COQ6 mutations in human patients produce nephrotic syndrome with sensorineural deafness

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Steroid-resistant nephrotic syndrome (SRNS) is a frequent cause of end-stage renal failure. Identification of single-gene causes of SRNS has generated some insights into its pathogenesis; however, additional genes and disease mechanisms remain obscure, and SRNS continues to be treatment refractory. Here we have identified 6 different mutations in coenzyme Q10 biosynthesis monoxygenase 6 (COQ6) in 13 individuals from 7 families by homozygosity mapping. Each mutation was linked to early-onset SRNS with sensorineural deafness. The deleterious effects of these human COQ6 mutations were validated by their lack of complementation in coq6-deficient yeast. Furthermore, knockdown of Coq6 in podocyte cell lines and coq6 in zebrafish embryos caused apoptosis that was partially reversed by coenzyme Q10 treatment. In rats, COQ6 was located within cell processes and the Golgi apparatus of renal glomerular podocytes and in stria vascularis cells of the inner ear, consistent with an oto-renal disease phenotype. These data suggest that coenzyme Q10-related forms of SRNS and hearing loss can be molecularly identified and potentially treated.

Introduction

Nephotic syndrome (NS), a malfunction of the kidney glomerular filter, leads to proteinuria, hypoalbuninemia, and edema. Steroid-resistant NS (SRNS) represents a frequent cause of end-stage renal failure (ESRF), which requires renal replacement therapy for survival. Identification of single-gene causes of NS (1–7) has generated the first insights (8, 9) into its pathogenesis: (a) that single-gene causes of NS result in SRNS (10, 11) with very few exceptional cases that respond to treatment (3, 12); (b) that SRNS-causing genes are expressed in a specialized cell type, the glomerular podocyte (13); and (c) that the pathohistology ranges from the intrauterine-onset severe developmental phenotype of diffuse mesangial sclerosis (DMS) to the childhood-onset phenotype of focal segmental glomerulosclerosis (FGS). Two-thirds of all SRNS cases with onset in the first year of life (14) and 10%–28% of all childhood cases (15) are caused by single-gene mutations in 1 of only 4 genes, NPHS1 (1), NPHS2 (2), LAMB2 (16), and WT1 (17). However, the molecular cause of more than 80% of all cases of SRNS is unknown, and treatment options have yet to be discovered. We therefore performed total genome search for linkage to identify further causative recessive genes.

Authors note: Saskia F. Heering and Gil Chernin contributed equally to this work.

Conflict of interest: The authors have declared that no conflict of interest exists.

Citation for this article: J Clin Invest. 2011;121(5):2013–2024. doi:10.1172/JCI45693.
Results

**COQ6 mutations cause SRNS with sensorineural deafness (SND).** To identify further single-gene causes for SRNS, we performed a genome-wide search for linkage in 14 different consanguineous families with SRNS. Calculating lod under the hypothesis of locus heterogeneity yielded a significant maximum heterogeneity lod score of 4.9 (α = 5%) on human chromosome 14q24.3, covering a region of 6.4 Mb (Figure 1A). Of 7 families homozygous at this locus (SRNS2), families A1072 and F1082 from Turkey revealed haplotype sharing (Figure 1B), restricting the critical genetic region to 2.1 Mb under the hypothesis that an ancestor common to both families introduced the disease allele (i.e., homozygosity by descent). This interval contained 32 positional candidate genes (Figure 1C).

Exon sequencing of COQ6 yielded homozygous mutations in 3 of the 7 families homozygous at the SRNS2 locus (Table 1). In both affected individuals of family A1072, we detected a homozygous A353D substitution (Figure 1G and Table 1) that was also found in northern Lebanese family F252, as predicted from haplotype sharing at SRNS2 (Figure 1B). All 3 affected individuals that were examined in the northern Lebanese family F252 exhibited the homozygous change G225R (Figure 1G and Table 1). This mutation was shared by 3 affected individuals of family A234 from southern Turkey (Table 1), most likely as a founder effect. Both missense mutations altered amino acid residues that are uniformly conserved from affected individuals of family A1072, we detected a homozygous mutation of the 7 families homozygous at the SRNS2 locus (Table 1). In all 9 individuals with SRNS that were examined for hearing loss, there was SND (Table 1). Exon sequencing of all other 31 genes in family F1082, as predicted from haplotype sharing at SRNS2 (Figure 1B), restricting the critical genetic region to 2.1 Mb under the hypothesis that an ancestor common to both families introduced the disease allele (i.e., homozygosity by descent). This interval contained 32 positional candidate genes (Figure 1C).

All 11 affected individuals of the 5 families with 2 recessive COQ6 mutations had SRNS. They manifested with proteinuria at a median age of 1.2 years (range, 0.2–6.4 years) and progressed to ESRF by a median age of 1.7 years (range, 0.4–9.3 years); 5 individuals died in early childhood (median age, 5.0 years). Renal biopsy revealed FSGS in cases (Table 1 and Figure 2, A–C) and DMS in 1 case. Subject A234-21 presented with seizures, and subject F1082-21 had white matter abnormalities and seizures and died of multigain failure in sepsis; 2 other individuals had ataxia and facial dysmorphism (individuals F252-51 and A234-26, respectively; Table 1).

