


# Vestibular phenotype-genotype correlation in a cohort of 90 patients with Usher syndrome

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## Abstract

Usher syndrome has been historically categorized into one of three classical types based on the patient phenotype. However, the vestibular phenotype does not infallibly predict which Usher genes are mutated. Conversely, the Usher syndrome genotype is not sufficient to reliably predict vestibular function. Here we present a characterization of the vestibular phenotype of 90 patients with clinical presentation of Usher syndrome (59 females), aged 10.9 to 75.5 years, with genetic variants in eight Usher syndromic genes and expand the description of atypical Usher syndrome. We identified unexpected horizontal semicircular canal reactivity in response to caloric and rotational stimuli in 12.5% (3 of 24) and 41.7% (10 of 24), respectively, of our USH1 cohort. These findings are not consistent with the classical phenotypic definition of vestibular areflexia in USH1. Similarly, 17% (6 of 35) of our cohort with USH2A mutations had saccular dysfunction as evidenced by absent cervical vestibular evoked myogenic potentials in contradiction to the classical assumption of normal vestibular function. The surprising lack of consistent genotypic to vestibular phenotypic findings as well as no clear vestibular phenotypic patterns among atypical USH cases, indicate that even rigorous vestibular phenotyping data will not reliably differentiate the three USH types.

## KEYWORDS

atypical Usher syndrome, balance, novel variants, Usher syndrome, vestibular

## 1 | INTRODUCTION

Usher syndrome is inherited as an autosomal recessive disorder<sup>1-3</sup> with an estimated prevalence based on the clinical presentation of 3.2 to 6.2 per 100 000<sup>4</sup> to more recent estimates as high as one in 6000.<sup>5</sup> Usher syndrome is the most common cause of deaf-blindness, characterized

by progressive loss of vision due to retinitis pigmentosa (RP) with varying degrees of hearing loss and dysfunction of the vestibular system. First described in the nineteenth century, the classification of Usher syndrome evolved into three phenotypic types based solely on available diagnostic testing and in the absence of molecular genetic diagnostics. Despite over 100 years of clinical and basic research revealing

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phenotypic and genetic heterogeneity of Usher syndrome, the classification of Usher syndrome into phenotypically defined types I, II, and III remains a common practice.<sup>6</sup> Type I is characterized by congenital, profound sensorineural hearing loss (SNHL) and vestibular areflexia; type II by congenital, stable, moderate to severe SNHL with normal vestibular function; and type III by varying degrees of progressive SNHL with variable dysfunction of the vestibular system. The onset of RP is typically pre-pubertal in type I, post-pubertal in type II, and between the second and fourth decade of life in type III.<sup>1</sup>

To date, 12 genes are reported to underlie Usher syndrome, although three of them are disputed.<sup>7-9</sup> Each Usher syndrome gene is associated with one of the three clinical types. However, there are some reported examples of atypical RP,<sup>10</sup> auditory or vestibular manifestations in patients with variants in genes associated with Usher type I<sup>11-17</sup> and type II.<sup>18-24</sup> Some disparity exists because of previous technological limitations in clinical assessment. For example, much of the literature characterizing vestibular integrity in Usher syndrome describes only horizontal semicircular canal function<sup>25,26</sup> or uses age-of-independent-ambulation as an anamnestic proxy for congenital vestibular integrity.<sup>27-30</sup> Contemporary vestibular assessments can independently interrogate the function of all five vestibular sensory organs in the ear: the transducers of linear acceleration, gravity, and thus spatial orientation in the utricle and saccule, and the transducers of angular acceleration in each of the three semicircular canals. Methods such as dynamic posturography allow for a quantitative assessment of functional balance and can examine the contributions of vestibular, visual, and somatosensory cues toward postural stability.

This prospective study included vestibular testing of a group of 90 patients with clinical manifestations of Usher syndrome who had a molecular genetic confirmation of pathogenic variants in known Usher genes. Genotype-phenotype correlations were compared between three groups of patients with variants of eight genes usually associated with either clinically defined type I, type II, or type III Usher syndrome. Noteworthy atypical vestibular findings were observed in 32% (29 of 90) of the Usher syndrome patients in our study. This is consistent with an emerging body of data<sup>14,20,21,31</sup> suggesting that phenotypic boundaries between Usher types should not be assumed based on molecular diagnosis nor should clinical tests be used to infer a likely genotype.

## 2 | METHODS

### 2.1 | Participants

Ninety patients (59 females, 31 males) aged 10.9 to 75.5 years ( $M = 39.35$ ,  $SD = 15.91$ ) with genetic variants in Usher syndrome genes and clinically confirmed Usher syndrome, hereafter designated as USH1, USH2, and USH3, and no cochlear implantation or middle ear disease were seen between 2005 and 2013 for comprehensive auditory and vestibular testing at the Clinical Center of the National Institutes of Health (NIH) (05-EI-0096, Natural History and Genetic Studies of Usher Syndrome). The study was approved by the Combined Neuroscience Institutional Review Board at the NIH. Written,

informed consent was obtained from all patients and guardians of minor patients. Patients underwent a comprehensive ophthalmologic exam at the NIH, which included visual acuity, perimetry, electroretinography, and imaging documenting the presence of RP consistent with Usher syndrome. Visual field and visual acuity are presented in Table 2 and Table S5.

### 2.2 | Assessments

Criteria for data interpretation and test equipment used for individual tests are presented in Tables S1 and S2 in the supplement. Most patients completed all testing described below, although equipment malfunction and time constraints limited complete assessment of some patients (Table 1).

