



Genetic architecture and phenotypic landscape of *SLC26A4*-related hearing loss

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Abstract

Mutations of coding regions and splice sites of *SLC26A4* cause Pendred syndrome and nonsyndromic recessive hearing loss DFNB4. *SLC26A4* encodes pendrin, a transmembrane exchanger of anions and bases. The mutant *SLC26A4* phenotype is characterized by inner ear malformations, including an enlarged vestibular aqueduct (EVA), incomplete cochlear partition type II and modiolar hypoplasia, progressive and fluctuating hearing loss, and vestibular dysfunction. A thyroid iodine organification defect can lead to multinodular goiter and distinguishes Pendred syndrome from DFNB4. Pendred syndrome and DFNB4 are each inherited as an autosomal recessive trait caused by biallelic mutations of *SLC26A4* (M2). However, there are some EVA patients with only one detectable mutant allele (M1) of *SLC26A4*. In most European-Caucasian M1 patients, there is a haplotype that consists of 12 variants upstream of *SLC26A4*, called CEVA (Caucasian EVA), which acts as a pathogenic recessive allele in trans to mutations affecting the coding regions or splice sites of *SLC26A4*. This combination of an M1 genotype with the CEVA haplotype is associated with a less severe phenotype than the M2 genotype. The phenotype in EVA patients with no mutant alleles of *SLC26A4* (M0) has a very low recurrence probability and is likely to be caused by other factors.

Introduction

Hereditary hearing loss can be either syndromic, which includes abnormalities affecting other organs and tissues, or nonsyndromic, which is not associated with other signs and symptoms. Nonsyndromic hearing loss phenotypes and loci can be categorized as autosomal dominant (termed DFNA), autosomal recessive (DFNB), X-linked (DFNX), or mitochondrial. DFNA, DFNB, and DFNX phenotypes and loci are numbered in the order the genetic loci were first reported. The causative genes have been identified for more than 70% of the reported loci (Van Camp and Smith 2021).

The same gene can underlie both syndromic and nonsyndromic hearing loss. *SLC26A4* (solute carrier family 26, member 4), formally known as *PDS*, is the causative gene for Pendred syndrome and DFNB4 (Everett et al. 1997; Li

et al. 1998). Pendred syndrome was originally described by Vaughan Pendred in 1896 as an autosomal recessive disorder comprised of goiter (thyroid gland enlargement) and severe congenital deafness (Pendred 1896). DFNB4 was first reported in 1995 as nonsyndromic congenital recessive hearing loss mapping to chromosome 7q31 (Baldwin et al. 1995). Both Pendred syndrome and DFNB4 are associated with enlargement of the vestibular aqueduct (EVA), which is also referred to as dilated or large vestibular aqueduct (DVA or LVA, respectively). DFNB4 is thus a form of nonsyndromic EVA (NSEVA). The term “large vestibular aqueduct syndrome (LVAS)”, introduced by Valvassori and Clemis in 1978, refers to the auditory phenotype associated with Pendred syndrome, DFNB4/NSEVA, and other forms of nonsyndromic hearing loss of unknown etiology associated with EVA. Large vestibular aqueduct syndrome is not actually a syndrome, as defined above, although it can be associated with a hearing loss syndrome, such as Pendred syndrome. In this review, we refer to Pendred syndrome and DFNB4 as *SLC26A4*-related hearing loss (Fig. 1).

Mutations of *SLC26A4* are one of the most common causes of hereditary hearing loss worldwide (Park et al. 2003). *SLC26A4* encodes pendrin, which is expressed in a restricted tissue distribution that includes the inner ear,

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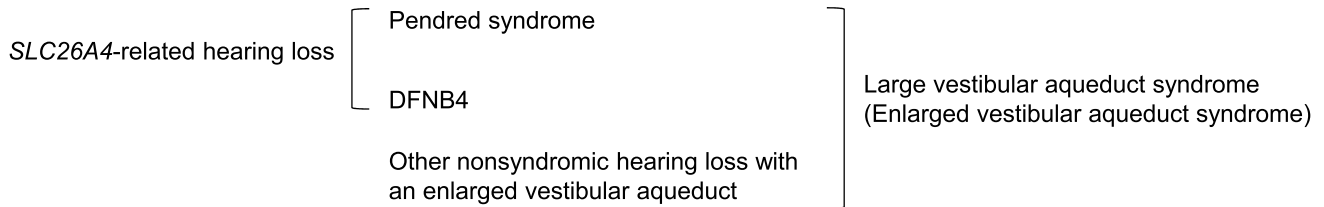