**COQ6 function.** The COQ6 gene extends over 13.2 kb and contains 12 exons (Figure 1, D and E). There are 18 putative isoforms resulting from alternative splicing (www.aceview.org). Full-length isoforms a and b contain 12 exons, but use alternative exons 1a and 1b (Supplemental Figure 1, A and B; supplemental material available online with this article; doi:10.1172/JCI45693DS1). Full-length isoforms were expressed in multiple tissues, including the kidney (Supplemental Figure 1, C–F). Using in situ hybridization analysis, we demonstrated Coq6 mRNA expression in the metanephric mesenchyme and forming nephrons of mouse kidney (Supplemental Figure 1, G–L). Isoform a (encoding a 54-kDa protein) is predicted to be expressed in mitochondria with a Predotar score of 0.81 (http://urgi.versailles.inra.fr/predotar) because of a mitochondrial leader peptide, whereas isoform b (encoding a 51-kDa protein), which uses an alternative exon 1, is considered only possibly mitochondrial, with a Predotar score of 0.45. Both isoforms encode a flavin-dependent mono-oxygenase with 3 flavin adenine dinucleotide-binding motifs (18). The amino acid sequence is highly conserved throughout evolution, with identity to the human COQ6 protein sequence of 66% for Danio rerio and 33% for the E. coli ortholog UbiH. The enzyme coenzyme Q10 mono-oxygenase 6 (COQ6) is required for biosynthesis of coenzyme Q10 (CoQ10, also referred to as ubiquinone) and is thought to catalyze one or more ring hydroxylation steps. Humans synthesize CoQ10 and yeast synthesizes CoQ8 (where CoQ8 designates a polyisoprenoid residue with n isoprenoid units). CoQ8 operates as a redox carrier in the mitochondrial respiratory chain shuttling electrons from respiratory chain complexes RCCI and RCCII to complex RCCIII (19). CoQ10 also serves as a lipid-soluble antioxidant and has previously been implicated in protection from cell damage by ROS (20).

Because rare recessive mutations have been described in syndromic and nonsyndromic forms of NS (21, 22) in other genes involved in CoQ10 biosynthesis (23–25), we performed sequencing of all exons of the following 11 candidate genes: PDSS1, PDSS2, COQ2, COQ3, COQ4, COQ5, COQ7, COQ8, COQ9, COQ10a, and COQ10b. We examined 42 individuals with SRNS who had extrarenal symptoms suggestive of mitochondrial disease or in whom only 1 heterozygous COQ6 mutation was found. However, we did not detect any further mutations. The 4 protein-truncating mutations in COQ6 that we detected in subjects A988, A1904, and A3331-21 (Figure 1G and Table 1) may be considered null alleles. Similarly, the fully conserved homozygous missense mutations G225R and A353D that we observed in 4 families with SRNS and SND may also represent loss-of-function mutations (Figure 1G and Table 1). To test this hypothesis, we examined all 6 COQ6 mutations for potential deleterious effects by complementation in *yeast* harboring the human mutations (Figure 1G and Table 1). Monogenic variants of childhood NS for potential deleterious effects by complementation in *coq6*-deficient yeast strains. Yeast cells harboring a deletion mutation in the *coq6* gene were unable to grow on yeast extract/peptone/glycerol media (YPG; in which glycerol acts as a nonfermentable carbon source) and were deficient in CoQ8 (Figure 2, D and E, and ref. 18). Expression of human WT *COQ6* with an aminoterminal yeast mitochondrial leader sequence rescued both YPG growth and CoQ8 content (Figure 2, D and E), although not as robustly as did yeast harboring the WT *COQ6* gene (pSrS1-1; Figure 2, D and E). Rescue of growth on YPG was observed with either low–copy number (pQM; Figure 2D) or high–copy number (pRCM; data not shown) expression constructs. Both constructs also rescued the deficiency in CoQ8 content (Figure 2E). In contrast, none of the *Coq6* constructs harboring the human mutations (Figure 1G and Table 1) were able to rescue the growth deficiency phenotype or CoQ8 content phenotypes (Figure 2, D and E), thereby demonstrating the deleterious effects of these mutations.