#### 2.2.1 | Audiologic evaluation

Audiologic evaluation included pure-tone threshold testing by air conduction (0.125, 0.25, 0.5, 1, 2, 3, 4, 6, and 8 kHz) and bone conduction (0.125, 0.25, 0.5, 1, 2, 3, 4 kHz). Pure-tone thresholds were classified for degree and type of hearing loss using a four-frequency (0.5/1/2/4 kHz) pure-tone average (4F-PTA) and three frequency (0.5/1/2 kHz) pure-tone average, respectively (Table S1). Here, we report findings for the ear with the better 4F-PTA.

#### 2.2.2 | Vestibular and balance assessment

Vestibular testing included measurement of the vestibulo-ocular reflex (VOR) elicited by stimulation of the horizontal semicircular canal during bithermal caloric irrigations and sinusoidal harmonic acceleration (SHA) using a rotary chair. The VOR to bithermal air-caloric stimulation (24 and 50°C) was classified as normal, unilateral hypofunction, bilateral hypofunction, or absent. Horizontal semicircular canal reactivity to SHA was recorded at octave frequencies between 0.01 and 0.64 Hz to extend assessment of the VOR beyond the traditional caloric stimulus, which is equivalent to 0.003 Hz. The VOR was interpreted as absent, present with normal gain, or present with reduced gain. All VOR responses were inspected independently by two audiologists to confirm presence of a response, operationally defined as appropriately beating nystagmus with a clear slow and fast phase temporally linked with chair velocity and caloric stimulation.

Cervical vestibular evoked myogenic potentials (cVEMP), which indirectly assess saccular function, were elicited via an air-conducted 0.5 kHz tone burst (Blackman gating, 2 ms rise/fall time, 0 ms plateau) presented monaurally via insert earphones at 100 to 107 dB nHL and a stimulus repetition rate of 5.1/s. Myogenic activity was recorded from surface electrodes placed on the ipsilateral sternocleidomastoid muscle (reference), sternum (active), and forehead (ground). The cVEMP was interpreted based on presence or absence of the P1-N1 response and interaural symmetry of the P1-N1 amplitude.

**TABLE 1** Patient characteristics and tests completed for each genetically determined Usher syndrome type

Usher type	Gene	Number of patients	Age in years, mean (SD)	Caloric testing (n)	SHA (n)	cVEMP (n)	SOT (n)
USH1		26	34.5 (15.8)	24	24	20	26
	<i>MYO7A</i>	11	31.7 (17.3)	11	11	9	11
	<i>USH1C</i>	3	37.9 (14.0)	3	3	3	3
	<i>CDH23</i>	6	46.2 (15.2)	4	5	2	6
	<i>PCDH15</i>	5	43.5 (16.6)	5	4	5	5
	<i>USH1G</i>	1	38.9	1	1	1	1
USH2		57	40.8 (15.3)	51	49	39	53
	<i>USH2A</i>	51	40.9 (15.8)	45	44	35	48
	<i>ADGRV1</i>	6	43.1 (12.6)	6	5	4	5
USH3		7	41.8 (18.2)	3	6	6	7
	<i>CLRN1</i>	7	41.8 (18.2)	3	6	6	7

Abbreviations: cVEMP, cervical vestibular evoked myogenic potential; SHA, sinusoidal harmonic acceleration; SOT, sensory organization test.

Functional balance was assessed by the sensory organization test (SOT), a subtest of platform posturography, which provides a measure of postural stability in conditions that rely on somatosensory, visual, or vestibular input. The SOT consists of a series of six conditions (1-6) during which an equilibrium score is calculated through measurement of the patient's sway on a force plate platform. During the first three conditions (1-3) the platform is fixed, and for the other three conditions (4-6) the unfixed platform moves with patient sway. Vestibular-dependent conditions (5, 6) are those where somatosensory and visual stimuli are removed or altered.<sup>32</sup> The vestibular contribution to postural stability was evaluated as normal, reduced, or absent based on the vestibular sensory analysis score (ratio of conditions 5-1). A conditionally-weighted SOT composite score (Table S1) was used to assess overall postural stability and fall risk.

### 2.3 | Genetic analysis

Genetic variants were identified by Sanger sequencing all the annotated exons of genes associated with Usher syndrome, or from whole-exome sequencing (WES) using Illumina or Applied Biosystems next-generation sequencing (NGS) platforms, or both. Details of Sanger sequencing<sup>33</sup> and NGS<sup>34</sup> have been previously reported. All patients were categorized based upon genotype into one of the following groups: USH1 (variants of *MYO7A*, *USH1C*, *CDH23*, *PCDH15*, or *USH1G*), USH2 (variants of *USH2A* or *ADGRV1*), or USH3 (*CLRN1*).

### 2.4 | Multiplex ligation-dependent probe amplification assay

In order to determine the copy number variation in *USH2A*, two multiplex ligation-dependent probe amplification (MLPA) probemixes were utilized (SALSA MLPA P361 & P362), whereas for *PCDH15* a single probemix was used (SALSA MLPA P292) according to manufacturer's instructions (MRC Holland, Amsterdam). Briefly, 100 nanograms of

DNA for the sample and the references was diluted in 5  $\mu$ l of low Tris-ethylenediamine tetraacetic acid and denatured at 98°C for 5 min, after which 3  $\mu$ l of MLPA probe mix and buffer was added at room temperature. The reaction mixture was denatured at 95°C for 1 min and incubated for 16-h at 60°C for probe hybridization with the target sequences. After the hybridization, ligation mixture (32  $\mu$ l) was added and incubated at 54°C for 15 min for the ligation of the hybridized probes, followed by heat inactivation step at 98°C for 5 min. Furthermore, fluorescent universal primer pair was used for multiplex polymerase chain reaction (PCR) amplification according to the kit protocol. For the analysis of the amplified PCR products, 0.7  $\mu$ l of each amplified PCR product was mixed with 0.2  $\mu$ l of GeneScan 500 LIZ dye Size Standard in 9  $\mu$ l of deionized formamide, which was denatured for 3 min at 86°C, followed by cooling for 2 min at 4°C. The samples were then run on 3730xl DNA Analyzer (Applied Biosystems). The genotype data files were analyzed using Coffalyser.Net software. Three control samples were included with each MLPA probemix run. The two deletions observed were characterized with long range PCR using LA Taq DNA polymerase (Takara, California) to validate MLPA results.

