A novel COCH mutation, V104del, impairs folding of the LCCL domain of cochlin and causes progressive hearing loss

I Nagy, M Horváth, M Trexler, G Répássy, L Patthy

MATERIALS AND METHODS
Selection of patients and gene analysis
Patients were selected from the cochlear implantation list of the Department of Otorhinolaryngology of Semmelweis University according to diagnostic criteria of the DFNA9 disorder (OMIM #601369): progressive hearing loss usually begins in the third decade of life as a high frequency loss with concomitant vestibular dysfunction.

Molecular analysis of cases of DFNA9 has identified five different mutations in this gene. Interestingly, all mutations causing DFNA9 type deafness disorder affect the LCCL domain of cochlin.

Our present investigation was aimed at identifying novel mutations affecting the LCCL domain of cochlin in order to gain more insight into the pathomechanism of DFNA9. Hungarian patients selected according to the diagnostic criteria of DFNA9 were screened for the presence of mutations affecting the LCCL domain. These studies identified one person heterozygous for a novel mutation in the coding region of COCH. The mutation has resulted in the deletion of Val104, a residue conserved in the human, mouse, and chicken cochlin sequences. It affects a critical β strand of the LCCL domain and was found to prevent refolding of recombinant LCCL domain expressed in E. coli.

Key points
• Autosomal dominant nonsyndromic sensorineural deafness 9 (DFNA9, OMIM #601369) is a rare, late onset hearing loss. In DFNA9 patients, hearing loss usually begins in the third decade of life as a high frequency loss with concomitant vestibular dysfunction.
• DFNA9 is caused by mutations in the COCH gene, which encodes cochlin, an extracellular matrix protein that contains an LCCL domain and two von Willebrand type A domains.
• Molecular analysis of cases of DFNA9 has identified five different mutations in this gene. Interestingly, all mutations causing DFNA9-type deafness disorder affect the LCCL domain of cochlin.
• Here we describe a novel COCH mutation in a Hungarian patient, which results in the deletion of Val104, a residue conserved in the human, mouse, and chicken cochlin sequences. The deletion affects a critical β strand of the LCCL domain and was found to prevent refolding of a recombinant LCCL domain expressed in Escherichia coli.

COLLECTED DATA
DNA from 17 hearing impaired persons from 14 different families was used for genetic analysis, and compared with DNA from 50 unrelated controls. A DNA sample was also collected from a relative of the proband identified in the present study. Genomic DNA (20 ng) was isolated from peripheral blood cells using the Puregene DNA Isolation kit (Gentra Systems, Minneapolis, MN, USA).

Mutation screening was performed only for exons 4 and 5 of COCH (NM 004086), which encode the LCCL domain of the protein. Intronic PCR primers (sense: 5'-CCACTATGGCCC AAGAAGCTCTAAAGGGAATG-3', antisense: 5'-GGGTTGGAGA ATATTACAGAATGAGAAC-3') were used to amplify the genomic region encompassing exon 5. Amplification products were purified using the Nucleospin Extract Kit (Macherey-Nagel GmbH, Düren, Germany).

Dideoxy sequencing of the PCR products for exons 4 and 5 was carried out using the primers 5'-CTGTCGATT TCCCTCCACCCTGTTG-3', flanking exon 4, and 5'-TGAAAAGTCTGGATAGATGTCCTT-3' flanking exon 5. To verify the sequence of the genomic DNA of the patient carrying a mutation in exon 5 of COCH, PCR primers (sense: 5'-CGTCTGAGTGTGTTGATAGACTCTTCAGCTG-3', antisense: 5'-GGGTTGAAGATTACAGAATGAGAAC-3') were used to amplify only the affected exon 5. The PCR product was blunt end ligated into Smal digested M13mp19 vector, and phages carrying the mutant or wild type alleles were sequenced. Restriction enzymes and the M13 sequencing kit used for dideoxy sequencing of cloned DNA were
were incubated at 25˚C for 60 minutes with constant stirring EDTA, and 0.1 mol/l dithiothreitol, pH 8.0. The mixtures dissolved in 0.1 mol/l Tris-HCl, 8 mol/l urea, 10 mmol/l and inclusion bodies containing recombinant protein were the recombinant proteins was induced with 100 μl IPTG, against 0.1 mol/l Tris-HCl and 10 mmol/l EDTA, pH 8.0 at 25˚C.

The fragment was cut with HindII and HindIII, and ligated in a PvuII/HindIII digested pmed23 expression vector. This construct encodes a fusion protein in which the first 35 amino acids of β galactosidase are fused to the mutant LCLC domain. Expression, refolding, and characterisation of the recombinant V104del mutant LCLC domain was performed using the same protocol as that used for the wild type protein and several other mutants of the LCLC domain.  Expression of the recombinant proteins was induced with 100 μmol/l IPTG and inclusion bodies containing recombinant protein were dissolved in 0.1 mol/l Tris-HCl, 8 mol/l urea, 10 mmol/l EDTA, and 0.1 mol/l dithiothreitol, pH 8.0. The mixtures were incubated at 25˚C for 60 minutes with constant stirring and the solubilised proteins were chromatographed on a Sephacryl S-300 column equilibrated with 100 mmol/l Tris-HCl, 8 mol/l urea, 10 mmol/l EDTA, and 0.1% 2-mercaptoethanol. Fractions containing pure fusion proteins were identified by SDS-PAGE, pooled and refolded by dialysis against 0.1 mol/l Tris-HCl and 10 mmol/l EDTA, pH 8.0 at 25˚C.