**Response to CoQ10 treatment.** Monogenic variants of childhood NS are characterized by a lack of response to therapy (26). Because successful CoQ10 treatment had been described previously in an...
Figure 1
Positional cloning of COQ6 mutations in individuals with NS and SND. (A) lod score profile across the human genome in affected children from 14 consanguineous kindred with SRNS. Parametric heterogeneity lod (HLOD) scores are plotted against human chromosomal mapping positions, concatenated from p-ter (left) to q-ter (right). (B) Within the SRNS2 locus, haplotypes from 250k SNP analysis are shown for 3 of the 7 families with homozygosity at the SRNS2 locus. Alleles are colored light green (AA), dark green (BB), and red (AB). (C) The 32 genes within the SRNS2 locus; 3 genes preferentially expressed in kidney podocytes are underlined. Mutations were found in COQ6. Transcriptional direction is indicated by < or >. (D) COQ6 extends over 13.2 kb and contains 12 exons (boxes). (E) Exon structure of COQ6 cDNA. Arrows indicate relative positions of mutations (see G). Positions of peptides for antibody generation are shown in yellow. (F) Domain structure of COQ6 protein.Extent of the mono-oxygenase domain is shown in relation to encoding exon position (E). (G) 6 different COQ6 mutations in 7 families with SRNS. Family number and amino acid change (see Table 1) are given above sequence traces. Arrows denote positions of mutations in relation to exons and protein domains. For the 2 missense mutations, G255R and A363D, full conservation across evolution of altered amino acid residues is illustrated.
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Additional mutations (heterozygous only detected in families A998 (R162X) and A1904 (W188X) (see Figure 1G). **ND**, no data or DNA available. Consang, Consanguinity. All mutations were absent of the 12 cranial components analyzed. This study would it also to the mitochondrial enzyme, COQ6, which is known to be important for the synthesis of CoQ10. In patients with COQ6 mutations, CoQ10 levels are typically reduced, leading to a decrease in the levels of COQ10 in the mitochondria. CoQ10 is a molecule that plays a crucial role in energy production within the mitochondria. It is synthesized from COQ2, which is another enzyme in the mitochondrial electron transport chain. Therefore, the combination of COQ2 and COQ6 mutations could lead to a decrease in the levels of COQ10 in the mitochondria, which may explain the symptoms observed in these patients. In conclusion, the study of COQ6 mutations is important for understanding the pathogenesis of NS and deafness and for developing targeted therapies for these conditions.
expressed full-length COQ6 isoform a spared Golgi expression, as demonstrated with Giantin as a Golgi marker (Figure 3F). Likewise, in podocyte cell lines, the cell type central to the disease mechanism of SRNS, α–COQ6-TPEP2 detected endogenous COQ6 in Golgi, but not in mitochondria (Figure 3G). The endogenous COQ6 expression pattern was confirmed with the antibody α–COQ6–925-1 (Supplemental Figure 3, A and B), which was derived from a different peptide (Figure 1E).

Endogenous COQ6, COQ7, and COQ9 colocalize to cell processes and Golgi in rat podocytes. Monogenic forms of SRNS are caused by dysfunction of the glomerular podocyte, a terminally differentiated cell critical for the filtering function of the kidney glomerulus. (13, 26). We therefore examined expression of the COQ6 protein in kidney. COQ6 was seen almost exclusively in glomeruli, rather than in tubules (Figure 4A). As predicted, within glomeruli, COQ6 was expressed specifically in podocytes, as marked by WT1 labeling (Figure 4A). Within podocytes, COQ6 was absent from mitochondria (labeled with COXIV; Figure 4A); conversely, it was expressed within cellular processes and within Golgi apparatus (Figure 4, B and C), which confirmed the results obtained in cell lines (Figure 3). Because nonmitochondrial localization and function have been previously described for CoQ6 (27), we hypothesized that nonmitochondrial expression would also apply to COQ7 and COQ9, which are known as mitochondrial proteins but share a multienzyme complex together with COQ6 for the biosynthesis of CoQ10 and CoQ6 (21). Indeed, upon immunofluorescence, both COQ6 and COQ7 fully colocalized to cellular processes and Golgi of rat glomerular podocytes (Figure 4, B and C), as did COQ7 and COQ9 (Supplemental Figure 3C). We demonstrated specificity of this signal for α–COQ6-TPEP2 by showing the absence of the podocyte signal after preabsorption with the cognate peptide TPEP2, in contrast to its presence after preabsorption with the noncognate peptide TPEP1 (Supplemental Figure 3D). In addition, COQ6 colocalized to podocyte cellular processes with podocin (Figure 4E), another gene product that, if mutated, causes a Mendelian form of SRNS (2). These findings demonstrate that COQ6, COQ7, and COQ9 are all 3 expressed in cellular processes and Golgi apparatus of podocytes rather than in mitochondria.
We then investigated expression of COQ6 in the inner ear, because hearing loss is the other phenotype in this oto-renal syndrome. Immunofluorescence studies using α–COQ6-TPEP2 revealed COQ6 expression in the spiral ganglion as well as in cells of stria vascularis and spiral ligament (Figure 4, F and G), which are involved in maintaining the high potassium concentration in the cochlear duct necessary for sound transduction of the hair cells of Corti organ.