### 2.5 | Data analysis

Data were analyzed using the SPSS, version 25 (IBM Corp). A one-way analysis of variance was performed to compare age between the genetically classified Usher types and subtypes, with a Tukey's post hoc for multiple comparisons. Because age-related loss of the cVEMP response has been reported,<sup>35</sup> a Mann-Whitney *U* was performed to compare the ages of patients with and without a cVEMP response based on the mutated genes in the USH2 group. Chi-square analysis was performed to identify any significant association between specific USH1 genes and presence vs absence of the VOR during SHA. A linear regression was conducted to investigate the effect of aging on the SOT composite score and a multiple regression was performed to investigate the effects of visual field and visual acuity on condition 4 (vision dependent) of the SOT. Statistical significance was set at  $P \leq 0.05$ .

**TABLE 2** Phenotypic characteristics and genetic variants for USH1 (n = 13) and USH2 (n = 16) patients with atypical vestibular findings

LMG ID	Gene	Allele 1	Allele 2	Age (years)	Degree of HL	Caloric test	SHA	cVEMP	SOT-VEST	Visual field <sup>a</sup>	Visual acuity <sup>b</sup>
USH1											
1687	CDH23	c.5237G > A, p.R1746Q	c.7872G > A	58.2	Profound	Absent	Low	—	Absent	18	50
1856	CDH23	c.3016G > A, p.E1006K	c.3369 + 1G > A	27.4	Profound	—	Low	Absent	Absent	19	40
1846	MYO7A	c.5392C > T, p.Q1798X	c.4951G > A, p.G1651S	68.5	Profound	Absent	Low	Absent	Absent	18	32
1862	MYO7A	c.1370C > T, p.A457V	c.401 T > A, p.I134N	21.5	Profound	BH	Absent	—	Low	126	20
1967	MYO7A	c.5428A > T, p.K1810X	c.6025G > A, p.A2009T	26.7	Profound	WNL	WNL <sup>c</sup>	Present	Low	56	25
1999 <sup>d</sup>	MYO7A	c.2904G > T, p.E968D	c.224dup, p.D75EfsX65	47.4	Profound	Absent	Low	Absent	Absent	25	100
2000 <sup>d</sup>	MYO7A	c.487G > A, p.G163R	c.1189G > A, p.A397T	48.9	Profound	Absent	Low	Absent	Absent	80	25
2001 <sup>d</sup>	MYO7A	c.487G > A, p.G163R	c.2904G > T, p.E968D	22.2	Profound	Absent	Low	Absent	Absent	85	20
2002 <sup>d</sup>	MYO7A	c.1189G > A, p.A397T	c.2904G > T, p.E968D	16.1	Profound	Absent	Low	Absent	Low	137	25
1863	PCDH15	c.4733_4736delTCAG; p.V1578AfsX6	<b>c.92-528C &gt; T</b>	56.7	Moderate	BH	Absent	Absent	Absent	140	25
2098	PCDH15	c.1737_1738insA, p.A580SfsX9	c.1304A > C, p.D435A	19.3	Profound	Absent	Low	Absent	Absent	32	25
1725	USH1G	c.113G > A, p.W38X	c.113G > A, p.W38X	38.8	Profound	Absent	Absent	Absent	Low	5	40
1920	USH1C	c.216G > A	c.216G > A	41.6	Profound	Absent	Low	Absent	Low	18	63
USH2											
1855	USH2A	c.2299delG, p.E767SfsX21	c.6383G > T, p.C2128F	59.8	Moderate	BH	WNL	—	WNL	0	LP
1903	USH2A	c.920_923dupGCCA, p.H308QfsX16	Exon 27 deleted	75.7	Severe	—	—	—	Low	0	HM
1970	USH2A	c.1859G > T, p.C620F	c.2276G > T, p.C759F	57.2	Moderate	WNL	WNL	Present	Low	10	20
2009	USH2A	c.920_923dupGCCA, p.H308QfsX16	c.11864G > A, p.W3955X	58.9	Severe	WNL	WNL	Absent	WNL	37	63
2062	USH2A	c.2299delG, p.E767SfsX21	c.2299delG, p.E767SfsX21	68.7	Profound	—	WNL	—	Absent	0	HM
2115	USH2A	c.1214delA, p.N405IfsX3	c.15017C > T, p.T5006M	17.0	Moderate	WNL	WNL	Absent	WNL	30	32
2142	USH2A	c.9469C > T, p.Q3157X	c.13040_13062delinsTCAGAAAGTCA, p.T4347IfsX22	28.2	Severe	UH	WNL	Present	WNL	140	16
2157	USH2A	c.956G > A, p.C319Y	c.15089C > A, p.S5030X	23.6	Moderate	—	WNL	Absent	WNL	80	32
2171	USH2A	c.2299delG, p.E767SfsX21	—	42.5	Moderate	WNL	WNL	Present	Low	11	32
2176	USH2A	c.2299delG, p.E767SfsX21	c.4714C > T, p.L1572F	43.1	Moderate	—	—	Absent	WNL	13	40
2177	USH2A	c.1679delC, p.P560IfsX31	<b>c.4133_4134dupTC, p.N1379SfsX54</b>	38.2	Moderate	UH	WNL	WNL	WNL	115	32
2193	USH2A	c.4758 + 1G > A	c.8584C > T, p.Q2862X	55.1	Severe	UH	Low	Present	WNL	4	63
2200	USH2A	c.1876C > T, p.R626X	<b>c.4396 + 2 T &gt; G</b>	48.7	Moderate	WNL	WNL	Absent	WNL	20	20
2217	USH2A	c.1541 T > C, p.I514T	c.5614_5620del	61.6	Moderate	WNL	WNL	Absent	Low	10	50

