Molecular Analysis of Aquaporin Genes 1 to 4 in Patients with Menière’s Disease

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Abstract
Background: Menière’s Disease (MD) is an episodic cochleovestibular dysfunction of unknown etiology, still lacking a specific test and therapy. The proposed theories on the pathophysiology include genetic factors and factors relating to inner ear homeostasis. Various aquaporins (AQP), water channels, expressed in the inner ear and the vestibular organ, are involved in homeostasis. Mutations in AQP genes could result in disturbed inner ear homeostasis and endolymphatic hydrops, and therefore be involved in the pathogenesis of MD. Aim: To search for mutations in AQP1 to 4 in patients suffering from MD. Methods: In patients with definite MD, DNA was extracted from whole blood. The coding sequences of AQP1 to 4 were amplified by PCR reaction and sequenced. Results: One sequence alteration, homozygous c.105G->C (conservative change without alteration of amino acid) in AQP3 was detected in 11 out of 34 patients but not in 100 control chromosomes. Conclusion:

By itself the detected alteration is unlikely to play a role in the pathogenesis of MD. However, together with an additional modifying gene an effect can not be excluded. Additional regions (introns, splice-sites) and other genes involved in inner ear homeostasis need to be analyzed to identify a possible molecular alteration in MD.

Introduction

Menière’s disease (MD) is a cochleovestibular disorder characterized by the classic triad of episodic vertigo, tinnitus and fluctuating hearing loss. No specific diagnostic test exists. The etiology of MD remains unclear. The proposed theories on the pathophysiology of MD include, among others, genetic factors related to inner ear homeostasis [1-4]. The strong evidence of a genetic predisposition to
MD mainly stems from family studies with a reported incidence of 7%. An autosomal dominant inheritance with reduced penetrance and anticipation was described [1, 4, 5]. A potential candidate gene, COCH, has been excluded by sequence analysis [6]. Other genes, such as aquaporins (AQP) and potassium channels, playing a role in the control of intralabyrinthine fluid dynamics, have been proposed in the etiology of MD based on association and animal study [7, 8].

AQP, water channels as their name suggests, are integral membrane proteins, which selectively transport water and also some small solutes, such as glycerol, along the osmotic gradient. AQP are ubiquitous in flora and fauna. In humans 11 isoforms (AQP 0-10) are described with different distribution and individual mode of action [9]. In the mammalian inner ear AQP 0-6, 7 and 9 can be detected in different structures of the cochlea, the vestibular organ and the endolymphatic sac [7, 10-15]. Among the AQPs, isoforms 1-4 are the best studied in the inner ear and have been proposed to be involved in the pathophysiology of MD. AQP1 has been detected in the intermediate cells of the stria vascularis in rats and in nonsensory epithelial cells in the spiral ligament in humans [16-18]. Likewise, the immunolocalization of AQP4 in humans closely resembles the one seen in animal models [7, 17, 19]. AQP2, along with AQP3 and 4, is coexpressed in the endolymphatic sac [10]. The important role of these three inner ear structures, stria vascularis, spiral ligament and endolymphatic sac, for fluid movement in the inner ear has been demonstrated in guinea pigs and in vitro studies [20, 21]. AQP2 is of special interest with regard to MD. The application of both Lithium and OPC-31260, two vasopressin-antagonists, led to a down-regulation of AQP2-mRNA in the inner ear and reduced endolymphatic hydrops, the histopathologic hallmark of MD, in experimental studies [22, 23]. However, a mutation screen of AQP2 in 12 individuals with MD did not show any mutations within the four coding exons and their intron-exon junctions [14].

An additional line of evidence for the important role of AQPs in the inner ear stems from hearing research. AQP4 knockout and transgenic mice showed impaired hearing but normal neural conduction time. Therefore, cochlear dysfunction was suggested as the primary cause for hearing impairment in these mice [15, 19]. However, in other knockout mice lacking AQP1,3 and 5 auditory brainstem response thresholds were not increased [15].

For these reasons, AQP5 represent good candidate genes for an etiologic involvement in the pathophysiology of MD. Molecular changes in these genes might lead to a disturbed homeostasis and development of endolymphatic hydrops in MD. The aim of this study was to search for mutations in AQP isofoms 1-4 in patients with MD.

Materials and Methods

Patients

34 patients (18 males and 16 females) with “definite” MD were included in the study. Definite MD was defined according to the diagnostic scale set up by AAO/HNS. Other causes of cochleovestibular pathology or concomitant illnesses were excluded by a questionnaire. All participants signed an informed consent, according to guidelines approved by the Ethics Committee, University Hospital of Basel and Cantonal Hospital of Aarau, before entering the study.