Coq6 knockdown in cultured podocytes induces apoptosis that is reversed by CoQ10 treatment. In order to study COQ6 function in glomerular podocytes, the cell type involved in the disease phenotype, we performed knockdown of Coq6 expression in vitro using a vector-based siRNA approach (28). Murine podocytes (29) were stably transfected with COQ6 siRNA constructs, and clones were analyzed by RT-PCR for Coq6 expression levels. We compared clones transfected using a scrambled siRNA oligonucleotide with non-transfected WT podocytes. The 3 clones that showed the highest degree of Coq6 downregulation (clones 1, 2, and 5) were selected for functional studies (Supplemental Figure 1M). First, we analyzed the growth behavior of Coq6 knockdown clones when kept in an undifferentiated and proliferative state (Figure 5A). When we seeded a defined number of cells and counted them after 24, 48, and 72 hours of cultivation, we found that the growth rate of the 3 Coq6 knockdown clones was strongly decreased, while the scrambled siRNA clone C proliferated at the same rate as WT cells (Figure 5A). This difference reached statistical significance after 24 hours for clones 2 and 5 ($P < 0.05$) and after 72 hours for clone 1 ($P < 0.005$; Figure 5A). As the scrambled siRNA clone C did not
show any difference in growth behavior compared with WT podocytes, the scrambled clone was used as negative control for further experiments. To analyze whether the diminished overall growth rate in podocytes after Coq6 knockdown is associated with activation of the intrinsic apoptotic pathway, we next determined the inner mitochondrial membrane potential ($\Delta \Psi_m$) in these podocyte clones by using the fluorescent dye tetramethylrhodamine ethylester (TMRE). Compared with control cells, all 3 knockdown clones showed a substantial drop in TMRE fluorescence (data not shown), indicative of an increased percentage of podocytes with depolarized $\Delta \Psi_m$.

We then analyzed activity of caspase-9 (Figure 5B), the major caspase downstream of mitochondria-mediated apoptosis (30). Using fluorometric immunosorbent enzyme assay (FIENA), we detected a more than 2-fold increase of caspase-9 activity in all 3 knockdown clones compared with control podocytes ($P < 0.005$; Figure 5B). Moreover, caspase-3, the final downstream executioner caspase of different apoptotic signaling pathways (31), showed significant elevation of activity for all 3 siRNA clones ($P < 0.05$; Figure 5C), consistent with the effect seen in zebrafish (see below). These data suggest that the observed decline in podocyte growth after Coq6 knockdown is caused, at least in part, by increased apoptosis. Since mitochondria-induced apoptosis is associated with depolarization of the inner mitochondrial membrane (32) as well as caspase-9 activation (30), it is likely that lack of growth upon Coq6 knockdown is caused by activation of the intrinsic apoptotic pathway. Because some of the SRNS patients in our study that carry COQ6 mutations responded partially to CoQ10 treatment, we then analyzed whether CoQ10 has a beneficial effect on the phenotype caused by knockdown...
of Coq6 expression in podocytes in vitro. When culturing podocyte clones 1, 2, and 5 in the presence of CoQ₁₀ at a concentration of 50 μM for 48 hours, we observed a decrease in caspase-9 and caspase-3 activities (Figure S5, B and C). Compared with clones cultured in the absence of CoQ₁₀, this decrease was statistically significant (P < 0.05), whereas we did not detect any changes in caspase activities of negative control clones (Figure S5, B and C).

To examine COQ6 loss of function in a vertebrate organism rather than cell lines, we performed morpholino oligonucleotide (MO) knockdown of coq6 in zebrafish. We demonstrate that coq6-MO4 MOs directed against zebrafish coq6 intron 7 splice donor blocked proper splicing of coq6 mRNA (see Supplemental Figure 1N). Negative controls were injected with 0.1 mM coq6 mismatch MO. Note the gray appearance of zebrafish heads upon differential interference contrast (DIC) microscopy as a sign of increased cell death. (E and F) Zebrafish dorsal head and lateral trunk views. Embryos were injected as indicated with 0.1 mM coq6-MO4 splice targeting MO (E), MO targeting the AUG translation start site (dcoq6 MO1; F), coq6 mismatch (mm) MO negative controls, or left uninjected (WT). Cells were stained by an antibody against cleaved caspase-3, a specific marker for apoptotic cells. Lens (asterisk), yolk sac (ys), and cloaca (arrow) are indicated. Scale bars: 1 mm (D); 100 μm (E and F).

