT TTT TTA CCA GAG CAA ACC GC-3′ and GJB2-2R, 5′-GGG CAA TGC GTT AAA CTT GC-3′ amplified a 722-bp fragment that was sequenced and checked for mutations using the connexin-deafness database.

**SEQUENCING THE SLC26A4 GENE**

Genomic primers were designed for all the coding exons (2-21) of the SLC26A4 gene (NM_000441.1; http://genome.ucsc.edu), using the Primer 3 Input (version 0.2; http://frodo.wi.mit.edu/cgi-bin/primer3/primer3_www.cgi). Polymerase chain reactions (PCRs) were performed in a total of 50 µL, using PCR Red-dyMix (ABgene; Epson, Surrey, England), including 1 µL of genomic DNA with a mean concentration of 200 ng/µL. The PCR cycling conditions were 95°C for 5 minutes, followed by a touchdown program of 60°C to 55°C and 30 cycles of 95°C for 30 seconds, 55°C for 30 seconds, and 72°C for 30 seconds. Two final steps followed at 72°C and 4°C for 10 minutes each. After verification of the PCR products by separation of 3 µL of reaction by electrophoresis on a 1% gel, the PCR products were purified by Wizard SV Gel and the PCR Clean-Up System (Promega, Madison, Wisconsin). Sequencing was performed using the same primers as those used for PCR: the ABI Prism BigDye Terminator Cycle Sequencing Ready Reaction Kit (Applied Biosystems, Foster City, California) and a DNA sequencer (model 377; ABI). Mutations were confirmed by sequencing in both directions.

**DETECTION OF THE SLC26A4 GENE:**

A restriction enzyme assay was designed. This method was based on the principle of PCR-mediated, site-directed mutagenesis, followed by BstZ17I digestion. The primer set consisted of a wild type (WT) forward primer, SLC26A4-13F: 5′-TCT TTT TTA CCA GAG CAA ACC GC-3′, and a modified reverse primer, SLC26A4-BstZ17I-R: 5′-AGATCCAGCCCAAGATGATGAGCATGAT-3′, that was modified at nucleotide 1662 (G→C). This modification is located 4 nucleotides downstream of the insertion site. The amplified WT fragment of 155 bp has a newly created restriction site for the BstZ17I enzyme; that is, the digestion occurs only in the modified WT fragment. The insertion of thymine 4 nucleotides upstream of the modification eliminates the restriction site. The PCR reactions were performed as described in the previous subsection in a total of 30 µL; 10 µL of the reaction mix was separated by electrophoresis on a 1% gel. The PCR product was digested by BstZ17I (37°C for 8 hours) and run on a 2% gel electrophoresis. Because a BstZ17I site is inserted in the modified primer, a BstZ17I digest of WT DNA produces 2 fragments of 126 bp and 29 bp; digestion of heterozygous DNA produces 3 fragments of 156 bp, 126 bp, and 29 bp; and c.1458_1459insT homozygous DNA results in 1 fragment of the 156-bp original PCR product size.

**COMPUTATIONAL ANALYSIS OF THE p.Ile487TyrfsX39 MUTATION**

Two independent predictions of a hypothetical model for the human pendrin protein sequence (UniProtKB/Swiss-Prot: O43511) were performed. The first prediction was provided by the UniProtKB/Swiss-Prot protein sequence database (entry version 34, release 7.0/49.0; February 7, 2006; http://www.expasy.org/sprot/) and is presented in Figure 1B. A second prediction was performed by the TMHMM program (version 1; February 2006; http://www.cbs.dtu.dk/services/TMHMM-2.0/) (data not shown).

