LETTER TO JMG

Development of a genotyping microarray for Usher syndrome

Frans P M Cremers, William J Kimberling, Maigi Külm, Arjan P de Brouwer, Erwin van Wijk, Heleen te Brinke, Cor W R J Cremers, Lies H Hoefsloot, Sandro Banfi, Francesca Simonelli, Johannes C Fleischhauer, Wolfgang Berger, Phil M Kelley, Elene Haralambous, Maria Bitner-Glindzicz, Andrew R Webster, Zubin Saihan, Elfride De Baere, Bart P Leroy, Giuliana Silvestri, Gareth J McKay, Robert K Koenekoop, Jose M Millan, Thomas Rosenberg, Tarja Joensuu, Eeva-Marja Sankila, Dominique Weil, Mike D Weston, Bernd Wissinger, Hannie Kremer

J Med Genet 2007;**44**:153–160. doi: 10.1136/jmg.2006.044784

Background: Usher syndrome, a combination of retinitis pigmentosa (RP) and sensorineural hearing loss with or without vestibular dysfunction, displays a high degree of clinical and genetic heterogeneity. Three clinical subtypes can be distinguished, based on the age of onset and severity of the hearing impairment, and the presence or absence of vestibular abnormalities. Thus far, eight genes have been implicated in the syndrome, together comprising 347 protein-coding exons.
Methods: To improve DNA diagnostics for patients with Usher syndrome, we developed a genotyping microarray based on the arrayed primer extension (APEX) method. Allele-specific oligonucleotides corresponding to all 298 Usher syndrome-associated sequence variants known to date, 76 of which are novel, were arrayed.
Results: Approximately half of these variants were validated using original patient DNAs, which yielded an accuracy of >98%. The efficiency of the Usher genotyping microarray was tested using DNAs from 370 unrelated European and American patients with Usher syndrome. Sequence variants were identified in 64/140 (46%) patients with Usher syndrome type I, 45/189 (24%) patients with Usher syndrome type II, 6/21 (29%) patients with Usher syndrome type III and 6/20 (30%) patients with atypical Usher syndrome. The chip also identified two novel sequence variants, c.400C>T (p.R134X) in *PCDH15* and c.1606T>C (p.C536S) in *USH2A*.
Conclusion: The Usher genotyping microarray is a versatile and affordable screening tool for Usher syndrome. Its efficiency will improve with the addition of novel sequence variants with minimal extra costs, making it a very useful first-pass screening tool.

Key points

- We developed a genotyping microarray for Usher syndrome based on the arrayed primer extension (APEX) method, which includes 298 Usher syndrome-associated sequence variants identified in eight genes. Seventy six variants have not been reported previously.
- Validation of half of these variants employing DNAs from the original Usher syndrome patients yielded a microarray accuracy of >98%. The efficiency of the microarray was analysed using DNAs from 370 novel unrelated Usher syndrome patients. Sequence variants were identified in 46% of patients with Usher syndrome type I, 24% of patients with Usher syndrome type II, 29% of patients with Usher syndrome type III and 30% of patients with atypical Usher syndrome.
- We conclude that this genotyping microarray represents a versatile and affordable screening tool for Usher syndrome. Its efficiency will improve with the addition of novel sequence variants with minimal extra costs, making it a very useful first-pass screening tool.

Patients with Usher syndrome (MIM 276900-2, MIM 276905, MIM 605472) have autosomal recessive retinitis pigmentosa (arRP) and sensorineural hearing impairment. In addition, vestibular dysfunction can be seen in a subset of patients. Usher syndrome occurs in ~1/20 000 individuals and represents 50% of all cases with deafblindness.[1–3] Three clinical subtypes can be distinguished.[4] Patients with Usher syndrome type I (USH1) show severe to profound congenital hearing loss, RP and vestibular areflexia. Patients with Usher syndrome type II (USH2) have moderate to severe hearing loss, RP and normal or variable vestibular function (Huygen *et al*, unpublished data). Usher syndrome type III (USH3) patients present with progressive hearing loss, RP and variable vestibular function. The eight genes known to be involved in Usher syndrome are *CDH23*, *MYO7A*, *PCDH15*, *USH1C* and *USH1G* for USH1, *USH2A* and *VLGR1* for USH2, and *USH3A* for USH3.[5–15] The *USH2A* gene is also implicated in arRP.[16–18] Likewise, mutations in *CDH23*, *MYO7A*, *PCDH15* and *USH1C* have been reported in patients with non-syndromic hearing impairment.[7 12 19–22]

Identification of the causal mutations is important for the early diagnosis of Usher syndrome, which is relevant for the decision whether or not to elect for a cochlear implant, for genetic counselling and for prenatal diagnosis. In addition, gene-specific treatments might become available in the near

Abbreviations: APEX, arrayed primer extension; arRP, autosomal recessive retinitis pigmentosa; RP, retinitis pigmentosa; SSCP, single strand conformation polymorphism; USHA, atypical USH; USH, Usher syndrome

Table 1 Characteristics of Usher genes

Gene	Protein coding exons	Amplicons for APEX analysis	Known pathologic variants
USH1			
CDH23	69	32	52
MYO7A	48	39	118
PCDH15	32	6	7
USH1G	2	2	4
USH1C	28	6	8
USH2			
USH2A	72	26	88
VLGR1	90	6	6
USH3			
USH3A	6	3	9
Total	347	120	292

future, necessitating knowledge of the underlying gene defect. Comprehensive molecular diagnostics for Usher syndrome has been hampered both by the genetic heterogeneity and the large number of exons for six of the eight known Usher genes. The five USH1 genes collectively contain 179 protein-coding exons, the two USH2 genes comprise 162 protein-coding exons, and the USH3 gene *USH3A* has six protein-coding exons, some of which are alternatively spliced (UCSC Human Genome Browser at http://genome.cse.ucsc.edu). Thus far, large-scale mutation screening has been carried out using single strand conformation analysis and denaturing gradient gel electrophoresis, with subsequent sequence analysis of fragments with an aberrant migration pattern. For routine analysis, these techniques are both time consuming and expensive.

In this study, we used microarray technology that was previously used for efficient mutation analysis of the *ABCA4* gene in patients with either autosomal recessive Stargardt disease or autosomal recessive cone-rod dystrophy,[23 24] as well as for seven genes implicated in Leber congenital amaurosis (LCA).[25 26] It is inherent to the arrayed primer extension (APEX) that it detects only known mutations and, therefore, its efficiency is highly dependent on the extent of earlier mutation analysis efforts. Here, we describe the first comprehensive Usher genotyping microarray which allows the identification of known Usher gene defects in a high-throughput and cost-effective manner.

METHODS

Patients

For validation purposes, we obtained genomic DNA from 158 patients with Usher syndrome in which the variants were originally identified. In order to test the efficiency of the Usher microarray (hereafter denoted ''evaluation''), 370 patients were studied. Of these, 170 unrelated Usher syndrome patients were ascertained in seven European countries: Belgium (20 patients), Denmark (10 patients), UK (34 patients), Germany (27 patients), Italy (20 patients), Spain (5 patients), Switzerland (7 patients) and the Netherlands (47 patients). A further 200 patients from the USA (Boys Town, Omaha) were ascertained. In total, we tested DNAs from 140 patients with USH1, 189 patients with USH2, 21 patients with USH3 and 20 patients with atypical Usher syndrome (USHA). The patients, except for 104 USH2 patients from the USA who were previously shown not to carry the *USH2A* c.2299delG (p.E767fs) mutation, had not been previously tested for the presence of Usher mutations. Research procedures were in accordance with institutional guidelines and the Declaration of Helsinki. Informed consent was obtained at each centre from all patients after the nature of procedures to be performed was fully explained.