**Figure 5**

COQ6 knockdown causes apoptosis in podocytes and zebrafish embryos. (A–C) Coq6 downregulation in cultured mouse podocytes induced apoptosis that was diminished by CoQ₁₀ treatment. Data are mean ± SEM. (A) Growth curve analysis of Coq6 knockdown clones. 20,000 podocytes were seeded per 24-well plate, plated, detached, and counted (n = 4). (B and C) Caspase-9 (B) and caspase-3 (C) activity in undifferentiated Coq6 knockdown clones by FIENA before and after CoQ₁₀ treatment. RFUs derived from cleaved capase-9 or capase-3 substrate peptide were measured in lysates from 1 × 10⁶ cells (n = 3). C, control clone; No Tx, no treatment. *P < 0.001, †P < 0.05 versus control; ‡P < 0.005, §P < 0.05 versus untreated. (D–F) coq6 knockdown in zebrafish embryos 28 hours after fertilization increases apoptosis. (D) coq6-MO4 directed against zebrafish coq6 intron 7 splice donor blocked proper splicing of coq6 mRNA (see Supplemental Figure 1N). Negative controls were injected with 0.1 mM coq6 mismatch MO. Note the gray appearance of zebrafish heads upon differential interference contrast (DIC) microscopy as a sign of increased cell death. (E and F) Zebrafish dorsal head and lateral trunk views. Embryos were injected as indicated with 0.1 mM coq6-MO4 splice targeting MO (E), MO targeting the AUG translation start site (dcoq6 MO1; F), coq6 mismatch (mm) MO negative controls, or left uninjected (WT). Cells were stained by an antibody against cleaved caspase-3, a specific marker for apoptotic cells. Lens (asterisk), yolk sac (ys), and cloaca (arrow) are indicated. Scale bars: 1 mm (D); 100 μm (E and F).
of COQ6 mutations is remarkably similar to that of mutations in COQ2 (23) and PDSS2 in humans (34) and Pds2 in mice (24), all of which respond to CoQ10 treatment (12, 35). Patients with defects in genes required for CoQ10 biosynthesis—PDSS2, COQ2, and COQ9—exhibit renal disease, and in some cases there is a dramatic response to CoQ10 therapy, but this is quite variable (36).

**Discussion**

In this study, we report what we believe to be a novel cause of SRNS that appears to respond to oral CoQ10 supplementation. CoQ10, an essential component of the mitochondrial electron transport chain and one of the most potent lipophilic antioxidants (37), is also required for pyrimidine nucleoside biosynthesis and has been implicated in the inhibition of apoptosis by its prevention of inner mitochondrial membrane collapse (38). In multiple studies, the deleterious effect of CoQ10 deficiency to mitochondria has been shown. CoQ10 deficiency can lead to the opening of the mitochondrial permeability transition pore (MPTP) directly, but an increased amount of ROS caused by CoQ10 deficiency can also induce the MPTP by opening of nonspecific high-conductance permeability transition pores in the mitochondrial inner membrane (39). Experiments in HEK293 cells recently showed that CoQ10 inhibits Bax-induced mitochondrial dysfunction and protects mitochondria from permeability transition pore opening (9). Here, we confirmed that COQ6 mutations that cause CoQ10 deficiency led to the upregulation of proapoptotic factors. Interestingly, CsA inhibits the MPTP through interaction with cyclophilin D, an essential component of the MPTP (40). We showed that incubation of COQ6 knockdown podocytes with CsA had a mild rescue effect and decreased activity of caspase-3. Patient A1072-22, who had been treated with CsA in the past, also showed partial remission of proteinuria after treatment with CsA.

Mutations in 5 other CoQ10 biosynthesis enzymes leading to CoQ10 deficiency have been recently implicated in other monogenic mitochondrialopathies, generally characterized by central nervous system signs and myopathy (22, 34, 41–43); 1 patient with mutations in PDSS2 and 5 patients with mutations in COQ2 also presented with SRNS (22, 34, 43). So far, the exact pathogenic mechanism has remained unclear. Interestingly, 1 patient with mutations in COQ2 was successfully treated with oral CoQ10 supplementation, showing progressive recovery of renal function and a reduced level of proteinuria until 5 years after completion of treatment (22). The podocyte-specific phenotype caused by PDSS2 mutations leading to primary CoQ10 deficiency was demonstrated in the Pds2 knockout mouse (24). Conditional knockouts targeted to renal tubular epithelium, monocytes, or hepatocytes did not show disease manifestation. It remains unclear why the podocyte in particular is affected by PDSS2-dependent CoQ10 deficiency.

Interestingly, the presentation of primary CoQ10 deficiency caused by genetic mutations is very heterogeneous. It seems that the mutations in PDSS2 and COQ2 are partial loss-of-function mutations. Therefore, the phenotypes (ATP synthesis, ROS production) may depend on the content of Q in the cell, which is determined by the severity of the mutation. Mutations in PDSS2, for example, cause reduced ATP synthesis in cultured fibroblasts, but no increase in ROS production, whereas mutations in COQ2 cause no difference in ATP synthesis in cultured fibroblasts, but increase ROS production (36). One could speculate that different cell types and/or tissues react differently to ROS and ATP synthesis defects according to their antioxidant defense mechanisms or the level of respiratory activity, explaining the wide spectrum of clinical features. Based on the surprising Golgi localization of COQ6, COQ7, and COQ9, we speculate that the antioxidant function of Q/SH2 in certain cells, such as podocytes, may depend on targeted synthesis of CoQ in the Golgi for delivery to the plasma membrane, which in the podocyte constitutes an enormous surface area that must contain vulnerable lipid components. Whereas most other forms of monogenic childhood NS are characterized by a lack of response to therapy (10, 16, 17, 44), the identification by mutation analysis of individuals with NS caused by CoQ10 biosynthesis defects, as described here, is important because those individuals may respond to treatment with CoQ10.