A list of current known human mutations in the pendrin protein, demonstrated by colored circles in Figure 1B, was made based on 2 resources, the UniProtKB/Swiss-Prot database and the study by Tsukamoto et al.hores of the current known human mutations in the pendrin protein, demonstrated by colored circles in Figure 1B, was made based on 2 resources, the UniProtKB/Swiss-Prot database and the study by Tsukamoto et al.9

**LOCALIZATION OF THE YFP CHIMERAS**

The SLC26A4 c.1458_1459insT mutation was created by PCR mutagenesis using the QuikChange Site-Directed Mutagenesis Kit (Stratagene, La Jolla, California) and subcloned into the yellow fluorescent protein (YFP) expression vector pEYFP-C1 (“p” indicates plasmid) (Clontech, Mountain View, California). Cell cultures and expression of chimeras were performed as previously described.15

©2008 American Medical Association. All rights reserved.
Figure 1. A novel mutation in SLC26A4 (PDS) is responsible for nonsyndromic sensorineural hearing loss in a Jewish Israeli patient of Iranian origin. A, The sequencing of SLC26A4 revealed a 1458-1459insT mutation in exon 13, leading to a predicted stop codon at position 526 (p.Ile487TyrfsX39) in the affected individual. B, A potential model of the human pendrin amino acid sequence and its membrane arrangement is predicted by the UniProtKB/Swiss-Prot database (http://www.expasy.org/sprot). Known missense, deletion (del), and stop mutations are demonstrated with colored circles. The current list of human mutations was made based on the study by Tsukamoto et al. and the UniProtKB/Swiss-Prot database. C, The reported mutation, p.Ile487TyrfsX39, leads to a 40 amino acid change in the pendrin protein sequence beginning at position 487 and terminating with a stop codon at position 526. A hypothetical model of the disrupted pendrin protein with the subsequent premature truncation is demonstrated, showing the mutation within a transmembrane domain and the stop codon within an intracellular domain. COOH and NH2 indicate the carboxyl group and amino group of amino acids, respectively.
CONFOCAL LASER-SCANNING MICROSCOPY

The COS7 cells were imaged in Dulbecco's Modified Eagle's Medium (Biological Industries, Kibbutz Beit Haemek, Israel) without phenol red but supplemented with 20 mM of Hepes (pH, 7.4). Transfection and imaging were performed in Labtek chambers (Nunc, Naperville, Illinois). A laser scanning microscope (PASCAL; Zeiss, Jena, Germany) equipped with an Axiovert 200 inverted microscope (Zeiss) and Ar 514 nm laser line was used for EYFP. The confocal images were captured using a 63x1.4 numerical aperture objective with a pinhole diameter equivalent to 1 to 2 Airy units.

RESULTS

SLC26A4 GENE c.1458-1459insT MUTATION DETECTION

The SLC26A4 gene was sequenced in a proband with NSHL and EVA after excluding mutations in GJB2 by sequencing. The c.1458_1459insT mutation was detected on both alleles (Figure 1A). The SLC26A4 gene contains 21 exons that encodes a predicted protein of 780 amino acids. The mutation c.1458_1459insT in exon 13 causes a frameshift at position 487, leading to a stop codon at position 526 of the pendrin protein, p.Ile487TyrfsX39.

COMPUTATIONAL ANALYSIS OF THE PREDICTED TRUNCATED PENDRIN PROTEIN

Two methods were employed to make a prediction of the 3-dimensional structure of the pendrin protein, the UniProtKB/Swiss-Prot protein sequence database (http://www.expasy.org/sprot) and the TMHMM program (http://www.cbs.dtu.dk/services/TMHMM-2.0/). According to both, our reported mutation, p.Ile487TyrfsX39, leads to an amino acid change within a potential transmembrane domain and a stop codon within a potential intracellular domain (Figure 1B).

PROBABILITY OF THE c.1458_1459insT MUTATION IN THE ISRAELI JEWISH POPULATION

Deaf probands (n = 203), in whom mutations in the exon 2 of the connexin 26 were excluded, were screened for the c.1458_1459insT mutation by the restriction enzyme assay described in the subsection titled “Detection of c.1458_1459insT.” Three individuals with Mondini dysplasia were included in this population. The 203 probands were WT for SLC26A4. In total, the approximated probability of the c.1458_1459insT mutation in the SLC26A4 gene among the Jewish deaf population in Israel is 0.5% (1 in 204).