Aquaporin mutation analysis

Genomic DNA was isolated from a 5mL EDTA blood sample using the Qiamp DNA Blood Maxi Kit (Qiagen, Basel, Switzerland) according to the manufacturer’s instructions. The following primers were used to amplify the coding exons and intron-exon junctions of AQP1 to 4 (genbank accession no. NM_198098, NM_012909, NM_001079794, NM_001650):

AQP1-F(forward) (Exon 1); 5’GCT CCT CTC AGA GGG AAT TGA GC3’
AQP1-R(reverse) (Exon 1); 5’AAC CAG TGC TTT GGC CAG CTT GT3’
AQP1-F(forward) (Exon 1); 5’GCT CTC AGA GGG AAT TGA GC3’
AQP2-F(forward) (Exon 1); 5’CCT GCC TGT TCT TCT TCC TG3’
AQP2-R(reverse) (Exon 1); 5’ATT CCT GCC CTT TCT TCT TCT 3’
AQP2-F(forward) (Exon 2); 5’GCA CGT GGG AAA AAC CTG T3’
AQP2-R(reverse) (Exon 2); 5’GTG TCT CAC CGT TGG GCC CAG T3’
AQP2-F(forward) (Exon 3); 5’ATC CCT GCC CCT TCC TCT TCT T3’
AQP2-R(reverse) (Exon 3); 5’ATC CCT GCC CCT TCC TCT TCT T3’
AQP2-F(forward) (Exon 4); 5’AGT GAC TTT GGC CAG CTT GT3’
AQP2-R(reverse) (Exon 4); 5’AGT GAC TTT GGC CAG CTT GT3’

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AQP3-R (Exon 4): 5’CCA TGA GCT ACC AAG GCA AC3’
AQP3-F (Exon 5/6): 5’TGC AGC TCA CCC TGT TCT C3’
AQP3-R (Exon 5/6): 5’GGA CAG TCA GTG GAT GCT CA3’
AQP4-F (Exon 1); 5’CAG GCA ATG AGA GCT GCA C3’
AQP4-R (Exon 1): 5’TGC CTA AGA AGG CAC AAA CA’
AQP4-F (Exon 2): 5’CCT GGG TGT AGT GGC TTC TG3’
AQP4-R (Exon 2): 5’TGC AAG AAG CTT GGA GTC CT3’
AQP4-F (Exon 3/4): 5’CTC TTG CTT CAA TTC TGA TGG A3’
AQP4-R (Exon 3/4): 5’CTGTAGGAAGATGGGAACTATCA3’
AQP4-F (Exon 5): 5’GC TGC TCA ATG GAA TAG CTT 3’
AQP4-R (Exon 5): 5’TGG AAG GAA ATC TGA GGA CAG 3’

PCR conditions were as follows: AQP 1 (Exon 1-4), AQP 2 (Exon 1-4): initial denaturation at 94 °C for 10 minutes; 40 cycles at 94 °C for 15 seconds, 58 °C for 20 seconds and 72 °C for 40 seconds; final elongation at 72 °C for 4 minutes.

The annealing temperatures for AQP 3 (Exon 2-6) and AQP 4 (Exon 1-5) were 56 °C. The PCR was carried out on an Eppendorf Mastercycler Gradient (Vaudaux-Eppendorf, Basel, Switzerland).

For DNA sequencing, PCR products were purified using the QIAquick PCR Purification kit (Qiagen, Basel, Switzerland). The sequencing reaction was performed using the Big Dye Terminator Cycle Sequencing kit (Applied Biosystems, Rotkreuz, Switzerland), according to the manufacturer’s guidelines. After purification using the DyeEx 2.0 Spin Kit (Qiagen, Basel, Switzerland) sequencing products were analyzed on an ABI PRISM 310 Genetic Analyzer (Applied Biosystems, Rotkreuz, Switzerland). Each fragment was sequenced twice following independent PCR amplification to assure accurate sequence results. The sequences were analyzed using the Sequencher 4.0 software (Gene Codes Corporation, Ann Arbor, MI).

Results

Patients

The mean age at onset of disease was 45 (range 24 to 65). The mean duration was 10 years (2-28).

The majority of patients were sporadic cases and suffered from unilateral disease. Family history was positive in 4 cases. The whole frequency range was affected in most patients with at least moderate severity. For the patients where data was available, working status was normal in about 80% (Table 1).