Molecular methods

Microarrays were designed and manufactured according to arrayed primer extension (APEX) technology.[27 28] A detailed description of the methodology can be found elsewhere (www.asperbio.com).[29 30] In brief, 5′-modified sequence-specific oligonucleotides are arrayed on a glass slide. In general, these oligonucleotides are designed with their 3′ end immediately adjacent to the variable site. PCR-amplified and fragmented target nucleic acids are annealed to oligonucleotides on the slide, followed by sequence-specific extension of the 3′ ends of primers with dye-labelled nucleotide analogues (ddNTPs) by DNA polymerase. The APEX reaction is, in essence, a sequencing reaction on a solid support.

A total of 120 amplicons from eight genes (table 1) were amplified as described previously.[23] Primer sequences are available on request. In the amplification mixture, 20% of the dTTP was substituted by dUTP.[29] The amplification products were concentrated and purified (GENErALL PCR kit; General Biosystems, Seoul, Korea). The fragmentation of amplification products was achieved by adding thermolabile uracil *N*-glycosylase (Epicenter Technologies, Madison, WI) and heat treatment.[29] One-sixth of every amplification product was used in the primer extension reaction on the Usher microarray. Each APEX reaction consisted of fragmented and pooled denatured PCR products, 4 U Thermo Sequenase DNA Polymerase (Amersham Biosciences, Little Chalfont, UK), 1× reaction buffer and 1.4 μM final concentration of each fluorescently labelled ddNTP: Texas Red-ddATP, fluorescein-ddGTP (Amersham Biosciences), Cy3-ddCTP and Cy5-ddUTP (NEN, Boston, Massachusetts, USA). The reaction mixture was applied to a microarray slide for 15 min at 58℃. The reaction was stopped by washing the slide at 95℃ in Milli-Q water.[31] The slides were imaged with the Genorama QuattroImager (Asper Biotech, Tartu, Estonia) and the sequence variants were identified by Genorama Genotyping software (Asper Biotech).[23 30]

Array-identified variants were confirmed by direct sequencing with the ABI PRISM Big Dye Terminator Cycle Sequencing V2.0 Ready Reaction Kit and the ABI PRISM 3730 DNA analyser (Applied Biosystems, Foster City, California, USA).

RESULTS

Construction of the Usher genotyping microarray

We compiled a list of 298 previously published and communicated sequence variants from the coding region and adjacent intronic sequences of the eight Usher genes: *CDH23*, *MYO7A*, *PCDH15*, *USH1C*, *USH1G*, *USH2A*, *USH3A* and *VLGR1* (see supplementary table 1 available at http://jmg.bmj.com/supplemental). Intronic sequence variants were included when they were predicted to affect splicing, that is, altering the strictly conserved splice site sequences (nucleotides −2A or −1G of 3′ splice sites; nucleotides +1G or +2T of 5′ splice sites), causing transversion of one or a few of the pyrimidines (−5 through −14) of a 3′ splice site, changing a −3C nucleotide of a 3′ splice site, changing a +3, +4, +5 or +6 nucleotide of a 5′ splice site, or exonic nucleotides being part of splice sites, to a less favourable nucleotide. In addition, we included the putatively benign sequence variants c.5156A>G (p.Y1719C) in *MYO7A* and c.688G>A (p.V230M), c.1434G>C (p.E478D), c.2052A>G (p.Q684Q, possible cryptic splice site), c.2137G>C (p.G713R) and c.2522C>A (p.S841Y) in *USH2A*. Each sequence variant was queried in duplicate by the software, from both the sense and the antisense strand (Genorama Genotyping software).

We also included four variants on the chip despite the fact that there are inconsistencies in their notations in the original publications or erroneous genomic sequence data: *CDH23* c.3880>T (p.Q1294X),[12] *MYO7A* c.269G>C (p.R90P),[32] *MYO7A* c.4039_4053del (p.R1347_F1351del),[33] and *USH2A* c.233T>G (p.F78V). The *USH1C_ABCC8* 122 815-bp deletion[7] is not represented on the chip.

Validation of the Usher genotyping microarray

We collected DNA samples from 158 patients with Usher syndrome and at least one known variant. All variants, except two, *CDH23* c.3617C>G and *MYO7A* c.223delG, were reliably identified. For the two unidentified variants (false negatives), primers have been redesigned and will be retested (see supplementary table 1 available at http://jmg.bmj.com/supplemental). For the remaining 140 variants, no DNA samples from the original patients were available as positive controls. However, the wild-type sequences of these variants were robustly identified. Since 102 of these variants represent nucleotide substitutions, the identification of the wild-type sequence can be regarded as a positive control since the same 25 mers are employed for the identification of both the wild-type and mutant nucleotides. However, we cannot exclude the possibility of erroneous sequence variant annotations, which we observed for a number of mutations in the respective original publications. Thirty eight non-validated variants represent insertions/deletions for which in some instances oligonucleotides linked to the microarray for detection of the wild-type allele differed from that for detection of the mutant allele.

Evaluation of the Usher genotyping microarray

The efficiency of the Usher microarray was evaluated using a total of 370 patients: 140 USH1, 189 USH2, 21 USH3 and 20 USHA. The results are given both separately and combined for the novel Usher patients from Europe and the USA (table 2). The European patients originated from eight Western European countries, that is, the Netherlands (12.7%), the UK (8.1%), Germany (7.3%), Belgium (5.4%), Italy (5.4%), Denmark (2.7%), Switzerland (1.9%) and Spain (1.4%). The majority of the patients from the USA were of European descent. For USH1, genotyping using the microarray revealed the highest percentage of patients with either one or two mutations, 51% for the European patients, 30% for the patients from the USA and 46% when both groups are combined. When counting mutated alleles, these percentages were 34%, 23% and 31%, respectively. The best results were observed for the USH1 patients of Danish origin in whom a mutation was found in 80% (8/10) of cases or in 65% (13/20) of alleles.

For USH2 the percentages of patients with variants were 25%, 24% and 25%, respectively. The percentages for detected USH2 alleles were 20%, 14% and 18%, respectively. A total of 104 of the patients with USH2 from the USA were pre-screened for the p.E767fs mutation and patients heterozygous or homozygous for this mutation were not included. This pre-screening did not influence the genotyping detection rate for the microarray which was 23% of the patients and 15% of the alleles. The numbers of patients with USH3 or USHA were relatively low. Consequently, the sensitivity of the microarray for these patient groups, although rather good in the present cohorts of patients, cannot be reliably assessed.