In addition, 310 controls with normal hearing were screened, including 21 who were of Iranian ethnic origin, and they were WT for SLC26A4 as well. No carriers of the mutation were detected.

LOCALIZATION OF YFP-WT VS YFP-MUTATED PENDRIN

We observed YFP-WT PDS in the plasma membrane and in the endoplasmic reticulum (ER) (Figure 2A), whereas the YFP-1458_1459insT was completely retained in the ER in transfected COS7 cells, seen as an elaborated reticulum extending off the nuclear envelope (Figure 2B).

COMMENT

The mutation c.1458_1459insT leads to a predicted stop codon at position 526 of the pendrin protein (p.Ile487TyrfsX39). Although the putative truncated protein produced is only two-thirds the length of the WT
pendrin and is missing 1 or 2 transmembrane domains, the affected individual has NSHL with EVA, but not PS. Localization experiments of the mutated protein show that the YFP-L445W-1459nsT is retained in the ER, whereas the WT pendrin targets the PM. Retention of pendrin in the ER is a major mechanism for PS and was observed for other mutations involved in PS, including L236P, T416P, G384E, and V239D.13,14 In another study,15 mutations in pendrin associated with NSHL were also shown to cause retention of the mutated protein in the ER, as was observed for mutations causing PS. These findings suggest involvement of modifier genes, and/or nutritional factors, including iodine uptake, which determine the thyroid phenotype and determine the difference between PS and NSHL. This hypothesis is supported by mutations found to be involved both in PS and in NSHL in individual patients, either with PS or with NSHL.16

In our study, the affected individual homozygous for the mutation has NSHL associated with EVA, but no goiter is present. However, the thyroid phenotype usually does not develop until the second decade of life or even at a later age, so PS cannot be ruled out in the proband in this study because he may develop goiter in the future.

The novel c.1458_1459insT mutation in the SLC26A4 gene was detected in 1 family only, and no carriers were identified. The low probability obtained in Israel might due to the small population of hearing-impaired patients with EVA and to the small control group of Jews originating in Iran. However, because the SLC26A4 gene is involved in up to 4% of NSHL in some populations,1 we study strongly suggests that it would be beneficial to test for this novel mutation in the Israeli deaf population with associated temporomandibular bone malformations.

Submitted for Publication: March 20, 2007; final revision received June 17, 2007; accepted August 7, 2007.

Correspondence: Zippora N. Brownstein, PhD, Department of Human Molecular Genetics and Biochemistry, Sackler School of Medicine, Tel Aviv University, Tel Aviv 69978, Israel (brownste@post.tau.ac.il).

Author Contributions: Drs Brownstein, Gilony, Migirov, Hirschberg, and Avraham and Mr Dror had full access to all the data in the study and take responsibility for the integrity of the data and the accuracy of the data analysis. Study concept and design: Brownstein and Avraham. Acquisition of data: Brownstein, Dror, Gilony, Migirov, Hirschberg, and Avraham. Analysis and interpretation of data: Brownstein, Dror, Hirschberg, and Avraham. Drafting of the manuscript: Brownstein, Gilony, Migirov, and Avraham. Critical revision of the manuscript for important intellectual content: Brownstein, Dror, Hirschberg, and Avraham. Obtained funding: Migirov and Avraham. Administrative, technical, and material support: Brownstein, Gilony, and Avraham. Study supervision: Avraham. Financial Disclosure: None reported.

Funding/Support: This study was supported by grant R01 DC005641 from the National Institutes of Health, the European Commission FP6 Integrated Project EUROHEAR LSHG-CT-2005-512063, the German-Israeli Foundation for Scientific Research and Development, and the Berte and Alan Hirschfield Fund.

Additional Contributions: We thank the members of the family studied for their cooperation and support throughout the project. Jeanne Shepshelovich, MSc, from the laboratory of Dr Hirschberg, generated the PDS constructs.

REFERENCES