**Methods**

**Subjects**

We obtained blood, tissue samples, and pedigrees following informed consent from individuals with NS and/or from their parents. Human subject research was approved by the University of Michigan Institutional Review Board. The diagnosis of NS was made by a pediatric nephrologist based on either chronic or recurrent high-grade proteinuria (>40 mg/m²/h) or persistent low-grade proteinuria (>4 mg/m²/h) (45). Steroid-sensitive NS and SRNS were defined according to standard criteria (45, 46). Renal biopsies were evaluated by a reference renal pathologist. Age at onset of ESRF was defined as age at first renal replacement therapy, i.e., dialysis or renal transplantation. Clinical data were obtained using a standardized questionnaire (www.renalgenes.org).

**Genetic mapping and exon sequencing**

We performed a genome-wide search for linkage by homozygosity mapping using the 250k Affymetrix SNP microarray (47). Data were evaluated by calculating nonparametric lod scores and scoring for homozygosity (Zₜₘₜ) across the whole genome in order to identify regions of homozygosity. The GENEHUNTER-MODSCORE program (48) was used to calculate multipoint lod scores assuming recessive inheritance with complete penetrance, a disease allele frequency of 0.001, and the marker allele frequencies for individuals of mixed European descent specified by Affymetrix. Parametric and nonparametric lod scores were plotted over genetic distance across the entire human genome using GENEHUNTER-MODSCORE (http://www.genehunter.info/). See Supplemental Table 2 for exon sequencing primers.

**COQ6 mRNA expression**

The probe for human Northern blot analysis was obtained by digesting the COQ6 isoform a coding region cloned into pCRITOFPO with EcoRI and was radiolabeled with α-³²P dCTP (Amersham Biosciences) using the Random Primers DNA Labeling System kit (Invitrogen) and successively purified with QuickSpin columns (Roche) according to the manufacturer’s protocol. Radiolabeled probes were hybridized to a commercial preblotted membrane (FirstChoice Human Blot 1 membrane; Ambion) containing 2 μg/lane poly(A)⁺ RNA from 10 human tissues. Prehybridization and hybridization were both performed in a 50% formamide buffer at 42°C, with a working concentration of 1.5 × 10⁶ cpm and 0.1 mg salmon sperm DNA per milliliter. The excess probe was removed by washing at 65°C for 15 minutes using a 0.1% SDS, 0.1x sodium chloride–sodium citrate buffer solution. Radioactivity was detected with a Storm PhosphorImager (Molecular Dynamics) after overnight exposure. Selective amplification of COQ6 isoform b was carried out using primers in exon 1b and in exon 4. Simultaneous amplification of isoform a and isoform b was carried out using primers on exon 2 and on exon 4. PCR conditions were 94°C for 3 minutes followed by 35 cycles of 94°C for 30 seconds,
55°C for 30 seconds, and 72°C for 30 seconds and a final extension step of 72°C for 7 minutes. Amplified fragments were also purified from agarose gel and sequenced. Primer sequences were as follows: exon 1b forward, 5′-TCTAGCTTTGGCGTCTGTT-3′; exon 2 forward, 5′-CTTCTAAGGTTTATATATATATATTCAATCGAAG-3′; exon 4 reverse, 5′-CTTCTG-GATCCATGATGACATCATTCT-3′.

Generation of plasmids
Yeast COQ6 was amplified from genomic DNA extracted from a WT BY4741 strain and cloned in pCM189 vector. Site-specific mutagenesis was performed using the QuickChange kit (Stratagene) according to the manufacturer’s protocol. To generate constructs that expressed the gene under the control of the endogenous yeast coq6 promoter, the different pCM189–yeast COQ6 constructs were digested with SacI and MscI (to eliminate the CYC1 promoter and control elements); religated with a fragment encompassing the yeast COQ6 promoter, the 5′ end of the gene, and the MscI site; amplified from genomic DNA; and cut accordingly. Plasmid maps were described previously (49). Yeast growth and transformation were performed as described below.

COQ6-GFP expression studies
The complete coding region of full-length human COQ6 isoform a, lacking termination codon but including the Kozak sequence, was PCR amplified from pCRITTOPO-COQ6 and subcloned into the HindIII and BamHI sites of pEGFP-N1 (BD Biosciences — Clontech). The correctness of the construct was verified by direct sequencing. HeLa cells stably expressing mitochondrially targeted red fluorescent protein (50) were grown on coverslips in complete DMEM (Sigma-Aldrich) containing 10% fetal bovine serum until 70% confluent, then transfected with the purified plasmid using Effectene Transfection Reagent (Qiagen) according to the manufacturer’s instructions. Cells were visualized after 48 hours using a Nikon Video Confocal microscope.

In situ hybridization analysis in mice
Whole-mount in situ hybridization was performed following a standard procedure with digoxigenin-labeled antisense riboprobes (51). Stained specimens were transferred in 80% glycerol prior to documentation. In situ hybridization on 10-μm paraffin sections was done as described previously (52).

Immunofluorescence
Rat kidneys were perfusion-fixed with paraformaldehyde/lysine/periodate bath. Thereafter, the COQ6 expression was stained with an antibody (rat anti-GFP, Sigma-Aldrich) and visualized using a confocal microscope.