Fig. 1 Classification of diseases with hearing loss and an enlarged vestibular aqueduct

thyroid, and kidney (Everett et al. 1997, 2001; Royaux et al. 2003). Pendrin functions as a nonspecific exchanger of anions (e.g., Cl^- and I^-) and bases (e.g., HCO_3^- and OH^-) across apical plasma membranes of epithelial cells.

Clinical phenotype

SLC26A4-related hearing loss is associated with inner ear malformations, hearing loss, vestibular dysfunction, and thyroid abnormalities.

Inner ear malformations

EVA is a completely penetrant feature of *SLC26A4*-related hearing loss. The vestibular aqueduct, a bony canal surrounding the endolymphatic duct and a portion of the endolymphatic sac, is abnormally dilated in EVA ears. There are two commonly used radiologic definitions of EVA. The original (Valvassori) criterion of a midpoint VA diameter > 1.5 mm (Valvassori and Clemis 1978) has largely been replaced by the “Cincinnati criteria” of a midpoint diameter ≥ 1.0 mm or an operculum diameter ≥ 2.0 mm (Fig. 2A) (Boston et al. 2007; Vijayasekaran et al. 2007). Enlargement of the endolymphatic duct and sac are also observed by magnetic resonance imaging (MRI) of ears with *SLC26A4*-related hearing loss (Fig. 2B). *SLC26A4*-related hearing loss and EVA can be bilateral or unilateral. In a North American EVA cohort, 25% of subjects with unilateral EVA had one or two mutant alleles of *SLC26A4* (Chattaraj et al. 2013).

Another characteristic inner ear deformity in *SLC26A4*-related hearing loss is incomplete partition type II (IP-II). IP-II is a deformity in which the middle and apical turns of the cochlear duct coalesce to form a cystic apex, resulting in 1.5 turns instead of the normal 2.5 turns (Sennaroglu and Saatci 2002). A combination of IP-II and EVA (Mondini dysplasia) was present in the temporal bones of the 8-year-old deaf boy reported by Carlo Mondini in 1791 (Mondini 1997). The incidence of IP-II in EVA ears ranges from 21.7 to 73.9% (Forli et al. 2020; King et al. 2010; Mey et al. 2019b). The more common cochlear anomaly in *SLC26A4*-related hearing loss is hypoplasia or deficiency of the cochlear modiolus, which can be detected by MRI or computed