(Continues)

TABLE 2 (Continued)

LMG ID	Gene	Allele 1	Allele 2	Age (years)	Degree of HL	Caloric test	SHA	cVEMP	SOT-VEST	Visual field <sup>a</sup>	Visual acuity <sup>b</sup>
2069	ADGRV1	p.S4880fs	p.P194H or p.R2959Q	36.9	Moderate	UH	WNL	WNL	WNL	19	40
2219	ADGRV1	<b>c.954_955insAATC, p.Q318NfsX8</b>	<b>c.11771delT, p.V3924LfsX11</b>	29.9	Moderate	UH	WNL	Present	WNL	105	32

Note: Bolded text in table identifies novel genetic variants (Allele 1 and Allele 2) and atypical clinical findings. Transcript Accession number: MYO7A: NM\_000260.4, USH1G: NM\_173477.5, PCDH15: NM\_033056.4, CDH23: NM\_022124.6, USH1C: NM\_005709.4.

Abbreviations: BH, bilateral hypofunction; cVEMP, cervical vestibular evoked myogenic potential; HL, hearing loss; HM, hand motion perception; SHA, sinusoidal harmonic acceleration; SOT-VEST, sensory organization test-vestibular component; UH, unilateral hypofunction; WNL, within normal limits.

<sup>a</sup>Visual field represents the horizontal extent of the central continuous field in degrees.

<sup>b</sup>Visual acuity measured in Snellen obtained using an ETDRS chart.

<sup>c</sup>Estimated as WNL based on visual inspection of response, data were not saved.

<sup>d</sup>1999, 2000, 2001, and 2002 are members of family LMG353 and phase is known to be in trans-based on sequencing of both parents.

## 3 | RESULTS

### 3.1 | Genotype

Twenty-six of 90 (28.9%) patients had deleterious variants in USH1 genes, 57 (63.3%) in USH2 genes, and seven (7.8%) in USH3 genes (Table 1). All had two biallelic deleterious variants apart from the eight patients with only a single variant in USH2A. In two of these eight (25%) patients with only a single causative variant, we were also able to identify a second copy number variant (CNV) of USH2A (Table S6), which was confirmed by long range PCR (Figure S3). Most of the variants are pathogenic or likely pathogenic according to ACMG<sup>36</sup> classification in all but one variant of ADGRV1 (p.K5421M) in LMG 212, which is predicted to be a variant of uncertain significance. There was not a significant difference in age between patients in each of the three Usher groups ( $F(2) = 1.64, P = 0.199$ ), nor was there a difference in age within the USH1 subgroups, nor the USH2 subgroups classified by genotype ( $F(4) = 0.60, P = 0.66$ ;  $F(1) = 0.95, P = 0.76$ , respectively).

### 3.2 | Auditory phenotype

All patients had bilateral SNHL of varying degrees (Figure S1). Twenty-five of 26 (96%) patients in the USH1 group had profound hearing loss and one patient with biallelic mutations in PCDH15 had bilateral moderate hearing loss. In the USH2 group, the degree of hearing loss was most often moderate ( $n = 38, 66.7%$ ), although some patients had severe ( $n = 17, 29.8%$ ) or profound ( $n = 2, 3.5%$ ) hearing loss. Four of seven (57%) patients in the USH3 group had severe hearing loss, while the remaining three (43%) had profound hearing loss.

### 3.3 | Vestibular and balance phenotype

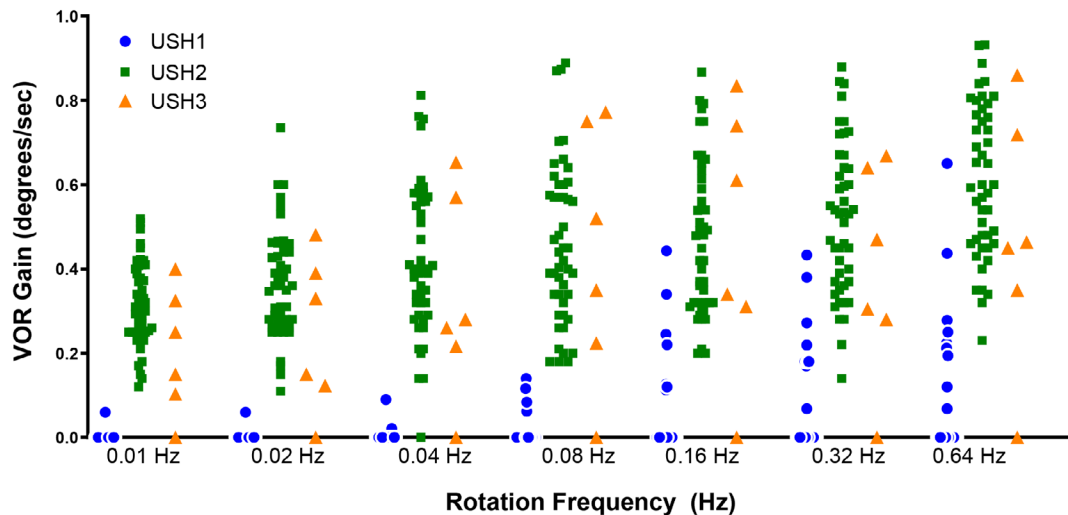
The results for individual vestibular assessments are described below for each Usher type. The spectrum of phenotypic and genetic findings for each patient with atypical results is presented in Table 2 and findings for those with typical results are presented in Table S5.