The *USH2A* variant c.2299delG (p.E767fs) was previously described as a common mutation in Caucasian patients with USH2, comprising between 13% and 39% of *USH2A* alleles.[34–38] The genotyping presented here revealed a second common mutation, c.11864G>A (p.W3955X) in exon 61 of this gene. This nonsense mutation truncates the long isoform of the USH2A protein.[39] Three of 47 European patients with USH2 were heterozygous for this allele, twice in combination with the p.E767fs mutation. In USH2 patients from the USA, 15 alleles with this mutation were detected in 13 of 142 patients. In total, 18 of 61 mutant alleles (30%) identified in patients with USH2 were p.W3955X. However, since some of the USH2 patients were pre-screened for the common p.E767fs mutation, this percentage was probably higher than would be expected in an unselected patient cohort. For the European patients this percentage was only 16% (3/19). The p.W3955X mutation was also heterozygously present in a patient with USHA in whom the second mutation was not identified. Haplotype analysis has to be performed to determine whether the p.W3955X mutation is a founder mutation as has been shown for p.E767fs.[40]

Table 2 Identification of Usher mutations in patients from Europe and the USA

	USH1 patients				USH2 patients				USH3 patients				USHA patients			
Country	**Total**	**0 all**	**1 all**	**2 alls**	**Total**	**0 all**	**1 all**	**2 alls**	**Total**	**0 all**	**1 all**	**2 alls**	**Total**	**0 all**	**1 all**	**2 alls**
Belgium, Germany, and Netherlands	51	27	12	12	35	25	5	5	3	3	0	0	5	4	1	0
Switzerland					5	5	0	0	2	2	0	0				
Italy, Spain	13	5	8	0	3	2	0	1	1	0	1	0	8	5	2	1
Denmark	10	2	3	5												
UK	29	16	12	1	4	3	0	1	1	0	0	1				
Total Europe	103	50	35	18	47	35	5	7	7	5	1	1	13	9	3	1
Patients with mutation		53/103 = 51%				12/47 = 25%				2/7 = 29%				4/13 = 31%		
Mutant alleles		71/206 = 34%				19/94 = 20%				3/14 = 21%				5/26 = 19%		
USA	37	26	5	6	38	29	7	2	14	9	3	1	7	5	1	1
Patients with mutation		11/37 = 30%				9/38 = 24%				4/14 = 29%				2/7 = 29%		
Mutant alleles		17/74 = 23%				11/76 = 14%				5/28 = 18%				3/14 = 21%		
Total	140	76	40	24	85	64	12	9	21	14	4	2	20	14	4	2
Patients with mutation		64/140 = 46%				21/85 = 25%				6/21 = 29%				6/20 = 30%		
Mutant alleles		88/280 = 31%				30/170 = 18%				8/42 = 19%				8/40 = 20%		
USA pre-screened					104	80	17	7								
Patients with mutation						24/104 = 23%										
Mutant alleles						31/208 = 15%										

The number of cases with two alleles represent those cases for which two sequence variants were detected in the same gene. all, alleles.

Of the mutations detected, 191 were re-evaluated by sequence analysis and only two could not be confirmed (false positives), which illustrates the robustness of the method. One mutation, c.496+1G>A in the *USH1C* gene, was not detected by the microarray but was detected afterwards by sequence analysis (false negative). Segregation analysis could be performed in relatives of 11 probands in whom at least two variants were detected by chip analysis. In one of these families, the analysis revealed that two *CDH23* variants were present on the same allele. For the remaining 10 probands the results are compatible with both alleles each carrying one mutation.

Identification of novel variants in Usher genes

Since all four nucleotides are available during primer extension, the APEX technology allows the detection of new nucleotide variants for positions that were already known to be variant and are represented by an assay on the microarray. In this way two novel variants were detected and confirmed by sequence analysis. In *PCDH15*, c.400C>T is predicted to cause the nonsense mutation p.R134X. At this position the substitution of a guanine for a cytosine was already described to cause the missense mutation p.R134G in a family with non-syndromic hearing loss.[21] In the *USH2A* gene, a c.1606T>A was detected, which is predicted to cause an amino acid substitution p.C536S. The nucleotide substitution c.1606T>C (p.C536R) was reported by Dreyer *et al*[34] in one of 31 unrelated patients with USH2 who also carried the p.E767fs variant.

Variants in genes known to be associated with a different USH type

In a number of patients, variants were detected that did not correspond with the type of Usher syndrome in the patient (table 3). In five patients with USH1, one or two mutations were detected in the *USH2A* gene. In USH2 patients, variants were detected in the *MYO7A* gene and also in the *USH3A* gene, and in USH3 patients variants were seen in *MYO7A* and in *USH2A*. Whether the heterozygous mutations in the *MYO7A* gene are indeed causative such that mutations in *MYO7A* can also cause USH2 and USH3, remains to be determined. In many cases, the clinical diagnosis may be ambiguous. This is also true for the heterozygous *USH2A* mutations in patients with USH1 and USH3 and *USH3A* mutations in patients with USH2.

In patients with USHA, mutations were detected in *MYO7A*, *USH2A* and *CDH23* (table 3).

Table 3 Variants in genes known to be associated with a different USH type and variants associated with atypical USH (USHA)

Patient	Phenotype	Allele 1	Allele 2
H2524	USH1	*USH2A* p.560fs	
JD6381	USH1	*USH2A* p.E767fs	
03-03704	USH1	*USH2A* p.L555V	
57	USH1	*USH2A* p.R4115C	
QUB4/B5	USH1	*USH2A* p.C536S	*USH2A* p.H548S
D3900	USH2	*USH3A* p.N48K	*USH3A* p.N48K
H2774	USH2	*USH3A* p.N48K	
0303158	USH2	*USH3A* p.S50fs	
D9569	USH2	*MYO7A* p.R1240Q	
0401876	USH2	*MYO7A* c.736-3C>T	
D8903	USH3	*MYO7A* p.Q1798X	
D9804	USH3	*MYO7A* p.E1359fs	
H2156	USH3	*USH2A* p.V218E	
O2	USH3	*USH2A* p.E767fs	
H0200	USHA	*MYO7A* p.R1743W	*MYO7A* p.R1743W
MM52	USHA	*MYO7A* p.R1861X	*MYO7A* p.R1861X
RP683	USHA	*CDH23* p.T1209A	
21730	USHA	*CDH23* p.R1060W + p.D1341N	
T56	USHA	*USH2A* p.L555V	
H1362	USHA	*USH2A* p.W3955X	

Variants identified in two Usher genes

In nine patients, variants in two different genes were detected, that is, in four samples used for validation and in five patients tested for evaluation of the chip (table 4). In three of the nine cases, a variation in a second gene was present in addition to two mutations in one of the other Usher genes. As segregation analysis could not be performed for any of these cases, we cannot conclude that they represent true digenic inheritance, whether the variant in the second gene contributes to the severity of the phenotype or whether the results are merely a coincidence. However, in one of the cases with three sequence variants, two in *USH2A* and one in *MYO7A*, the *USH2A* mutations are protein truncating. These truncating mutations are most likely sufficient to cause the disease and thus only a modifying effect for the p.R1343S variant in *MYO7A* seems plausible. A second case had two truncating mutations in *MYO7A* in addition to p.P608R in USH1C. Also for this case, the third variant might modify the phenotype but is not likely to be primarily disease causing. The combination of variants in the *MYO7A* and *USH2A* genes were seen in six of the eight cases with variants in two Usher genes, which is not unexpected since these genes are causative in the majority of the patients with USH1 and USH2, respectively, and thus are expected to exhibit the highest carrier frequencies.