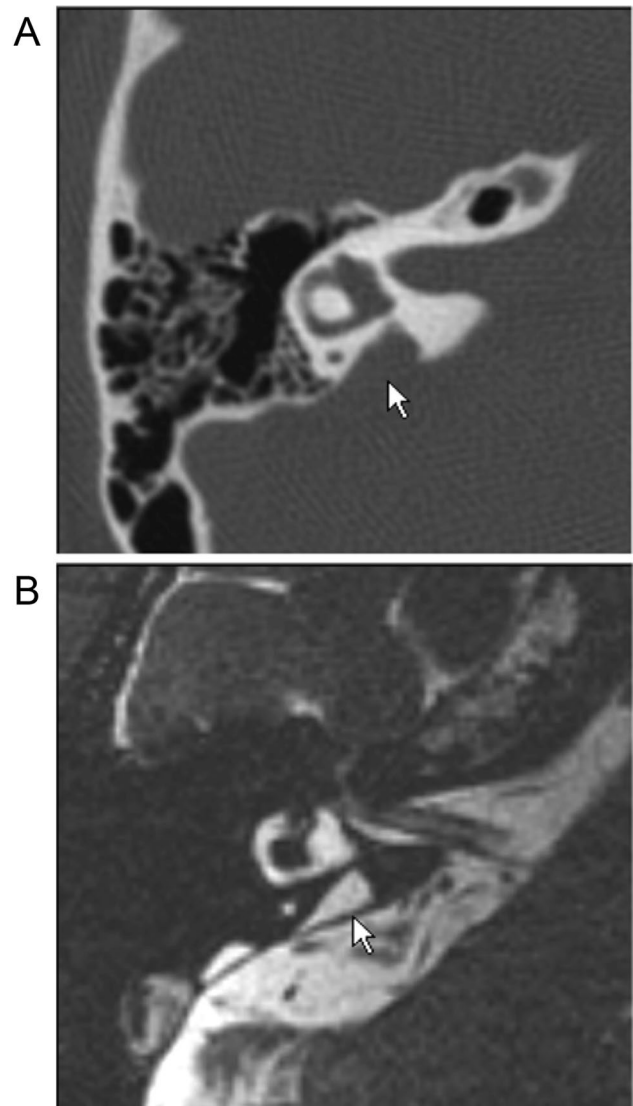


Fig. 2 Radiologic imaging of an enlarged vestibular aqueduct. Axial computed tomography (CT) scan (top) and magnetic resonance image (MRI) (bottom) of the same right ear with an enlarged vestibular aqueduct. Arrows in the top and bottom panels indicate the same location corresponding to the enlarged endolymphatic sac and duct represented by isodensity on CT and high signal intensity on MRI. Reproduced from <https://www.nidcd.nih.gov/health/enlarged-vestibular-aqueducts-and-childhood-hearing-loss>

tomography (CT) (Goldfeld et al. 2005; Lemmerling et al. 1997).

Audiological phenotype

The stereotypical presentation of *SLC26A4*-related hearing loss is a fluctuating or progressive sensorineural hearing loss (SNHL) with a pre-, peri- or even postlingual onset (Jackler and De La Cruz 1989; Levenson et al. 1989). The severity, laterality, and age of onset of SNHL are highly variable. Audiometry of *SLC26A4*-related hearing loss often shows air-bone gaps (indicative of conductive hearing loss) at low frequencies which results in mixed hearing loss (both sensorineural and conductive) in the presence of a normal middle ear. This is attributed to a “third-window” effect of EVA, in which the power of sound transmission within the labyrinth is shunted away from the cochlea (Merchant et al. 2007). The fluctuation or progression of the SNHL can occur in a stepwise incremental fashion and can be precipitated by minor head trauma or barotrauma. A study of 109 patients in Denmark with *SLC26A4*-related hearing loss demonstrated that the average level of hearing loss progressed and reached 80 dBHL by 6 years of age, whereas almost one half of the patients passed neonatal hearing screening (Mey et al. 2019a). This observation highlights the postnatal onset of SNHL in many ears with EVA.

Vestibular phenotype

Vestibular dysfunction also occurs in *SLC26A4*-related hearing loss. The reported prevalence of vestibular symptoms is 4–47% among patients with EVA (Antonelli et al. 1998; Berrettini et al. 2005; Grimmer and Hedlund 2007; Jackler and De La Cruz 1989; Jung et al. 2016; Valvassori and Clemis 1978; Yang et al. 2016; Zalewski et al. 2015). The symptoms can include episodic rotatory vertigo, clumsiness, head-tilting and vomiting, and a delayed onset (> 18 months of age) of independent ambulation. Abnormal results of vestibular function tests, including the caloric test, rotational chair test, video head impulse test (vHIT), and the cervical vestibular evoked myogenic potential (cVEMP) test, have been reported for some patients with EVA (Jung et al. 2016, 2017; Sheykhleslami et al. 2004; Yang et al. 2016; Zalewski et al. 2015; Zhou and Gopen 2011; Zhou et al. 2017). In a North American cohort of patients with EVA, 21 (32.8%) of 64 patients had caloric abnormalities, six (25.0%) of 24 patients had abnormal results of rotational chair testing, and two (22.2%) of 9 patients had abnormal cVEMP results (Zalewski et al. 2015). There was no correlation between the severity of hearing loss and vestibular signs and symptoms or abnormal vestibular test results. In a cohort of 31 Korean patients with biallelic mutations in *SLC26A4*, 16 patients (45.2%) had unilateral caloric weakness and two

patients (6.4%) had bilateral caloric weakness (Jung et al. 2016). Among 10 patients undergoing both the caloric test and vHIT in the Korean cohort, four patients (40%) had unilateral caloric weakness and one patient (10%) had abnormal vHIT results (Jung et al. 2017). These results suggest that the pathophysiologic mechanism of *SLC26A4* mutations in vestibular systems may differ from that in the auditory system.