#### 3.3.1 | Caloric testing

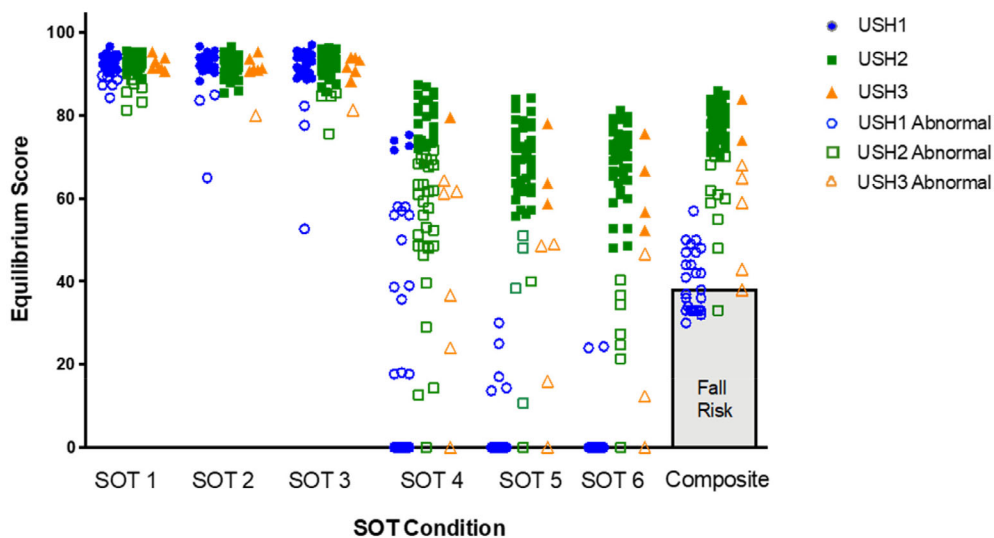
An absent VOR to caloric stimulation was documented in 21 of 24 (87.5%) patients with USH1 who had caloric testing. Three (12.5%) patients had a measurable VOR to caloric stimulation; two had bilateral hypofunction (biallelic pathogenic variants in PCDH15 and MYO7A, respectively) and the other had a clinically normal response (biallelic pathogenic variants in MYO7A). Forty-five of 51 (88%) patients with USH2 had a normal VOR response to caloric stimulation and six (12%) had reduced VOR responses and a negative history of vertigo. Four patients (8%) with USH2A mutations had reduced VOR reactivity; one (2%) had bilateral hypofunction and three (6%) had unilateral hypofunction. Additionally, two patients with USH2C mutations (ADGRV1) also had







**FIGURE 2** Gain of the vestibulo-ocular reflex (VOR) induced during rotary chair testing for individual patients grouped by genetically defined type of Usher syndrome [Colour figure can be viewed at [wileyonlinelibrary.com](#)]



**FIGURE 3** Sensory organization test (SOT) equilibrium scores for all six conditions (averaged over three trials) and composite score for all patients. Filled symbols represent scores that fall within the normal range by age, unfilled symbols are scores below the fifth percentile for age. Composite scores that fall within the shaded gray area indicate patients are considered at risk for falls [Colour figure can be viewed at [wileyonlinelibrary.com](#)]

90 patients with all three types of Usher syndrome. Previously published studies have employed a limited set of vestibular or balance tests, most commonly the caloric test.<sup>16,31</sup>

Normal saccular function, as measured by the cVEMP test, rarely occurs in patients with USH1. We anticipated that saccular function would be absent based on the classically defined clinical phenotype of profound SNHL and vestibular areflexia. This was the case for all but one of the patients in our USH1 group (LMG1967) who has biallelic pathogenic variants of *MYO7A* and a measurable VOR to both caloric and rotational stimulation of the horizontal semicircular canals. While Magliulo et al<sup>23</sup> described unilateral normal cVEMP responses in three of four patients with clinically defined Usher syndrome type I, the lack of genetic confirmation and the patients' past histories of vertigo raises doubt about the Usher syndrome diagnosis.<sup>37</sup> To our knowledge, ours is the first report of bilateral normal saccular function in a patient with genetically confirmed USH1.

Dysfunction in the saccular otolith pathway can exist in patients with *USH2A* pathogenic variants in the absence of current or past vertigo. We anticipated normal saccular function in patients with USH2 based on the classically described phenotype that includes normal vestibular function. We documented bilateral abnormal saccular function in six (17%) of 35 patients with mutations in *USH2A*. While there are known age-related changes in the cVEMP including absence of the P1-N1 response that increases from 7% in the fifth decade to 32% in the eighth decade,<sup>35</sup> age did not explain absence of a cVEMP in our *USH2A* group. Magliulo et al<sup>24</sup> reported bilateral saccular dysfunction in two of five patients with genetically confirmed USH2 (one with mutations in *USH2A*, one with mutations in *ADGRV1*) and histories of sporadic vertigo. Here, we extend the observation of saccular dysfunction in *USH2A* to those with no current or past history of vertigo.

Traditional phenotypes would dictate an absence of vestibular response for patients with USH1. Our study confirms residual

vestibular and balance function for patients with pathogenic variants in *USH1* genes including *MYO7A*, *CDH23*, or *USH1G*, and extends this observation to patients with mutations in *PCDH15* or *USH1C*. There was evidence of residual horizontal semicircular canal function in 46.2% of our *USH1* subgroup (Table 2), documented by the presence of a VOR to rotary or caloric stimulation. Conversely, a normal vestibular response for patients with *USH2* would be classically expected, however both unilateral and bilateral reduced VOR gain for six patients in this group was observed during rotational and caloric stimulation. Others have reported atypical caloric responses in patients with *USH1*<sup>11,16</sup>; we extend this observation to patients with *USH2*.