USH variants with questionable pathogenicity

Several sequence variants in Usher genes have previously been described for which pathogenicity was uncertain. A number of these were included in the microarray and, based on the results of the evaluation experiment, were regarded as polymorphisms. Nine alleles with the missense variant p.E478D[17 41] in the *USH2A* gene were detected in patients with all three types of Usher syndrome and in three patients, one of each with USH1, USH2 and USH3, this variant was present in addition to two pathogenic mutations. The frequency in controls was determined for the Jewish population (0/120 alleles).[41] However, we detected this variant in three out of 180 control alleles from the Dutch population. The *USH2A* variant p.V230M was detected nine times in patients with all three types of Usher syndrome. In these patients, only one putative pathogenic *USH2A* mutation was detected in addition to the p.V230M variant. Dreyer *et al*[34] did not detect this variant in controls, although Jian Seyedahmadi *et al*[17] detected similar frequencies in patients and controls. The *USH2A* variant p.G713R was described by Dreyer *et al*[34] as likely to be pathogenic since it was not detected in controls. However, Jian Seyedahmadi reported that the variant did not co-segregate with the disease in some families. In the present genotyping, the p.G713R variant was detected as the only variant heterozygously in two patients with USH1 and in one patient with USH3. In an USH2 patient it was detected in addition to a truncating mutation. This variant was not present in an affected sib of one of the USH1 patients. The *USH2A* variant c.2052A>G (p.Q684Q)[42] was described as possibly creating a cryptic splice site. This nucleotide substitution was detected once in an USH2 patient as the only variant. The USH2A variant p.S841Y was previously described to be present in two of 186 control alleles.[38] In the present genotyping this variant was detected in one USH1 patient with one *MYO7A* mutation and in one USH1 patient with one mutation in *CDH23*.

Najera and co-workers questioned whether the variant p.Y1719C in *MYO7A* was disease-causing[33] since it was detected

Table 4 Usher syndrome patients with sequence variants in two Usher genes

Patient	Phenotype	Allele 1	Allele 2	Allele 3
Val-1	USH1	*CDH23* p.R2833G	*MYO7A* p.R302H	
Val-2	USH1	*MYO7A* p.A1340T	*USH1C* p.R80fs	
Val-4	USH2	*USH2A* p.C1002fs	*MYO7A* p.R302H	
H0151	USH2	*USH2A* p.C419F	*MYO7A* p.E1359fs	
H0165	USH2	*USH2A* p.R317R	*MYO7A* p.T1566M	
H2264	USH2	*USH2A* p.E767fs	*MYO7A* p.R1743W	
Val-3	USH2	*USH2A* p.K182fs	*USH2A* p.E767fs	*MYO7A* p.R1343S
H0900	USH2	*USH2A* p.V218E	*USH2A* p.W3955X	*MYO7A* p.T165M
P99-0345	USH1	*MYO7A* p.Q121fs	*MYO7A* p.Q121fs	*USH1C* p.P608R

in 3/168 control alleles. We detected this variant in four patients with all three different types of Usher syndrome, two of whom did not have an additional variant in one of the Usher genes. This does not support a causative effect of the mutation.

DISCUSSION

A cost-effectiveness comparison of APEX mutation analysis with other medium and high-throughput mutation detection techniques

Routine mutation analysis of patients suffering from a genetically heterogeneous disease has been severely hampered by the high costs associated with application of conventional analysis techniques for comprehensive mutation screening. Despite the fact that most Usher syndrome patients can be reliably grouped into one of two main clinical groups, a systematic mutation analysis of either the USH1 or USH2 genes still requires the analysis of 179 and 162 protein coding exons, respectively. As depicted in table 5, the APEX-based mutation detection array is an affordable and flexible system as new alleles can be added without the need to design completely new screening platforms. The main disadvantage is its low efficiency in early versions since it relies on the extent of previous mutation analysis studies performed using other techniques. The Affymetrix resequencing technique has two disadvantages. First, heterozygous deletions larger than 1 bp and all insertions and duplications are missed because the complexity of the microarray would increase disproportionally if matching primers were added to the chip. These variants comprise 47/292 (16%) of all pathologic USH variants. Second, the screening costs, including development costs, are quite high, prohibiting the use of this technique in a routine laboratory setting.

A direct comparison of efficiency with other mutation detection techniques is not straightforward since no comprehensive mutation detection studies have yet been performed for more than one Usher gene. For USH1, the most commonly used technique is single strand conformation polymorphism (SSCP) analysis, which yielded between 19% and 48% of mutant alleles in *MYO7A*,[32 33 43] which is comparable to our overall efficiency (31% of alleles; table 2). For USH2, SSCP and sequence analysis of exons 1–21 of *USH2A* yielded 23% and 38% of mutant alleles, respectively,[17 38] which is higher than with the APEX technology (18%). The relatively low yield of USH2 alleles is due to the fact that the *USH2A* gene was expanded only recently from 21 to 73 exons[39] and because comprehensive mutation analysis of this gene lags behind *MYO7A*.

Thus, efficiencies for the Usher chip at the moment can be best compared to the recently developed APEX chip for LCA, which is comparable in complexity (contains ~300 variants found in seven genes) and yields on average 20–28% of LCA alleles.[25 26] The Usher microarray chip is particularly useful for the analysis of patients with USHA, who have been shown to carry mutations in the *MYO7A*, *CDH23* and *USH2A* genes.

The overall efficiency of the Usher chip in the future is expected to increase in proportion to the addition of new variants. We propose the use of this mutation chip as a first-pass screening tool for all Usher patients. In patients with one or no variant, capillary-based heteroduplex analysis of the larger genes (*CDH23*, *MYO7A*, *PCDH15*, *USH1C*, *USH2A*, *VLGR1*) or sequence analysis of the smaller genes (*USH1G*, *USH3A*) can be performed. Novel variants from these studies can subsequently be added to the chip, resulting in a gradual increase in its efficiency. The Usher syndrome mutation detection chip can be obtained from Asper Ophthalmics (Tartu, Estonia; http://www.asperophthalmics.com/UshersyndromeDNAtest.htm).

Table 5 A comparison of mutation detection techniques for Usher syndrome

	Advantages	Disadvantages
APEX	Robust Versatile (addition of new variants with little extra costs) Cheap (<€200) Medium throughput Not highly dependent on DNA quality	Detects only known variants Low efficiency in early stages Less efficient for analysing patients of other ethnic backgrounds Requires specialised expertise Sequence confirmation required
Sequence analysis	Robust Versatile Easy set-up	High costs (>€1000 for *MYO7A* or *USH2A*)
Capillary-based heteroduplex analysis	Robust Medium throughput Relatively cheap	Polymorphic sequences difficult to analyse Sequence analysis necessary for mutation identification
Resequencing (Affymetrix)	Fully automated Detects known and new nucleotide substitutions	High costs (~€600) No detection of heterozygous deletions >1 nt and all duplications/insertions (47/292 (16%) pathologic USH variants) Addition of tested genes requires new chip design

Deficiencies in the Usher chip and other conventionally used mutation detection techniques

Currently, none of the standard mutation analysis techniques is able to identify heterozygous deletions that span one or both amplicon primers. As a result, we have no knowledge whatsoever about the frequency of deletions of this kind. Therefore, a customised probe set needs to be designed that can identify copy-number changes, for example, multiplex ligation dependent probe amplification or quantitative PCR.[44] Likewise, deep intronic mutations affecting splicing are missed as RNA analyses are not part of standard procedures due to restricted expression of the Usher genes.

