Abstract

Hearing loss is the most frequent sensory disorder, with an incidence of 1:1500 live newborns. In more than 50% of patients, it is associated with a genetic cause, while in up to 30% of cases, it is related to syndromic entities. We performed a literature review of studies on congenital hearing loss of genetic origin in the Mexican population. We identified eight reports that showed that the pathogenic variants most frequently associated with hearing loss are related to the GJB2 gene, although in a low percentage (3%). Other mutations were identified in the GJB6, SLC26A4, or CHD23 genes. On this basis, a possible diagnostic strategy in Mexican patients with hearing loss is to consider an initial screening of these three genes. If these genes were negative for pathogenic variants, the following steps would be to consider second-generation sequencing analysis focused on panels of genes associated with hearing loss, isolated or syndromic, and if necessary, to perform exome or whole-genome analysis. Establishing an etiologic cause is critical in clinically evaluating patients with congenital hearing loss and their families. It can help determine rehabilitation strategies, such as hearing aids or cochlear implants and provide information on disease progression and genetic counseling in this population.

Keywords: Congenital hearing loss. Congenital deafness. Mexican population. GJB2. GJB6.

Pérdida auditiva congénita: revisión de la etiología genética en la población mexicana

Resumen

La pérdida auditiva es la alteración sensorial más frecuente, con una incidencia de 1:1500 recién nacidos vivos. En más del 50% de los pacientes se asocia con una causa genética, mientras que en más del 30% de los casos se asocia con entidades sindrómicas. Se llevó a cabo una revisión de la literatura de las investigaciones sobre la pérdida auditiva congénita de origen genético en la población mexicana. Se identificaron ocho reportes en los que se demostró que las variantes patogénicas más frecuentemente asociadas con pérdida auditiva se encuentran en el gen GJB2, aunque en un porcentaje bajo (3%). Se identificaron otras mutaciones en los genes GJB6, SLC26A4 o CHD23. Con base en esta información, una posible estrategia diagnóstica en pacientes mexicanos con pérdida auditiva es considerar un primer paso en el tamiz diagnóstico con los tres genes mencionados. Si estos genes fueran negativos para variantes patogénicas, el siguiente paso
Congenital hearing loss in Mexico

Congenital hearing loss can be classified according to its type as conductive (related to external or middle ear pathology), sensorineural (associated with internal ear and spiral ganglion pathologies), neural (associated with VIII cranial nerve alterations), and mixed (associated with pathologies including two or more of the above categories). The classification of hearing impairments has important implications for their treatment. For example, the primary indication for a cochlear implant is exclusively related to the hearing thresholds indicated when congenital hearing loss is classified as severe or profound neurosensorial loss. Congenital hearing loss (of any type) in patients with early-onset bilateral sensorineural deafness cases have been considered to have a genetic cause. The other half corresponds to non-genetic causes. Environmental factors include, for example, infections such as those associated with TORCH (toxoplasmosis, rubella, cytomegalovirus, herpes simplex, and HIV), the diagnosis of cytomegalovirus, ototoxic drugs, prematurity, hypoxia at birth, hyperbilirubinemia, or even the permanence of the patient in neonatal intensive care units for more than five days.

Genetic factors of congenital hearing loss

When analyzing the possible genetic etiology of congenital hearing loss, one of the first aspects to consider is whether it is a syndromic presentation (a situation that represents up to 30% of cases of all types of hereditary hearing loss) or whether it is an isolated characteristic (which corresponds up to 70% of patients).
Syndromic genetic causes of hearing loss include Usher, Pendred, Waardenburg, and Norrie syndromes. In this regard, Bahena et al. conducted an interesting study on a group of 59 patients with combined retinal and hearing impairment but no intellectual disability. Most of the patients were Iranian, and seven unrelated Mexican patients were included in this study. Through exome analyses, the authors were able to elucidate all Mexican cases, as several pathogenic or probably pathogenic genetic variants were identified in the MYO7A (three patients), USH1G (one patient), and USH2A (two patients) genes. This study is also an example of the genetic heterogeneity observed in the Mexican population regarding the etiology of syndromic hearing loss.