Our platform posturography findings revealed that 19% (5 of 26) of patients with *USH1* were unexpectedly able to maintain sufficient postural stability to prevent a fall during vestibular-dependent SOT conditions. This suggests that some individuals with *USH1* are able to utilize alternative sensory input (eg, somatosensory) to maintain postural stability in vestibular dependent environments. Similarly, we hypothesized that patients with *USH2* would have normal postural stability on vestibular-dependent conditions. While this was the case for the majority of our *USH2* group, we observed reduced postural stability and falls for 9% (5 of 53) of our cohort.

Visual-field, but not visual acuity, correlates with postural stability in patients with Usher syndrome. Specifically, there was a reduction in postural stability in patients with Usher syndrome that not only resulted from reduced or absent vestibular function but also correlated with declining visual-field. This same relationship was not observed with visual acuity. We confirm previous reports identifying an overall aging effect on postural stability.<sup>32</sup> Our posturography data

further support and expand upon observations by Caldani et al<sup>17</sup> that patients with Usher syndrome have reduced postural stability that results from deficits in visual and vestibular contributions to balance.

Platform posturography can be used to assess fall risk using the SOT composite score. Whitney et al,<sup>38</sup> found that a composite score  $\leq 38$  on SOT is associated with an increased risk for falls over the preceding six-months. Based on this criterion, we found that 13 (50%) of those with *USH1* and one (2%) with *USH2* would be identified as being at risk for falling (Figure 3). These findings have implications for personalized and targeted counseling and (re)habilitation of postural stability and balance in patients with Usher syndrome. This study also extends knowledge of postural stability in *USH1* and *USH2*, which has been previously limited to one study in a genetically confirmed population,<sup>17</sup> and supplements the comprehensive report of variable SOT findings in *USH3*.<sup>39</sup>

As with most biological systems, age has a deleterious effect on visual and vestibular physiology. Age was a significant factor in the declining postural stability observed in the patients within our cohort. As such, age is likely a significant compound comorbidity in the declining balance function in patients with Usher syndrome, and may, create an added disadvantage for instability.

All four patients diagnosed with *USH1* in family LMG353 (Figure 4) had an atypical finding of measurable VOR gain on SHA (rotational) testing. Four variants of *MYO7A*, a gene classically associated with *USH1*, were confirmed to segregate among these four patients (ID: 1999-2002) (Figure 4). Of the four variants, two were pathogenic (c.2904G>T, p.E968D; c.224dupA, p.Asp75Glufs\*65) and were present in father, whereas the mother had two likely pathogenic variants (c.487G>C, p.G163R; c.1189G>A, p.A397T), while the

### LMG353

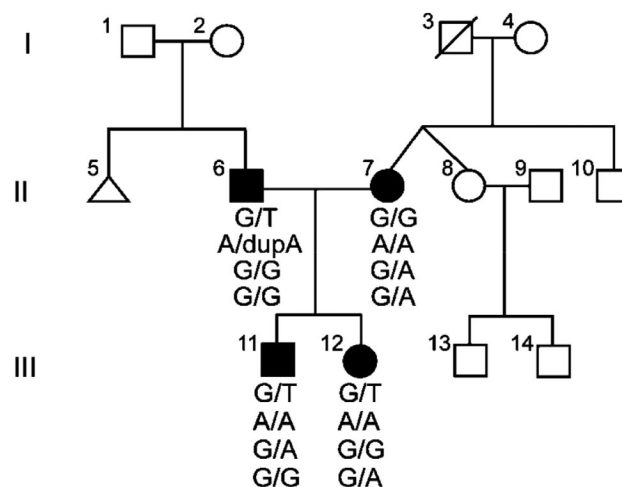
*MYO7A*: c.2904G>T (p.Glu968Asp)

*MYO7A*: c.224dupA (p.Asp75Glufs\*65)

*MYO7A*: c.487G>A (p.Gly163Arg)

*MYO7A*: c.1189G>A (p.Ala397Thr)

■ ● Usher syndrome Type I  
□ ○ unaffected  
◻ deceased  
△ spontaneous abortion



**FIGURE 4** Pedigree of family LMG353 segregating atypical Usher syndrome. Squares and circles represent male and female patients. Four different variants of *MYO7A* are cosegregating with the phenotype in four patients (ID: 1999-2002) with atypical Usher syndrome. Genotypes are mentioned under each patient



offspring had one pathogenic and one likely pathogenic variant each. These variants are present in compound heterozygosity and are predicted to be pathogenic by various *in silico* tools.<sup>5,40-42</sup>

In our study of 90 patients with Usher syndrome, 105 likely pathogenic variants were identified in genes definitively known to underlie the disease<sup>43</sup> (Table 2, Table S5). We identified 13 novel variants in four of the Usher syndrome genes (Table 2 and Table S4). Previously reported pathogenic variants were also identified in our cohort in the *USH1C*, *MYO7A*, *CDH23*, and *USH1G* genes. In eight patients, only one variant of an Usher gene was identified after exome sequencing. However, using MLPA analyses, we identified a CNV as the second allele in the *USH2A* gene in two of these eight cases (Table S6) and confirmed by long range PCR of approximately 5Kb deletions (Figure S3). Whereas, for the remaining six individuals we could not rule out the possibility of noncoding regulatory variants disrupting transcription or splicing; five had a classical Usher syndrome phenotype and one (LMG2171) had clinical findings considered atypical due to low scores on vestibular dependent SOT conditions. Additionally, in our cohort of 90 USH subjects, we did not identify variants in *CIB2*, *PDZD7*, and *HARS* which are either debatable USH genes or are very rare contributors to Usher syndrome.<sup>7,8</sup>

Our findings have implications for the diagnosis and management of patients with Usher syndrome, as they fail to confirm uniform genotype-phenotype correlations. This is especially important in the neonatal population who may be screened for hearing loss at birth and subsequently identified as having congenital deafness and two pathogenic variants in genes associated with both Usher syndrome and nonsyndromic deafness.<sup>44</sup> In this case, demonstration of intact vestibular function is not sufficient to rule out Usher syndrome and continued surveillance for the onset of RP is warranted.