Pathogenicity of variants in Usher genes

When a known mutation is detected in both copies of one of the Usher genes, one can confidently conclude that these mutations are disease-causing. Two alleles were found in 24/140 (17%) USH1 patients, 9/85 (11%) USH2 patients, 2/21 (10%) USH3 patients and 2/20 (10%) USHA patients. However, when one mutated allele is observed, the chance that a false conclusion is made regarding causality of this particular variant for the phenotype in that patient, differs for each of the Usher syndrome genes. For the *MYO7A* gene in USH1 patients, the percentage of patients with a false interpretation based on the presence of one mutated allele for this gene was calculated to be 2.4; for the *USH2A* gene in USH2 patients, this percentage was calculated to be 0.8.[45] For diagnoses based on one allele with a missense mutation, this percentage is likely to be higher due to the fact that the pathogenicity of this type of mutation is difficult to prove. Due to the small sizes of the families with Usher syndrome and the fact that samples of other family members are often not available, it is mostly not possible to perform segregation analysis to prove the pathogenicity of a specific sequence variant.

We also included on the microarray a number of sequence variants that we assume are not pathogenic. The results in the present study support this assumption. However, it cannot be excluded that these variants can modulate the disease severity in a way comparable to that of a sequence variant in Bardet-Biedl syndrome. An exonic nucleotide substitution that affects splicing of the *MGC1203* RNA modulates the phenotype of patients with Bardet-Biedl syndrome with mutations in the *BBS1* gene because the BBS1 and MGC1203 proteins interact.[46] Since both the USH1 and USH2 proteins are known be part of an Usher interactome,[47–52] phenotypic modulation might well be possible and was already suggested in a family with homozygous *USH3A* mutations in the affected members and a mutated *MYO7A* gene in one of them.[53 54]

Digenic inheritance in Usher syndrome?

Since Usher proteins interact with each other and form dynamic protein complexes, digenic or oligogenic inheritance of Usher syndrome would not be surprising. Indications for digenic inheritance involving mutations in the *PCDH15* and *CDH23* genes have been obtained for two USH1 patients and a patient with USHA,[55] but no elaborate segregation analysis was reported to strengthen this observation. The large number of patient DNAs screened in the present study is specifically suitable for detection of rare cases exhibiting digenic inheritance of the syndrome. From the nine cases with sequence variants in two different genes, one is unlikely to follow digenic inheritance since two truncating mutations in one of the genes were present. *PCDH15* and *CDH23*, previously implicated in digenicity, were not involved in any of the remaining eight cases. Segregation analysis could not be performed for any of the cases and therefore, we cannot confirm or exclude digenic inheritance.

Use of the Usher microarray for patients with non-syndromic arRP and hearing impairment

Mutations in the *USH2A* gene have been described to be a common cause of RP and the p.C759F mutation is almost exclusively detected in patients with non-syndromic RP. Based on their results of screening exons 1–21 of the gene, Jian Seyedahmadi *et al*[17] estimated that *USH2A* mutations are present in 7% of all RP cases in the USA and screening of only one third of exons 22–73 increased this to 16% for arRP patients.[56] Since all *USH2A* mutations detected in RP patients are represented on the Usher microarray, this is also suitable for this patient population. However, a mutation array with known mutations in a large number of RP genes, including *USH2A*, has been developed[57] and is more suitable for mutation detection in patients with RP.

Mutations in the USH1 genes *CDH23* (DFNB12), *MYO7A* (DFNA11, DFNB2), *PCDH15* (DFNB23) and *USH1C* (DFNB18) can cause non-syndromic hearing loss.[51] Among these genes, *CDH23* seems to be the most frequently involved in non-syndromic hearing loss. The hearing loss in DFNB12 patients ranges from moderate to profound, but also patients with hearing loss that started as mild in childhood have been described to have mutations in *CDH23*.[20] So far, there are no indications that mutations in the USH1 genes are a common cause of non-syndromic hearing loss. However, more extensive mutation analysis in this patient category is necessary to determine the value of the present microarray for this group of patients.

ELECTRONIC DATABASE INFORMATION

The UCSC Human Genome Browser is at http://genome.cse.ucsc.edu, the Asper Biotech website is at http://www.asperbio.com and the Asper Ophthalmics web site is at http://www.asperophthalmics.com/UshersyndromeDNAtest.htm

ACKNOWLEDGEMENTS

We thank Drs Rando Allikmets, Alfredo Ciccodicola and Carmela Ziviello for helpful discussion and Drs Ronald Admiraal, Andreas Gal, Cristiana Marchese, Ronald Pennings, Maria PiaManitto and Hanna Västinsalo for the ascertainment of patients and Krysta Voesenek, Saskia van der Velde and Christel Beumer for technical assistance

The supplementary table 1 is available at http://jmg.bmj.com/supplemental

Authors' affiliations

F P M Cremers, A P de Brouwer, L H Hoefsloot, Department of Human Genetics, and Nijmegen Centre for Molecular Life Sciences, Radboud University Nijmegen Medical Centre, Nijmegen, The Netherlands
W J Kimberling, P M Kelley, M D Weston, The Usher Syndrome Center, Boys Town National Research Hospital, Omaha, Nebraska, USA
M Külm, Asper Biotech, Tartu, Estonia
E van Wijk, H te Brinke, C W R J Cremers, H Kremer, Department of Otorhinolaryngology, Radboud University Nijmegen Medical Centre, Nijmegen, The Netherlands
S Banfi, Téléthon Institute of Genetics and Medicine, Naples, Italy
F Simonelli, Department of Ophthalmology, Second University of Naples, Naples, Italy
J C Fleischhauer, Department of Ophthalmology, University Hospital Zurich, Zurich, Switzerland
W Berger, Division of Medical Molecular Genetics and Gene Diagnostics, Institute of Medical Genetics, University of Zurich, Zurich, Switzerland
E Haralambous, M Bitner-Glindzicz, Clinical and Molecular Genetics Unit, Institute of Child Health, London, UK
A R Webster, Z Saihan, Molecular Genetics, Institute of Ophthalmology, UCL, London, UK
E De Baere, Center for Medical Genetics, Ghent University Hospital, Ghent, Belgium

B P Leroy, Department of Ophthalmology, Ghent University Hospital, Ghent, Belgium
G Silvestri, G J McKay, Centre for Vision Science, School of Biomedical Science, Queen's University Belfast, Belfast, Northern Ireland, UK
R K Koenekoop, Ocular Genetics Laboratory, McGill University Health Center, Montreal, Canada
J M Millan, Unidad de Genetica y Diagnostico Prenatal, Hospital Universitario La Fe, Valencia, Spain
T Rosenberg, Gordon Norrie Centre for Genetic Eye Diseases, National Eye Clinic for the Visually Impaired, Hellerup, Denmark
T Joensuu, E-M Sankila, The Folkhalsan Institute of Genetics, Biomedicum Helsinki, and Department of Ophthalmology, University of Helsinki, Helsinki, Finland
D Weil, Unité de Génétique des Deficits Sensoriels, Institut Pasteur, Paris, France
B Wissinger, Molecular Genetics Laboratory, University Eye Hospital, Tübingen, Germany

This study was supported by the Forschung contra Blindheit - Initiative Usher Syndrom e.V. (FPMC, CWRJC and HK), Oogfonds Nederland, Gelderse Blinden Vereniging, Stichting Blindenhulp, Algemene Nederlandse Vereniging ter Voorkoming van Blindheid, Rotterdamse Vereniging Blindenbelangen, Stichting voor Ooglijders, the Dr. F.P. Fischer Stichting (CWRJC and HK), the Heinsius-Houbolt Stichting (FPMC, HK and CWRJC,), The Italian Telethon Foundation (SB), the Northern Ireland HPSS R&D Office (GMK), the Deutsche Forschungsgemeinschaft - KFO134 (BW), Paul Schiller Foundation, Zurich, Switzerland (JF an WB), The Danish Society of the Blind (TR), F.I.S. PI04/0918, FAARPEE (JMM), the Big Lottery Fund, the British Retinitis Pigmentosa Society and Deafness Research UK (MB-G), Fonds voor Wetenschappelijk Onderzoek Vlaanderen FWO 3G004306 (BPL and EDB) and the Ulla Hjelt Foundation (E-MS). The work was partially supported by a grant from the Foundation Fighting Blindness and by a grant from the NIH-NIDCD/ 5P01DC01813 (WJK).