RESULTS AND DISCUSSION

Sequence analysis of the region encoding the LCLC module of COCH of one hearing impaired patient indicated that the patient was heterozygous for a deletion in this region. To determine the precise location and size of the deletion we cloned the affected region into M13mp19 in order to separate the mutant and wild type alleles. Single strand sequencing of phages confirmed that one of the alleles had the wild type sequence, whereas the mutant allele carried a deletion of nucleotides 367–369 in exon 5. The deletion of three nucleotides results in the deletion of a Val104 residue without causing a frameshift. No mutation in the LCLC domain was detected in the other 16 patients with hearing loss or in the 50 control individuals.

The hearing loss of the proband (born in 1943) was first observed at the age of 32 years to have severe vertigo, nausea, vomiting, and perceptive hearing impairment of the left ear. After 4 years, severe hearing loss appeared in the right ear as well. Severe to profound hearing loss across all frequencies was developed by the fifth decade. The patient received a cochlear implant at the age of 46 years but it did not improve his hearing. The latest examinations (at the age of 60 years) showed total cochleovestibular areflexia on both ears and the patient feels weak vertigo in the dark. He has no brothers or sisters. His father died in 1944 at the age of 30 years, his mother is 93 years old without any hearing problems. He has only one daughter (29 years old), who has no hearing problems.

Expression and characterisation of the recombinant V104del LCCL domain

The DNA fragment encoding the LCCL module of the V104del mutant protein of the proband was produced by a two step PCR strategy. Firstly, we amplified exon 4 and 5 of the mutant COCH gene separately by using 5'-GGAGGATGCTGACGGCCTCCTGATCCTACAGT-3' (sense) and 5'-GAGTTCTGTATCCCTGTTGACGCGCGCCA-3' (antisense) primers for exon 4, and 5'-TGGGGGTCTGCCTCCACAGGGAGTATCGCAACTC-3' (sense) and 5'-GGGAACTACGAGGTACTGTAAGAAAGACG-3' (antisense) primers for exon 5. For exon 4, the template was the genomic DNA of the proband, while for the mutant exon 5 we used the M13mp19 clone containing the mutant allele of exon 5. The two cDNA fragments were linked in a second reaction with 5'-GGAGGATGCTGACGGCCTCCTGATCCTACAGT-3' (sense), 5'-GGGAACTACGAGGTACTGTAAGAAAGACG-3' (antisense).

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In order to examine the effect of the mutation on the structure of the LCCL domain we expressed the mutant V104del LCCL domain, and dialysis led to complete precipitation of the recombinant protein. As the deletion of Val104 affects a conserved residue of the β6 strand structure of the LCCL domain (figs 1 and 2), it seems likely that this deletion affects an essential structural element of the LCCL fold, impairing its ability to form the native structure. In this respect, the V104del mutation is similar to most other DFNA9 causing mutations identified so far, which also impair refolding of recombinant LCCL domain (table 1).

In our opinion, this novel mutation provides additional support for the notion that the characteristic cosinophilic deposits in DFNA9 affected inner ear structures could be the result of accumulation and aggregation of aberrant, mutated cochlin. Recent studies have indeed shown that DFNA9 mutations do not impair secretion and post-translational processing of cochlin produced by mammalian cells. It seems likely that in vivo the mutations may lead to slow aggregation of cochlin over a longer time course, consistent with the late onset and progressive nature of this disorder.

### Table 1
Comparison of the V104del mutation with other DFNA9 mutations

<table>
<thead>
<tr>
<th>Mutation</th>
<th>Genotype</th>
<th>Age of onset</th>
<th>Refolding of LCCL domain</th>
</tr>
</thead>
<tbody>
<tr>
<td>V104del</td>
<td>Heterozygous</td>
<td>4th decade</td>
<td>Impaired*</td>
</tr>
<tr>
<td>I109N</td>
<td>Heterozygous</td>
<td>2nd–3rd decade</td>
<td>–</td>
</tr>
<tr>
<td>V66G</td>
<td>Heterozygous</td>
<td>2nd–3rd decade</td>
<td>Impaired*</td>
</tr>
<tr>
<td>G88E</td>
<td>Heterozygous</td>
<td>5th decade</td>
<td>Impaired*</td>
</tr>
<tr>
<td>W117R</td>
<td>Heterozygous</td>
<td>5th decade</td>
<td>Preserved*</td>
</tr>
<tr>
<td>P115S</td>
<td>Heterozygous</td>
<td>4th decade</td>
<td>Impaired*</td>
</tr>
</tbody>
</table>

*Present work.

### REFERENCES
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