One limitation of this study was the small number of patients with mutations in genes other than *MYO7A* for USH1 and *USH2A* for USH2. Such limited sample sizes prevent meaningful statistical analyses for differences among USH1 genes and between *USH2A* and *ADGRV1* for USH2. Moreover, although we were able to identify biallelic pathogenic variants in the majority of patients, for some cases due to lack of parental gDNA samples we were unable to perform a segregation analysis to determine the phase of the two variants whether they are in the *cis* or *trans*. Another limitation was that a complete vestibular test battery could not be performed in some patients due to time limitations, combined with a lack of studies investigating the utricle and vertical semicircular canals. It is recommended that future studies expand the vestibular phenotype even further to include utricular function through ocular-VEMP and assessment of the anterior and posterior semicircular canals.

Our results provide comprehensive evidence of a lack of a definitive vestibular genotype-phenotype correlation for 29 of 90 (32%) patients in our cohort with Usher syndrome, 28 of whom had biallelic mutations in USH genes. Excluding the six patients with just one known pathogenic variant in an Usher syndrome gene does not alter this conclusion, as only one of these individuals presented with discordant clinical findings. The lack of definitive genotypic to vestibular phenotypic findings, and no clear vestibular patterns among atypical

cases, indicates that vestibular results are not an infallible criterion for differentiating the USH types, nor is the Usher syndrome genotype sufficient to reliably predict vestibular function.

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## CONFLICT OF INTEREST

The authors declare no potential conflict of interest.

## PEER REVIEW

The peer review history for this article is available at <https://publons.com/publon/10.1111/cge.13868>.

## DATA AVAILABILITY STATEMENT

The data that support the findings of this study are available from the corresponding author upon reasonable request.

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## REFERENCES

- Friedman TB, Schultz JM, Ahmed ZM, Tsilou ET, Brewer CC. Usher syndrome: hearing loss with vision loss. *Adv Otorhinolaryngol*. 2011; 70:56-65.
- Griffith AJ, Friedman TB. Chapter 26. In: Wackym PA, Snow JB, eds. *Ballenger's Otorhinolaryngology Head and Neck Surgery*. Vol 1. Shelton: People's Medical Publishing House; 2016.
- Petit C. Usher syndrome: from genetics to pathogenesis. *Annu Rev Genomics Hum Genet*. 2001;2:271-297.
- Lentz J, Keats BJB. Usher syndrome type I. In: Adam MP, Ardinger HH, Pagon RA, et al., eds. *GeneReviews([R])*. Seattle, WA: University of Washington; 1993.
- Kimberling WJ, Hildebrand MS, Shearer AE, et al. Frequency of Usher syndrome in two pediatric populations: implications for genetic screening of deaf and hard of hearing children. *Genet Med*. 2010;12(8):512-516.
- Yan D, Liu XZ. Genetics and pathological mechanisms of Usher syndrome. *J Hum Genet*. 2010;55(6):327-335.
- Booth KT, Azaiez H, Kahrizi K, et al. PDZD7 and hearing loss: more than just a modifier. *Am J Med Genet A*. 2015;167(12):2957-2965.
- Booth KT, Kahrizi K, Babanejad M, et al. Variants in *CIB2* cause DFNB48 and not USH1J. *Clin Genet*. 2018;93(4):812-821.
- Sanjurjo-Soriano C, Erkilic N, Baux D, et al. Genome editing in patient iPSCs corrects the most prevalent *USH2A* mutations and reveals intriguing mutant mRNA expression profiles. *Mol Ther Methods Clin Dev*. 2020;17:156-173.
- Nolen R, Hufnagel R, Friedman T, et al. Atypical and ultra-rare Usher syndrome: a review. *Ophthalmic Genet*. 2020;41(5):401-412. <https://doi.org/10.1080/13816810.2020.1747090>[Epub].