Mutation analysis

Mutation analysis of AQP subtypes 1-4 revealed one sequence alteration in the coding sequences and intron-exon junctions of these genes after comparison with the published cDNA sequences. The homozygous change c.105G->C (p.L35L) in exon 1 of AQP3 was found in 11 patients (Fig. 1). It was not detected
in 100 control chromosomes and represents a novel variant. As it is not altering the amino acid, it was classified as a conservative change.

Discussion

Menière’s disease is suggested to be of multifactorial origin, with one of the contributing factors being genetic [4, 7]. The distribution of AQPs in the cochlea and vestibular system, their known role as transporters of water and small solutes, the ability of vasopressin to induce endolymphatic hydrops are indicative of a possible role of AQPs in MD [7]. This study analyzed the coding sequences of the AQP isoforms 1-4 in patients with MD, the majority being sporadic cases. After sequencing analysis of the coding regions and exon–intron boundaries one single variation, c.105G->C, in AQP 3 was found in 11 patients (32%). Although this percentage is intriguingly high, the amino-acid is not changed and therefore a mutational role must be considered with caution. However, it is possible that protein structure is slightly altered, that together with a modifying gene the function of AQP3 is changed in a way, which leads to development of endolymphatic hydrops. The existence of a modifying gene would also explain the high clinical variability seen in patients with MD. Nevertheless, without functional analysis, which is difficult to perform in this context, this proposal remains a supposition. The selection of the patients was done with great care to achieve a homogenous sample size. However, it is possible that protein structure is slightly altered, that together with a modifying gene the function of AQP3 is changed in a way, which leads to development of endolymphatic hydrops. The existence of a modifying gene would also explain the high clinical variability seen in patients with MD. Nevertheless, without functional analysis, which is difficult to perform in this context, this proposal remains a supposition. The selection of the patients was done with great care to achieve a homogenous sample size. However, it is possible that, in view of the lack of specific diagnostic tests, some patients might be wrongly classified as having MD. These patients will not necessarily exhibit genetic alterations. This might explain the number of patients in this study without the c.105G->C variation.

No other mutation was found in any of the patients. One explanation might be the fact that we cannot exclude either mutations in the cis transcription regulatory elements or promoter region, nor possible cryptic splice-site mutations. Splice-site mutations in the inner ear, for example, have been described for Pendrin, a deafness gene causing Pendred syndrome and enlarged vestibular aqueduct [24]. Also, in AQP3 deficient humans, a homozygous transition in the 5’-donor splice site of intron 5 leading to the skipping of exon 5 has been found [25]. Other mutational mechanisms have been described for the AQP genes 1 and 2. In AQP1, three individuals have been found with nonsense and missense mutations, encoding a nonfunctioning molecule but no obvious clinical defect [26]. Still, the total deficiency of AQP1 has been studied and subtle evidence for shortened red cell life span and reduced membrane surface area has been observed [27]. Additionally, AQP1-null individuals have limited capacity to concentrate urine [28]. Over 30 mutations in AQP2 play a role in autosomal-recessive or autosomal-dominant nephrogenic diabetes insipidus (OMIM 222000 and 125800, respectively) [29]. Typically, missense mutations and small deletions have been found. In most cases, these AQP2 mutant proteins are misrouted and cannot be expressed at the luminal membrane [30]. However, Goji et al. reported non-functional channels not impaired in their routing to the plasma membrane [31]. In this study, sequencing analysis would have detected these types of mutations. In addition, homozygous deletions can be ruled out, as all exons of AQP 1-4 could be amplified in all patients. A possible effect of the published mutations on hearing and balance cannot be evaluated, as neither hearing status nor vertigo have been described or measured in the patients with reported mutations in AQP1-3.

Quantitative differences in the expression of the different aquaporin subtypes as well as mutations in other - not yet analyzed - subtypes of AQPs might contribute to MD. The complex function of AQPs has been shown for the cochlea by Huang et al. [12]. The cellular localization and developmental expression were studied. The region-specific expression of AQPs have suggested compensatory and parallel pathways for water transport in the inner ear. The divergent expression might point to a concerted action of AQPs to maintain fluid regulation in the inner ear. The interaction and the high functional complexity of AQPs underlie the difficulty in studying a possible involvement of AQPs in human diseases. Further molecular-genetic research must be performed before a definitive statement concerning a possible etiologic role in MD can be made.
Conclusions

The evidence from expression and functional studies points to a clear involvement of AQP genes in inner ear homeostasis. The detection of a conservative change in AQP3 in about a third of patients suffering from MD in this study and its absence in controls might be a first indication of a possible involvement of AQP3s in the development of MD. But the definite role of AQP3s remains to be elucidated.

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References