Thyroid phenotype

Pendred syndrome is characterized by the presence of thyroid abnormalities. Goiter is incompletely penetrant and does not typically present until adolescence. Thus, Pendred syndrome often presents prior to the onset of goiter as non-syndromic hearing loss (Madeo et al. 2009). Ultrasonography can detect thyroid structural abnormalities with a higher sensitivity and specificity than manual palpation. The underlying, more penetrant thyroid phenotype is a deficiency of iodine organification in the biosynthesis of thyroid hormone. This is thought to reflect deficient transport of iodide anions by pendrin in the luminal plasma membrane of thyroid follicular cells. The perchlorate discharge test is the most sensitive clinical diagnostic method to detect the iodide organification defect (Madeo et al. 2009). Fraser clinically defined Pendred syndrome as congenital deafness, goiter, and a positive perchlorate discharge test (Fraser 1965). The perchlorate discharge test was previously used to distinguish between Pendred syndrome and DFNB4/NSEVA before the availability of reliable *SLC26A4* mutation testing. Subclinical or frank hypothyroidism in Pendred syndrome ranges from 0 to 79% (Ladsous et al. 2014; Madeo et al. 2009; Reardon et al. 1999; Soh et al. 2015). Thyroid serologic testing is not useful as an initial diagnostic screen for Pendred syndrome but is helpful for the management of thyroid-related symptoms.

Genetics

Pendred syndrome and DFNB4 are each inherited as an autosomal recessive trait. Thus, a conclusive genetic test for those phenotypes is expected to detect two mutant alleles (M2), either as homozygous or compound heterozygous mutations, of *SLC26A4*. However, there are some EVA patients with only one detectable mutant allele (M1), or with no mutant alleles (M0), identified through sequence analysis of the coding regions and adjacent splice sites of *SLC26A4*. The relative proportion of M2, M1, and M0 genotypes is variable in different populations. In North American Caucasian EVA patients, approximately 25% of patients are M2, another 25% are M1, and the other 50% are M0 (Choi et al. 2009a, b; Pryor et al. 2005). In East Asia, including China, Korea, or Japan, 67–90% of EVA patients have M2 genotypes and 8–21% have M1 genotypes (Choi et al. 2009c;

Miyagawa et al. 2014; Reyes et al. 2009; Wang et al. 2007; Zhao et al. 2013). This observation suggested the existence of one or more etiologic factors for EVA that are more common in European-Caucasian populations than in east Asian populations.

The prevalence of EVA among siblings of M1 probands is approximately 0.25, which is expected for an autosomal recessive trait (Choi et al. 2009a). This observation, as well as co-segregation of EVA with *SLC26A4*-linked markers on both chromosomes 7, suggested the existence of a second undetected pathologic variant in noncoding regions of *SLC26A4* in M1 patients (Choi et al. 2009a). In contrast, the probability of EVA in a non-twin sibling of an M0 EVA patient is nearly zero, indicating that EVA in M0 patients is not inherited as a Mendelian trait (Choi et al. 2009a).

Recently, a shared haplotype comprised of 12 variants located in introns or intergenic regions upstream of *SLC26A4* was identified as a recessive mutant allele when present in trans to a pathogenic variant of *SLC26A4* in Caucasian M1 families (Fig. 3) (Chattaraj et al. 2017). The *SLC26A4*-linked haplotype, termed CEVA (Caucasian EVA), was present on 7 of 10 mutation-negative chromosomes in a North American Caucasian M1 EVA cohort and 6 of 6 mutation-negative chromosomes in a Danish M1 EVA cohort. In contrast, the observed prevalence of the CEVA haplotype among Caucasian control chromosomes is 28 of 1006, which is significantly lower than among M1 patients ($p < 0.0001$). Thus, the association of CEVA with EVA is statistically significant and CEVA is likely to act as a pathogenic recessive allele in M1 patients. The CEVA haplotype was also found on 11 of

126 chromosomes in a North American Caucasian M0 EVA cohort, which is significantly higher ($p = 0.0042$) than the prevalence among Caucasian controls. The CEVA haplotype does not co-segregate with EVA in M0 patients, indicating that CEVA is not the major etiologic factor of EVA in M0 patients. Although several M0 patients are heterozygous for variants of unknown significance (p.Met775Thr and p.Glu29Gln) and homozygous for the CEVA haplotype, the pathogenic role of CEVA in these patients remains unclear.