Competing interests: None declared.

Correspondence to: F P M Cremers, Department of Human Genetics, Radboud University Nijmegen Medical Centre, PO Box 9101, 6500 HB Nijmegen, The Netherlands; F.Cremers@antrg.umcn.nl

Received 14 June 2006
Revised 15 August 2006
Accepted 22 August 2006
Published Online First 14 November 2006

REFERENCES

1 **Rosenberg T**, Haim M, Hauch AM, Parving A. The prevalence of Usher syndrome and other retinal dystrophy-hearing impairment associations. *Clin Genet* 1997;**51**:314–21.
2 **Spandau UH**, Rohrschneider K. Prevalence and geographical distribution of Usher syndrome in Germany. *Graefes Arch Clin Exp Ophthalmol* 2002;**240**:495–8.
3 **Mazarita ML**, Ploughman LM, Rawlings B, Remington E, Arnos KS, Nance WE. Genetic epidemiological studies of early-onset deafness in the U.S. school-age population. *Am J Med Genet* 2003;**46**:486–91.
4 **Smith RJH**, Berlin CI, Hejtmancik JF, Keats BJ, Kimberling WJ, Lewis RA, Moller CG, Pelias MZ, Tranebjaerg L. Clinical diagnosis of the Usher syndromes. Usher Syndrome Consortium. *Am J Med Genet* 1994;**50**:32–8.
5 **Weil D**, Blanchard S, Kaplan J, Guilford P, Gibson F, Walsh J, Mburu P, Varela A, Levilliers J, Weston MD, Kelley PM, Kimberling WJ, Wagenaar M, Levi-Acobas F, Larget-Piet D, Munnich A, Steel KP, Brown SDM, Petit C. Defective myosin VIIA gene responsible for Usher syndrome type 1B. *Nature* 1995;**374**:60–1.
6 **Eudy JD**, Weston MD, Yao SF, Hoover DM, Rehm HL, Ma-Edmonds M, Yan D, Ahmad I, Cheng JJ, Ayuso C, Cremers C, Davenport S, Moller C, Talmadge CB, Beisel KW, Tamayo M, Morton CC, Swaroop A, Kimberling WJ, Sumegi J. Mutation of a gene encoding a protein with extracellular matrix motifs in Usher syndrome type IIa. *Science* 1998;**280**:1753–7.
7 **Bitner-Glindzicz M**, Lindley KJ, Rutland P, Blaydon D, Smith VV, Milla PJ, Hussain K, Furth-Lavi J, Cosgrove KE, Shepherd RM, Barnes PD, O'Brien RE, Farndon PA, Sowden J, Liu X-Z, Scanlan MJ, Malcolm S, Dunne MJ, Aynsley-Green A, Glaser B. A recessive contiguous gene deletion causing infantile hyperinsulinism, enteropathy and deafness identifies the Usher type 1C gene. *Nat Genet* 2000;**26**:56–60.
8 **Verpy E**, Leibovici M, Zwaenepoel I, Liu X-Z, Gal A, Salem N, Mansour A, Blanchard S, Kobayashi I, Keats BJB, Slim R, Petit C. A defect in harmonin, a PDZ domain-containing protein expressed in the inner ear sensory hair cells, underlies Usher syndrome type 1C. *Nat Genet* 2000;**26**:51–5.
9 **Ahmed ZM**, Riazuddin S, Bernstein SL, Ahmed Z, Khan S, Griffith AJ, Morell RJ, Friedman TB, Riazuddin S, Wilcox ER. Mutations of the protocadherin gene PCDH15 cause Usher syndrome type 1F. *Am J Hum Genet* 2001;**69**:25–34.
10 **Alagramam KN**, Yuan H, Kuehn MH, Murcia CL, Wayne S, Srisailpathy CR, Lowry RB, Knaus R, Van Laer LL, Bernier FP, Schwartz S, Lee C, Morton CC, Mullins RF, Ramesh A, Van Camp G, Hageman GS, Woychik RP, Smith RJ. Mutations in the novel protocadherin PCDH15 cause Usher syndrome type 1F. *Hum Mol Genet* 2001;**10**:1709–18.
11 **Bolz H**, von Brederlow B, Ramírez A, Bryda EC, Kutsche K, Nothwang HG, Seeliger M, del C. -Salcedó Cabrera M, Caballeró Vila M, Pelaez Molina O, Gal A, Kubisch C. Mutation of *CDH23*, encoding a new member of the cadherin gene family, causes Usher syndrome type 1D. *Nat Genet* 2001;**27**:108–12.
12 **Bork JM**, Peters LM, Riazuddin S, Bernstein SL, Ahmed ZM, Ness SL, Polomeno R, Ramesh A, Schloss M, Srisailpathy CRS, Wayne S, Bellman S, Desmukh D, Ahmed Z, Khan SN, Der Kaloustian VM, Li XC, Lalwani A, Riazuddin S, Bitner-Glindzicz M, Nance WE, Liu X-Z, Wistow G, Smith RJH, Griffith AJ, Wilcox ER, Friedman TB, Morell RJ. Usher syndrome 1D and nonsyndromic autosomal recessive deafness DFNB12 are caused by allelic mutations of the novel cadherin-like gene *CDH23*. *Am J Hum Genet* 2001;**68**:26–37.
13 **Joensuu T**, Hamalainen R, Yuan B, Johnson C, Tegelberg S, Gasparini P, Zelante L, Pirvola U, Pakarinen L, Lehesjoki AE, de la Chapelle A, Sankila EM. Mutations in a novel gene with transmembrane domains underlie Usher syndrome type 3. *Am J Hum Genet* 2001;**69**:673–84.
14 **Weil D**, El-Amraoui A, Masmoudi S, Mustapha M, Kikkawa Y, Laine S, Delmaghani S, Adato A, Nadifi S, Zina ZB, Hamel C, Gal A, Ayadi H, Yonekawa H, Petit C. Usher syndrome type I G (USH1G) is caused by mutations in the gene encoding SANS, a protein that associates with the USH1C protein, harmonin. *Hum Mol Genet* 2003;**12**:463–71.