Yeast studies
Yeast growth. The S. cerevisiae coq6-null mutants W303ΔG63 (Mat α ade2-1 his 3-1,15 leu2-3,112 trpl-1 ura3-1 ΔCOQ6-HIS3; ref. 18) and W303ΔCOQ8 (Mat α ade2-1 his 3-1,15 leu2-3,112 trpl-1 ura3-1 ΔCOQ8-HIS3; ref. 54) were used in this study. Yeast growth media were prepared as described previously (55): YPD, containing 1% yeast extract, 2% peptone, and 2% dextrose; YPGal, containing 1% yeast extract, 2% peptone, 2% galactose, and 0.1% dextrose; YPG, containing 1% yeast extract, 2% peptone, and 3% glycerol; and SD-Ura, containing 0.18% nitrogen base without amino acids, 2% dextrose, 0.14% NaH₂PO₄, 0.5% (NH₄)₂SO₄, and a complete amino acid supplement (56), minus uracil. Solid plate media contained 2% agar.

Yeast transformation. Yeast was subjected to transformation as described previously (57), with either a low-copy number (pQM; ref. 58) or a high-copy number (pRCM; ref. 59) yeast expression plasmid. These vectors were used to prepare plasmids containing the human COQ6 open reading frame with an in-frame aminoterminal yeast mitochondrial leader sequence (pQM_hCOQ6-MLS and pRCM_hCOQ6-MLS). Each of the following mutations in human COQ6 were introduced by site-directed mutagenesis (Stratagene): R162X, W188X, G255R, A335D, W447X, and Q461fsX478. See Supplemental Table 1 for a complete list of plasmids used in yeast transformation experiments.

Lipid extraction and analysis. Yeast cells were grown in YPGal and harvested during log phase growth (1.0 OD₆₀₀nm). Lipid extracts were prepared from yeast whole cells as described previously (60). Lipids were separated by reverse-phase high-performance liquid chromatography with a Phenyl-hexyl column (Phenomenex 5-μm, 100 × 4.6 mm). The column was equilibrated with a mobile phase consisting of 95:5 methanol/2-propanol with 2.5 mM ammonium formate as solvent A and a flow rate of 650 μl/min. Upon sample injection, the percentage of solvent B (2-propanol with 2.5 mM ammonium formate) was increased linearly from 0% to 5% over 6 minutes, and the flow rate was also increased linearly to 800 μl/min. The flow rate and mobile phase were linearly changed back to initial conditions by 8 minutes. Q was quantified with an Applied Biosystems-MDS Sciex 4000 Q Trap (hybrid triple-quadrupole linear ion trap analyzer with autosampler and a Turbo-V source equipped with ESI and APCl sources) as described previously (35). The samples were analyzed in multiple reaction monitoring (MRM) mode; MRM transitions were as follows: m/z 591.6/197.1 for Qc; m/z 610.6/197.1 for Qh; with ammonium adduct; m/z 455.6/197.1 for Qa (Sigma-Aldrich), used as internal standard.

Podocyte expression studies
Preparation of CoQ₉₄ solution for use in cell culture. Pure CoQ₉₄ in powder form (Kaneka Corp.) was dissolved in 1 mL of molecular biology-grade isopropanol at a concentration of 10 mM by heating it briefly in a 95°C water bath. Thereafter, the CoQ₉₄ solution was diluted 1:10 in podocyte culture media to a final stock concentration of 1 mM and reheated for an additional 5 minutes at 95°C with gentle shaking. This CoQ₉₄ stock solution was stored at 4°C, protected from light for up to 4 weeks, and diluted immediately before use at 1:20 in cell culture medium to a final working concentration of 50 μM.

Podocyte culture. Immortalized murine podocytes were cultured as described previously (29). For treatment studies of undifferentiated podocytes, cells were cultivated in the presence of 50 μM CoQ₁₀, 1 μM dexamethasone (Sigma-Aldrich), or 1 μM CsA (Sigma-Aldrich) for 48 hours. For analysis of differentiated podocytes, undifferentiated podocytes were cultured under nonpermissive conditions in the presence of 1 μM dexamethasone for 14 days. Cultivation was then continued in the absence of dexamethasone for an additional 48 hours. For determination of cell number and growth curve analysis, cells were seeded in 24-well plates at 20,000 cells/well. After 24, 48, or 72 hours, cells were trypsinized and counted using a hemocytometer. Experiments were done 4 times with at least 3 independent replicates.

COQ6 RNAi
For the targeted downregulation of protein expression in podocytes, we used the pSuper RNAi System (OligoEngine) (28) following the manufacturer’s instructions and as done previously (61). Briefly, we cloned a 60-nt oligo including a 19-nt COQ6 target sequence and a hairpin (5′-TTCAGAGCAGC-ACATATAGTTGGCGTCTGTT-3′).
GA-3’) into a modified pSuper vector, which also encoded for a zeocin selection marker (61). After transfection of undifferentiated podocytes using FuGene 6 (Roche) followed by zeocin selection at 500 μg/ml for 7-10 days, appearing podocyte clones were covered by cloning chambers, trypsinized, and expanded separately from each other in culture medium containing 100 μg/ml of zeocin. In total, 5 different COQ6 targeting sequences were used (clone 1, AACAGATGCAGCTCTCATT; clone 2, AATGACGTCATCATG-TATG; clone 3, CTGGGCCAGATCGAAGTAA; clone 4, AACTGGTATGGTGTCGTGA; clone 5, AAGGATCGGCTCCATAGTA) as well as 1 scrambled control sequence (5’-CCGGCATCGCCCTGCTGGC-3’). Stable transfected clones were expanded and used for RNA isolation and functional studies.