Digenic inheritance of a heterozygous mutation in *SLC26A4* in combination with a heterozygous mutation in either the *FOXI1* or *KCNJ10* gene was proposed for M1 nonsyndromic EVA patients (Yang et al. 2007, 2009), but other studies have not been able to replicate or reproduce these findings (Chen et al. 2012; Jonard et al. 2010; Landa et al. 2013; Pique et al. 2014). A more recent study proposed digenic inheritance of point mutations in *EPHA2* and *SLC26A4* in two Japanese patients in Pendred syndrome (Li et al. 2020).

Genotype–phenotype correlation

The number of mutant alleles of *SLC26A4* is correlated with inner ear morphology, auditory, and thyroid phenotypes in Caucasian population (Table 1).

The M2 genotype is tightly correlated with bilateral EVA (Azaiez et al. 2007; Choi et al. 2009b; Pryor et al. 2005). King et al. could detect no significant relationship between EVA size and the number of mutant alleles of *SLC26A4*. In

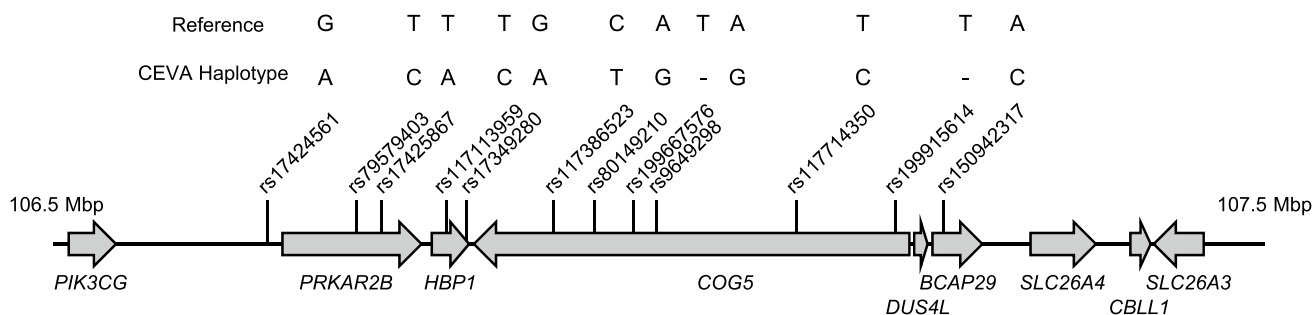


Fig. 3 Genetic map of the *SLC26A4*-linked CEVA (Caucasian EVA) haplotype. Twelve uncommon variants in intergenic regions or introns of genes including *PIK3CG*, *PRKAR2B*, *HBP1*, *COG5*, *DUS4L*, and *BCAP29*, are located within a linkage disequilibrium

block spanning a 613-kb region upstream of *SLC26A4*. Two variants (rs199667576 and rs199915614) are single-nucleotide deletions and ten are single-nucleotide substitutions

Table 1 Phenotypes and probability of EVA associated with *SLC26A4* test results

# mutant alleles	0	1	2
EVA	Unilateral or bilateral	Unilateral or bilateral	Bilateral
Mean pure-tone average (0.5/1/2/4 kHz)	Moderate	Moderate	Severe-profound
Thyroid iodine organification	Normal	Normal	Abnormal
Probability of EVA in each sibling	~0 (non-twin siblings)	1 in 4	1 in 4

contrast, a 2019 study suggested that the M2 genotype is associated with enlarged size and presence of “high-protein” contents in the endolymphatic sac seen on MRI (Mey et al. 2019b). Others have reported a significant association of the number of mutant alleles of *SLC26A4* with the presence of IP-II (Forli et al. 2020; King et al. 2010; Mey et al. 2019b).