15 **Weston MD**, Luijendijk MWJ, Humphrey KD, Moller C, Kimberling WJ. Mutations in the VLGR1 gene implicate G-protein signaling in the pathogenesis of Usher syndrome type II. *Am J Hum Genet* 2004;**74**:357–66.
16 **Rivolta C**, Sweklo EA, Berson EL, Dryja TP. Missense mutation in the *USH2A* gene: association with recessive retinitis pigmentosa without hearing loss. *Am J Hum Genet* 2000;**66**:1975–8.
17 **Jian Seyedahmadi B**, Rivolta C, Keene JA, Berson EL, Dryja TP. Comprehensive screening of the USH2A gene in Usher syndrome type II and non-syndromic recessive retinitis pigmentosa. *Exp Eye Res* 2004;**79**:167–73.
18 **Jian Seyedahmadi B**, Berson EL, Dryja TP. USH3A mutations in patients with a prior diagnosis of Usher syndrome type I, Usher syndrome type II, and nonsyndromic recessive retinitis pigmentosa. *Invest Ophthalmol Vis Sci* 2004;**45**:E-Abstract 4726.
19 **Liu X-Z**, Walsh J, Mburu P, Kendrick-Jones J, Cope MJTV, Steel KP, Brown SDM. Mutations in the myosin VIIA gene cause non-syndromic recessive deafness. *Nat Genet* 1997;**16**:188–90.
20 **Astuto LM**, Bork JM, Weston MD, Askew JW, Fields RR, Orten DJ, Ohliger SJ, Riazuddin S, Morell RJ, Khan S, Riazuddin S, Kremer H, Van Hauwe P, Moller CG, Cremers CW, Ayuso C, Heckenlively JR, Rohrschneider K, Spandau U, Greenberg J, Ramesar R, Reardon W, Bitoun P, Millan J, Legge R, Friedman TB, Kimberling WJ. CDH23 mutation and phenotype heterogeneity: a profile of 107 diverse families with Usher syndrome and nonsyndromic deafness. *Am J Hum Genet* 2002;**71**:262–75.
21 **Ahmed ZM**, Morell RJ, Riazuddin S, Gropman A, Shaukat S, Ahmad MM, Mohiddin SA, Fananapazir L, Caruso RC, Husnain T, Khan SN, Riazuddin S, Griffith AJ, Friedman TB, Wilcox ER. Mutations of MYO6 are associated with recessive deafness, DFNB37. *Am J Hum Genet* 2003;**72**:1315–22.
22 **De Brouwer AP**, Pennings RJ, Roeters M, Van Hauwe P, Astuto LM, Hoefsloot LH, Huygen PL, van den Helm B, Deutman AF, Bork M, Kimberling WJ, Cremers FPM, Cremers CWRJ, Kremer H. Mutations in the calcium-binding motifs of CDH23 and the 35delG mutation in GJB2 cause hearing loss in one family. *Hum Genet* 2003;**112**:156–63.
23 **Jaakson K**, Zernant J, Külm M, Hutchinson A, Tonisson N, Hawlina M, Ravnic-Glavac M, Meltzer M, Caruso R, Testa F, Maugeri A, Hoyng CB, Gouras P, Simonelli F, Lewis RA, Lupski JR, Cremers FPM, Allikmets R. Genotyping microarray (gene chip) for the *ABCR* (*ABCA4*) gene. *Hum Mutat* 2003;**22**:395–403.
24 **Klevering BJ**, Yzer S, Rohrschneider K, Zonneveld M, Allikmets R, van den Born LI, Maugeri A, Hoyng CB, Cremers FPM. Microarray-based mutation analysis of the *ABCA4* (ABCR) gene in autosomal recessive cone-rod dystrophy and retinitis pigmentosa. *Eur J Hum Genet* 2004;**12**:1024–32.
25 **Zernant J**, Kulm M, Dharmaraj S, den Hollander AI, Perrault I, Preising MN, Lorenz B, Kaplan J, Cremers FPM, Maumenee I, Koenekoop RK, Allikmets R. Genotyping microarray (disease chip) for Leber congenital amaurosis: detection of modifier alleles. *Invest Ophthalmol Vis Sci* 2005;**46**:3052–9.
26 **Yzer S**, Leroy BP, De Baere E, de Ravel TJ, Zonneveld MN, Voesenek K, Kellner U, Martinez Ciriano JP, de Faber J-THN, Rohrschneider K, Roepman R, den Hollander AI, Cruysberg JR, Meire F, Casteels I, van Moll-Ramirez NG, Allikmets R, van den Born LI, Cremers FPM. Microarray-based mutation detection and phenotypic characterization of patients with Leber congenital amaurosis. *Invest Ophthalmol Vis Sci* 2006;**47**:1167–76.
27 **Pastinen T**, Partanen J, Syvanen AC. Multiplex, fluorescent, solid-phase minisequencing for efficient screening of DNA sequence variation. *Clin Chem* 1996;**42**:1391–7.
28 **Shumaker JM**, Metspalu A, Caskey CT. Mutation detection by solid phase primer extension. *Hum Mutat* 1996;**7**:346–54.
29 **Kurg A**, Tonisson N, Georgiou I, Shumaker J, Tollett J, Metspalu A. Arrayed primer extension: solid-phase four-color DNA resequencing and mutation detection technology. *Genet Test* 2000;**4**:1–7.
30 **Tonisson N**, Kurg A, Kaasik K, Lohmussaar E, Metspalu A. Unravelling genetic data by arrayed primer extension. *Clin Chem Lab Med* 2000;**38**:165–70.