11. Astuto LM, Bork JM, Weston MD, et al. CDH23 mutation and phenotype heterogeneity: a profile of 107 diverse families with Usher syndrome and nonsyndromic deafness. *Am J Hum Genet.* 2002;71(2):262-275.
12. Liu XZ, Hope C, Walsh J, et al. Mutations in the myosin VIIA gene cause a wide phenotypic spectrum, including atypical Usher syndrome. *Am J Hum Genet.* 1998;63(3):909-912.
13. Kalay E, de Brouwer AP, Caylan R, et al. A novel D458V mutation in the SANS PDZ binding motif causes atypical Usher syndrome. *J Mol Med.* 2005;83(12):1025-1032.
14. Bashir R, Fatima A, Naz S. A frameshift mutation in SANS results in atypical Usher syndrome. *Clin Genet.* 2010;78(6):601-603.
15. Blanco-Kelly F, Jaijo T, Aller E, et al. Clinical aspects of Usher syndrome and the USH2A gene in a cohort of 433 patients. *JAMA Ophthalmol.* 2015;133(2):157-164.
16. Zina ZB, Masmoudi S, Ayadi H, et al. From DFNB2 to Usher syndrome: variable expressivity of the same disease. *Am J Med Genet.* 2001;101(2):181-183.
17. Caldani S, Bucci MP, Tisne M, Audo I, Van Den Abbeele T, Wiener-Vacher S. Postural instability in subjects with Usher syndrome. *Front Neurol.* 2019;10:830.
18. Liu XZ, Hope C, Liang CY, et al. A mutation (2314delG) in the Usher syndrome type IIA gene: high prevalence and phenotypic variation. *Am J Hum Genet.* 1999;64(4):1221-1225.
19. Bernal S, Meda C, Solans T, et al. Clinical and genetic studies in Spanish patients with Usher syndrome type II: description of new mutations and evidence for a lack of genotype-phenotype correlation. *Clin Genet.* 2005;68(3):204-214.
20. Aller E, Jaijo T, Oltra S, et al. Mutation screening of USH3 gene (clarin-1) in Spanish patients with Usher syndrome: low prevalence and phenotypic variability. *Clin Genet.* 2004;66(6):525-529.
21. Garcia-Garcia G, Aparisi MJ, Jaijo T, et al. Mutational screening of the USH2A gene in Spanish USH patients reveals 23 novel pathogenic mutations. *Orphanet J Rare Dis.* 2011;6:65.
22. Steele-Stallard HB, Le Quesne Stabej P, Lenassi E, et al. Screening for duplications, deletions and a common intronic mutation detects 35% of second mutations in patients with USH2A monoallelic mutations on sanger sequencing. *Orphanet J Rare Dis.* 2013;8:122.
23. Magliulo G, Iannella G, Gagliardi S, et al. Usher's syndrome: evaluation of the vestibular system with cervical and ocular vestibular evoked myogenic potentials and the video head impulse test. *Otol Neurotol.* 2015;36(8):1421-1427.
24. Magliulo G, Iannella G, Gagliardi S, et al. Usher's syndrome type II: a comparative study of genetic mutations and vestibular system evaluation. *Otolaryngol Head Neck Surg.* 2017;157(5):853-860.
25. Smith RJ, Berlin CI, Hejtmancik JF, et al. Clinical diagnosis of the usher syndromes. Usher syndrome consortium. *Am J Med Genet.* 1994;50(1):32-38.
26. Kimberling WJ, Moller CG, Davenport SL, et al. Usher syndrome: clinical findings and gene localization studies. *Laryngoscope.* 1989;99(1):66-72.
27. Dammeyer J. Development and characteristics of children with Usher syndrome and CHARGE syndrome. *Int J Pediatr Otorhinolaryngol.* 2012;76(9):1292-1296.
28. Hope CI, Bunday S, Proops D, Fielder AR. Usher syndrome in the city of Birmingham—prevalence and clinical classification. *Br J Ophthalmol.* 1997;81(1):46-53.
29. Jatana KR, Thomas D, Weber L, Mets MB, Silverman JB, Young NM. Usher syndrome: characteristics and outcomes of pediatric cochlear implant recipients. *Otol Neurotol.* 2013;34(3):484-489.
30. Hmani-Aifa M, Ben Arab S, Kharrat K, et al. Distinctive audiometric features between USH2A and USH2B subtypes of Usher syndrome. *J Med Genet.* 2002;39(4):281-283.
31. Ben Rebeh I, Moriniere M, Ayadi L, et al. Reinforcement of a minor alternative splicing event in MYO7A due to a missense mutation results in a mild form of retinopathy and deafness. *Mol Vis.* 2010;16:1898-1906.
32. Faraldo-Garcia A, Santos-Perez S, Crujeiras R, Soto-Varela A. Postural changes associated with ageing on the sensory organization test and the limits of stability in healthy subjects. *Auris Nasus Larynx.* 2016;43(2):149-154.
33. Bork JM, Peters LM, Riazuddin S, et al. Usher syndrome 1D and non-syndromic autosomal recessive deafness DFNB12 are caused by allelic mutations of the novel cadherin-like gene CDH23. *Am J Hum Genet.* 2001;68(1):26-37.
34. Wang X, Zein WM, D'Souza L, et al. Applying next generation sequencing with microdroplet PCR to determine the disease-causing mutations in retinal dystrophies. *BMC Ophthalmol.* 2017;17(1):157.
35. Piker EG, Baloh RW, Witsell DL, Garrison DB, Lee WT. Assessment of the clinical utility of cervical and ocular vestibular evoked myogenic potential testing in elderly patients. *Otol Neurotol.* 2015;36(7):1238-1244.
36. Richards S, Aziz N, Bale S, et al. Standards and guidelines for the interpretation of sequence variants: a joint consensus recommendation of the American College of Medical Genetics and Genomics and the Association for Molecular Pathology. *Genet Med.* 2015;17(5):405-424.
37. Hartel BP, Pennings RJ, van Wijk E. Comment on "Usher's syndrome: evaluation of the vestibular system with cervical and ocular vestibular evoked myogenic potentials and the video head impulse test". *Otol Neurotol.* 2016;37(5):608.
38. Whitney SL, Marchetti GF, Schade AI. The relationship between falls history and computerized dynamic posturography in persons with balance and vestibular disorders. *Arch Phys Med Rehabil.* 2006;87(3):402-407.
39. Sadeghi M, Cohn ES, Kimberling WJ, Tranebjaerg L, Moller C. Audio-logical and vestibular features in affected subjects with USH3: a genotype/phenotype correlation. *Int J Audiol.* 2005;44(5):307-316.
40. Roux AF, Faugere V, Le Guedard S, et al. Survey of the frequency of USH1 gene mutations in a cohort of Usher patients shows the importance of cadherin 23 and protocadherin 15 genes and establishes a detection rate of above 90%. *J Med Genet.* 2006;43(9):763-768.
41. 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(2):173-181.
42. Sloan-Heggen CM, Bierer AO, Shearer AE, et al. Comprehensive genetic testing in the clinical evaluation of 1119 patients with hearing loss. *Hum Genet.* 2016;135(4):441-450.
43. DiStefano MT, Hemphill SE, Oza AM, et al. ClinGen expert clinical validity curation of 164 hearing loss gene-disease pairs. *Genet Med.* 2019;21(10):2239-2247.
44. Schultz JM, Bhatti R, Madeo AC, et al. Allelic hierarchy of CDH23 mutations causing NON-syndromic deafness DFNB12 or Usher syndrome USH1D in compound heterozygotes. *J Med Genet.* 2011;48(11):767-775.

## SUPPORTING INFORMATION

Additional supporting information may be found online in the Supporting Information section at the end of this article.

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