The severity of hearing loss in EVA ears is greater in M2 patients than in M0 or M1 patients (Albert et al. 2006; King et al. 2010; Mey et al. 2019a, b; Rose et al. 2017). The prevalence of cochlear implantation is lower in M0 or M1 ears in comparison to M2 ears (Rose et al. 2017). Hearing loss reaches severe to profound levels (> 80 dB HL) earlier in M0 patients (3.2 years of age) than in all patients with *SLC26A4*-related hearing loss (6.0 years of age) (Mey et al. 2019a). However, the prevalence of hearing fluctuation does not seem to be associated with the number of mutant alleles of *SLC26A4* (Rose et al. 2017).

The iodine organification defect, as detected by the perchlorate discharge test, is significantly correlated with the M2 genotype (Madeo et al. 2009; Pryor et al. 2005). Thyroid function measured by serologic testing is not associated with the number of mutant alleles (Madeo et al. 2009).

M1 patients carrying the CEVA haplotype have a normal thyroid phenotype and less severe hearing loss in comparison to M2 patients (Chao et al. 2019). In M0 patients, hearing loss was more severe in patients who carry CEVA in comparison to non-carriers (Chao et al. 2019). This result suggested that CEVA might act as a genetic modifier of the EVA phenotype, although it is not the cause of EVA, in M0 patients.

The genotype–phenotype correlation is different in East Asian populations. Auditory phenotypes are more strongly associated with the type, rather than the number of mutant alleles, of *SLC26A4* in a Korean cohort (Rah et al. 2015). Other studies in Japanese and Chinese populations have not detected an association of the type or number of mutant alleles with the auditory phenotype (Miyagawa et al. 2014; Reyes et al. 2009; Wu et al. 2010). Intrafamilial variability in individuals with the same biallelic *SLC26A4* mutations have been reported (Miyagawa et al. 2014; Song et al. 2014).

Pathophysiological mechanism

SLC26A4 is comprised of 21 exons that encode a 780-amino acid (86-kDa) protein called pendrin (Everett et al. 1997). Pendrin is a nonspecific exchanger of anions and bases that is expressed in the plasma membrane of epithelial cells (Choi et al. 2009b; Wasano et al. 2020). The coding regions of human *SLC26A4* and the mouse ortholog *Slc26a4* share 85% nucleotide identity and the predicted amino acid sequences are 87% identical (Everett et al. 1999). In the mouse inner ear, pendrin is expressed in the apical membrane of outer

sulcus and spindle cells located in the lateral wall of the cochlea, transitional cells of the vestibular organs, and mitochondria-rich cells (MRCs) of the endolymphatic sac (Dou et al. 2004; Royaux et al. 2003; Wangemann et al. 2004). During development, pendrin expression is first initiated in the endolymphatic sac at embryonic day (E) 11.5 (Kim and Wangemann 2011). The onset of expression in the cochlea and the vestibular organs occurs at E13.5–E16.5 (Kim and Wangemann 2011).

A mouse model lacking pendrin (*Slc26a4*^{Δ/Δ}) has profound hearing loss, vestibular dysfunction, and massively enlarged endolymphatic spaces from the cochlear duct to the endolymphatic sac (Everett et al. 2001). The endolymphatic spaces begin to enlarge at E14.5 and reach an approximately tenfold increase in size of the cochlear lumen at E18.5 in comparison to *Slc26a4*^{Δ/+} littermate controls (Kim and Wangemann 2010). Acidification of the endolymph occurs in the cochlea at E15.5 and in the endolymphatic sac at E17.5 due to the failure of HCO₃⁻ secretion by pendrin (Kim and Wangemann 2011). The two primary pathological alterations, luminal enlargement and acidification, may be followed by secondary consequences including increased K⁺ secretion by marginal cells, oxidative stress in the stria vascularis, loss of *Kcnj10* in intermediate cells, a loss of endocochlear potential, increase of Ca²⁺ concentration in the endolymph, formation of giant otoconia, and a degeneration of sensory cells and the stria vascularis (Jabba et al. 2006; Li et al. 2013b; Nakaya et al. 2007; Singh and Wangemann 2008; Wangemann et al. 2004, 2007).