RNA isolation and RT-PCR
RNA was isolated from 2 × 10^6 undifferentiated podocytes using the RNeasy kit (Qiagen) following the manufacturer’s protocol. Prior to RT-PCR, total RNA samples were digested with DNase I (Roche) and RNA was transcribed into cDNA using Superscript II (Invitrogen). For RT-PCR, 100 ng cDNA, AmpliTaq Gold DNA polymerase (Applied Biosystems), and sequence-specific, intron-spanning primers were used (COQ6 forward, CAGACACCGTGTACGACGTG; COQ6 reverse, CCAACAGCTTTGCTCTCAG; GAPDH forward, CATAGAG; GAPDH reverse, TATGTCGTGGAGTCTACTGG; GAPDH forward, TATGTCGTGGAGTCTACTGG; GAPDH reverse, AGTGTAGGCTAGCTCCATAT) as well as 1 scrambled control sequence (5’-CCGGCATCGCCCTGCTGGC-3’). Stable transfected clones were expanded and used for RNA isolation and functional studies.

To analyze changes in the ΔΨm of undifferentiated podocytes, we used TMRE (Invitrogen) as described previously (62). Briefly, 3 × 10^5 cells were trypsinized and incubated in 25 nM TMRE for 30 minutes at 37°C. The reaction was incubated at 95°C, 30 seconds at 53°C, and 30 seconds at 72°C) were run on a GeneAmp PCR System 9700 (Applied Biosystems). PCR reactions were analyzed on a 2% agarose gel, and ethidium bromide signals were captured with a Bio-Rad Gel Doc XR system.

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Zebrafish MO-mediated knockdown
MOs were obtained from Gene Tools. The nucleotide sequences of the translation-blocking (coq6-MO1) and splice-blocking (coq6-MO4) MOs against D. rerio coq6 were 5’-GCTTAGCTTTTACGCAGAGACGATC3’ and 5’-ACACATAAGGTCGCTCCGGAAAG-3’, respectively. The 5-bp mismatch controls for the MOs were as follows: coq6-MO1mm, 5’-GGTTACCTTTTACGCAGAGACGATC3’ and coq6-MO4mm, 5’-ACAATAAGGTCGCTCCGGAAAG-3’. Fertilized eggs were microinjected with the specified amount of MO dissolved in 0.1M KCl. For immunohistochemical labeling, embryos were fixed with 4% PFA in PBS (pH 7.4) and stained with antibody against activated caspase-3 (1:200; BD Biosciences) following standard protocols (63).

Statistics
To evaluate caspase-3 and -9 activity in cell lines, Pearson χ^2 test was used with a critical P value of 0.05 (Figure 5).

Databases
Genetic mapping was performed using http://genome.ucsc.edu (May 2004 freeze).

Accession numbers
Accession numbers of COQ6 orthologs were NP_872282 for Homo sapiens, NP_001038879 for D. rerio, and ZP_00723222 E. coli.

Acknowledgments
We thank the affected individuals and their families for participation. We thank Corina Năilescu for contribution of clinical data. This research was supported by grants from the NIH to F. Hildebrandt (DK076683 and DK086542), C.F. Clarke (GM45952), and R.C. Wiggins (DK46073 and P30 DK081943) and by a grant from the KMD Foundation and the Tharsher Research Fund to F. Hildebrandt. F. Hildebrandt is an Investigator of the Howard Hughes Medical Institute, a Doris Duke Distinguished Clinical Scientist, and the Frederick G.L. Huetwell Professor. H. Prokisch was supported by the Impulse and Networking Fund of the Helmholtz Association in the framework of the Helmholtz Alliance for Mental Health in an Ageing Society (HA-215), by the German Network for Mitochondrial Disorders (mitoNET 01GM0862 and 01GM0867), and by Systems Biology of Metabotypes (SysMBo 0315494A). The work was further supported by a grant from the German Research Foundation (DFG, SFB 423, TP B19) to M. Zenker, by the German Federal Ministry of Science and Education through the National Genome Research Network to G. Nürnberg and P. Nürnberg, by the European Community FP7 program (EUNEFRON 201590) to D. Müller, by Fondazione CARIPARO Telethon Italy (GGP09207) to L. Salvati, by a Spanish FIS grant (PI080500) to P. Navas, and by the Young Investigator Career Development Grant from the NephCure Foundation and the National Scientist Development Grant from the American Heart Association to C. Faul.

Received for publication November 6, 2010, and accepted in revised form February 9, 2011.

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