31 **Tonisson N**, Zernant J, Kurg A, Pavel H, Slavin G, Roomere H, Meiel A, Hainaut P, Metspalu A. Evaluating the arrayed primer extension resequencing assay of TP53 tumor suppressor gene. *Proc Natl Acad Sci U S A* 2002;**99**:5503–8.
32 **Bharadwaj AK**, Kasztejna JP, Huq S, Berson EL, Dryja TP. Evaluation of the myosin VIIA gene and visual function in patients with Usher syndrome type I. *Exp Eye Res* 2000;**71**:173–81.
33 **Najera C**, Beneyto M, Blanca J, Aller E, Fontcuberta A, Millan JM, Ayuso C. Mutations in myosin VIIA (MYO7A) and usherin (USH2A) in Spanish patients with Usher syndrome types I and II, respectively. *Hum Mutat* 2002;**20**:76–7.
34 **Dreyer B**, Tranebjaerg L, Rosenberg T, Weston MD, Kimberling WJ, Nilssen O. Identification of novel USH2A mutations: implications for the structure of USH2A protein. *Eur J Hum Genet* 2000;**8**:500–6.
35 **Leroy BP**, Aragon-Martin JA, Weston MD, Bessant DA, Willis C, Webster AR, Bird AC, Kimberling WJ, Payne AM, Bhattacharya SS. Spectrum of mutations in USH2A in British patients with Usher syndrome type II. *Exp Eye Res* 2001;**72**:503–9.
36 **Aller E**, Najera C, Millan JM, Oltra JS, Perez-Garrigues H, Vilela C, Navea A, Beneyto M. Genetic analysis of 2299delG and C759F mutations (USH2A) in patients with visual and/or auditory impairments. *Eur J Hum Genet* 2004;**12**:407–10.
37 **Ouyang XM**, Hejtmancik JF, Jacobson SG, Li AR, Du LL, Angeli S, Kaiser M, Balkany T, Liu XZ. Mutational spectrum in Usher syndrome type II. *Clin Genet* 2004;**65**:288–93.
38 **Pennings RJE**, te Brinke H, Weston MD, Claassen A, Orten DJ, Weekamp H, van Aarem A, Huygen PL, Deutman AF, Hoefsloot LH, Cremers FPM, Cremers CWRJ, Kimberling WJ, Kremer H. USH2A mutation analysis in 70 Dutch families with Usher syndrome type II. *Hum Mutat* 2004;**24**:185.
39 **van Wijk E**, Pennings RJE, te Brinke H, Claassen A, Yntema HG, Hoefsloot LH, Cremers FPM, Cremers CWRJ, Kremer H. Identification of 51 novel exons of the Usher syndrome type 2A (USH2A) gene that encode multiple conserved functional domains and that are mutated in patients with Usher syndrome type II. *Am J Hum Genet* 2004;**74**:738–44.
40 **Dreyer B**, Tranebjaerg L, Brox V, Rosenberg T, Moller C, Beneyto M, Weston MD, Kimberling WJ, Cremers CWRJ, Liu XZ, Nilssen O. A common ancestral origin of the frequent and widespread 2299delG USH2A mutation. *Am J Hum Genet* 2001;**69**:228–34.
41 **Adato A**, Weston MD, Berry A, Kimberling WJ, Bonne-Tamir A. Three novel mutations and twelve polymorphisms identified in the USH2A gene in Israeli USH2 families. *Hum Mutat* 2000;**15**:388.
42 **Weston MD**, Eudy JD, Fujita S, Yao S, Usami S, Cremers C, Greenberg J, Ramesar R, Martini A, Moller C, Smith RJ, Sumegi J, Kimberling WJ, Greenburg J. Genomic structure and identification of novel mutations in usherin, the gene responsible for Usher syndrome type IIa. *Am J Hum Genet* 2000;**66**:1199–210.
43 **Adato A**, Weil D, Kalinski H, Pel-Or Y, Ayadi H, Petit C, Korostishevsky M, Bonne-Tamir B. Mutation profile of all 49 exons of the human myosin VIIA gene, and haplotype analysis, in Usher 1B families from diverse origins. *Am J Hum Genet* 1997;**61**:813–21.
44 **Schouten JP**, McElgunn CJ, Waaijer R, Zwijnenburg D, Diepvens F, Pals G. Relative quantification of 40 nucleic acid sequences by multiplex ligation-dependent probe amplification. *Nucleic Acids Res* 2002;**30**:e57.
45 **Kimberling WJ**. Estimation of the frequency of occult mutations for an autosomal recessive disease in the presence of genetic heterogeneity: application to genetic hearing loss disorders. *Hum Mutat* 2005;**26**:462–70.
46 **Badano JL**, Leitch CC, Ansley SJ, May-Simera H, Lawson S, Lewis RA, Beales PL, Dietz HC, Fisher S, Katsanis N. Dissection of epistasis in oligogenic Bardet-Biedl syndrome. *Nature* 2006;**439**:326–30.
47 **Adato A**, Lefevre G, Delprat B, Michel V, Michalski N, Chardenoux S, Weil D, El-Amraoui A, Petit C. Usherin, the defective protein in Usher syndrome type IIA, is likely to be a component of interstereocilia ankle links in the inner ear sensory cells. *Hum Mol Genet* 2005;**14**:3921–2.
48 **Adato A**, Michel V, Kikkawa Y, Reiners J, Alagramam KN, Weil D, Yonekawa H, Wolfrum U, El-Amraoui A, Petit C. Interactions in the network of Usher syndrome type 1 proteins. *Hum Mol Genet* 2005;**14**:347–56.
49 **El-Amraoui A**, Petit C. Usher I syndrome: unravelling the mechanisms that underlie the cohesion of the growing hair bundle in inner ear sensory cells. *J Cell Sci* 2005;**118**:4593–603.
50 **Reiners J**, van Wijk E, Marker T, Zimmermann U, Jurgens K, te Brinke H, Overlack N, Roepman R, Knipper M, Kremer H, Wolfrum U. Scaffold protein harmonin (USH1C) provides molecular links between Usher syndrome type 1 and type 2. *Hum Mol Genet* 2005;**14**:3933–43.
51 **Reiners J**, Nagel-Wolfrum K, Jurgens K, Marker T, Wolfrum U. Molecular basis of human Usher syndrome: deciphering the meshes of the Usher protein network provides insights into the pathomechanisms of the Usher disease. *Exp Eye Res* 2006;**83**:97–119.
52 **van Wijk E**, van der Zwaag B, Peters T, Zimmermann U, te Brinke H, Kersten FF, Marker T, Aller E, Hoefsloot LH, Cremers CWRJ, Cremers FPM, Wolfrum U, Knipper M, Roepman R, Kremer H. The DFNB31 gene product whirlin connects to the Usher protein network in the cochlea and retina by direct association with USH2A and VLGR1. *Hum Mol Genet* 2006;**15**:751–65.
53 **Adato A**, Kalinski H, Weil D, Chaib H, Korostishevsky M, Bonne-Tamir B. Possible interaction between USH1B and USH3 gene products as implied by apparent digenic deafness inheritance. *Am J Hum Genet* 1999;**65**:261–5.
54 **Adato A**, Vreugde S, Joensuu T, Avidan N, Hamalainen R, Belenkiy O, Olender T, Bonne-Tamir B, Ben-Asher E, Espinos C, Millan JM, Lehesjoki AE, Flannery JG, Avraham KB, Pietrokovski S, Sankila EM, Beckmann JS, Lancet D. USH3A transcripts encode clarin-1, a four-transmembrane-domain protein with a possible role in sensory synapses. *Eur J Hum Genet* 2002;**10**:339–50.
55 **Zheng QY**, Yan D, Ouyang XM, Du LL, Yu H, Chang B, Johnson KR, Liu XZ. Digenic inheritance of deafness caused by mutations in genes encoding cadherin 23 and protocadherin 15 in mice and humans. *Hum Mol Genet* 2005;**14**:103–11.
56 **Jian Seyedahmadi B**, Berson EL, Dryja TP. Screening of 51 newly identified *USH2A* exons among patients with Usher syndrome type II and non-syndromic recessive retinitis pigmentosa. *Invest Ophthalmol Vis Sci* 2005;**46**:E-Abstract 1801.
57 **Allikmets R**, Zernant J, Jaakson K, Lopez I, Haamer E, Den Hollander AI, Ayuso C, Banfi S, Cremers FPM, Koenekoop RK. Analysis of autosomal recessive retinitis pigmentosa patients on the ARRP genotyping (disease chip). *Invest Ophthalmol Vis Sci* 2006;**47**:E-Abstract 1700.

CORRECTION

doi: 10.1136/jmg.2006.044222corr1

Davies JE, Rubinsztein DC. Polyalanine and polyserine frameshift products in Huntington's disease. *J Med Genet* 2006;**43**:893–6.

The journal apologises for an error that has occurred within the abstract of this paper, which should read as follows:

There may be a link between diseases caused by polyglutamine and polyalanine expansion mutations as it has been shown that the expanded CAG/polyglutamine tract within the *SCA3* gene can shift to the GCA/polyalanine frame.

Development of a genotyping microarray for Usher syndrome

Frans P M Cremers, William J Kimberling, Maigi Külm, et al.

J Med Genet 2007 44: 153-160 originally published online September 8, 2006
doi: 10.1136/jmg.2006.044784