The molecular mechanism of endolymphatic enlargement is likely to be impaired absorption of luminal Na⁺, Cl⁻ and water by the endolymphatic sac during development (Choi et al. 2011; Honda et al. 2017; Li et al. 2013a). MRCs comprise about 30% of endolymphatic sac epithelial cells (Dahlmann and von Düring 1995; Honda et al. 2017). MRCs have plentiful mitochondria and numerous apical microvilli, and express ion transport genes including *Slc26a4*, *Atp6v0a4*, *Atp6v1b1*, *Cftr* and the forkhead transcription factor *Foxi1* that regulates expression of those genes (Honda et al. 2017; Hulander et al. 2003; Raft et al. 2014; Vidarsson et al. 2009). This structure and gene expression profile are features shared with other ionocytes such as intercalated cells of the kidney, narrow and clear cells in the epididymis, and recently identified pulmonary ionocytes (Blomqvist et al. 2004, 2006; Montoro et al. 2018; Plasschaert et al. 2018; Scudieri et al. 2020). Human orthologs *ATP6V0A4* and *ATP6V1B1* encoding V-ATPase subunits are causal genes for distal renal tubular acidosis with deafness and EVA (Vidarsson et al. 2009). *Atp6v0a4*^{Δ/Δ} mice, *Atp6v1b1* mutant mice, and *Foxi1*^{Δ/Δ} mice all have an inner ear phenotype similar to that of *Slc26a4*^{Δ/Δ} mice (Hulander et al. 2003; Lorente-Canovas et al. 2013; Tian et al. 2017). MRCs, acting as “the inner ear ionocyte”, appear to be engaged in absorption of Na⁺ Cl⁻,

and thus water, by the endolymphatic sac and regulate the balance between secretion and absorption of the endolymph during inner ear development. Disruption of this pathway may be the underlying mechanism for enlargement of the endolymphatic sac, cochlea, and vestibular aqueduct (Honda et al. 2017).

Slc26a4 knockout and knockin mouse models result in auditory and inner ear phenotypes that are more severe than those observed in patients with *SLC26A4*-related hearing loss (Dror et al. 2010; Hu et al. 2021; Lu et al. 2011, 2014; Wen et al. 2019). A doxycycline-induced *Slc26a4*-insufficient mouse model has fluctuation of hearing associated with fluctuation of the endocochlear potential and more closely approximates the phenotype observed in human patients. In this model, the loss of hearing is closely correlated with loss of the endocochlear potential and structural abnormalities and degeneration of the stria vascularis (Ito et al. 2014; Jabba et al. 2006). Expression of *Slc26a4* in the endolymphatic sac, but not the cochlea, is required for the acquisition of normal ABR thresholds in mice, suggesting that the cochlear abnormalities occur secondarily to the endolymphatic sac dysfunction (Li et al. 2013a). The pathogenic link between endolymphatic sac and cochlea dysfunction is unknown but may include alterations of pH, ionic composition, size, or osmotic pressure of endolymph. Elucidation of this pathophysiological mechanism should inform our understanding and management of *SLC26A4*-related hearing loss.

Conclusions

Hearing loss associated with enlargement of the vestibular aqueduct is a penetrant feature of *SLC26A4*-related mutant phenotypes. The phenotypes range from nonsyndromic recessive sensorineural hearing loss DFNB4 to sensorineural hearing loss as part of Pendred syndrome. Some EVA patients, especially those of European or Caucasian ancestry, will only have one *SLC26A4* allele with a detectable mutation affecting the coding regions or splice sites. The phenotype associated with one mutant allele (M1) is generally less severe than that associated with two mutant alleles (M2). Recent studies have revealed the existence of an uncommon haplotype, called CEVA, located upstream of *SLC26A4* that acts as a pathogenic recessive allele in trans-configuration with the mutated *SLC26A4* gene in a majority of European-Caucasian M1 EVA patients. CEVA is associated with a milder phenotype than mutations affecting the coding regions or splice sites of *SLC26A4*. The pathogenesis of EVA in patients with no detectable mutations of *SLC26A4* is likely caused by other mechanisms. Studies of *Slc26a4*-insufficient or -null mice indicate that disruption of sodium chloride and fluid absorption by the developing

endolymphatic sac is the precipitating developmental event in the pathogenesis of *SLC26A4*-related hearing loss.

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Declarations

Conflict of interest On behalf of all authors, the corresponding author states that there is no conflict of interest.

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Consent for publication Not applicable.

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