When non-syndromic causes are considered, hearing loss can be classified according to the inheritance pattern; for example, 75–80% of patients have an autosomal recessive pattern, 20% are autosomal dominant, < 2% are X-linked, and < 1% are of mitochondrial origin. This information is relevant because, depending on the homozygous or heterozygous condition of the patient, the genetic possibility of expression can vary from 50% risk in the case of autosomal dominant pattern (in which the presence of a single mutated allele is sufficient to cause a clinical manifestation) to 25% risk for autosomal recessive diseases, in which the presence of two mutated alleles is required to generate a clinical alteration. Also, it influences prognosis and response to treatments, including the cochlear implantation.

According to the information on the Hereditary Hearing Loss Homepage website, several different genes have been identified to be associated with different inheritance patterns of non-syndromic hearing loss. For example, at the DFNA1 locus (OMIM #124900) is the DIAPH1 gene (OMIM *602121) on 5q31.3; at the DFNA2A locus (OMIM #600101) is KCNQ4 (OMIM *603537) on 1p34.2, and at the DFNA2B locus (OMIM #612644) is GJB3 (OMIM 603324) on 1p34.3; these are examples of autosomal dominant patterns. Examples of congenital hearing loss with an autosomal recessive inheritance pattern include the DFNB1A locus (OMIM #220290) with the GJB2 gene (OMIM 121011) on 13q12.11; GJB6 (OMIM 604418) on 13q12.11 and GJB3; DFNB1B with the mentioned GJB6, or DFNB2 (OMIM #600060) with MYO7A (*276903) on 11q13.5 (Table 1). As described in studies on second-generation DNA analysis, it is still impossible to reach a molecular diagnosis in 100% of the patients.

An important aspect in diagnosing, managing, and genetic counseling patients with congenital hearing loss is that its distribution is complex, as different variants predominate in different populations. For example, the c.35delG in GJB2 is the most common variant in Europeans/Americans of European ancestry, and its carrier frequency is ~2.5% in the United States. Carrier prevalence for c. 35delG is 1.5% worldwide, ranging from 0% to 5.7% in Belarus. Another example is a carrier prevalence of 2.5% for the p.V371T variant (from 0% up to 16.7% in Thailand); the c.167delT variant has a carrier prevalence of ~4% in the Ashkenazi population, and the c.235delC variant is the most common in Japan. As described above, considering ethnicity is critical when determining the optimal genetic analysis. When sequencing for the diagnosis of congenital hearing loss, there is a wide range of genotype frequency depending on the ethnicity of the patients.

Based on these considerations, the alteration's genetic etiology impacts the management and treatment of congenital hearing loss. Therefore, profile determination of the pathogenic variants in different populations allows for determining the resources and prognosis for each patient. As an example, 49 genes were identified in a study that performed genetic analysis of 1119 patients of different ethnicities, including 549 Caucasians, 128 Hispanics, 51 African Americans, 40 Asians, 25 Middle Easterns, 8 Ashkenazi Jews, 57 of mixed ethnicity, and seven patients described as of “other” ethnicity. In 75%, hearing loss was associated
### Table 1. Comparison of information regarding the different mutations related to hearing impairment in Mexican populations

<table>
<thead>
<tr>
<th>Author (year)</th>
<th>Studied population</th>
<th>Origin of the studied population in Mexico</th>
<th>Analyzed gene/ Gene and pathogenic variant</th>
<th>Methods used for genetic variables identification</th>
<th>Results</th>
</tr>
</thead>
</table>
| Arenas-Sordo et al. (2012) | 76 individuals | Not specified | GJB2, GJB6, del(GJB6-D13S1830) and del(GJB6-D13S1854), m.1555A > G in MTRNR1 | a) GJB2 sequencing  
b) GJB6 screening (sequencing) for two deletions: del (GJB6-D13S1830) and del (GJB6-D13S1854)  
c) MTRNR1 gene (m.1555A>G in) | Eight previously reported pathogenic variants and two polymorphic variants in GJB2. |
| Mendelsberg-Frisbein et al. (2013) | 11 individuals | Central: MEX: 6; MICH: 3; GUA: 1; CDMX: 1 | GJB2 c.35delG, c.235delC and c.167delT | Three GJB2 mutations were analyzed:  
a) c.35delG by direct sequencing  
b) c.167delT by PCR-RFLP with PstI.  
c) C.235delC by PCR-RFLP with ApaI | No deletions were detected in GJB6 or GJB2 IVS1 + 1G. |
| Hernández-Juárez et al. (2014) | 78 individuals/deafness | Northeastern: NLE, SLP, and TAM | GJB2 IVS1 + 1 G > A and GJB6 deletions | a) GJB2 nucleotide sequencing  
b) PCR-RFLP analysis to detect IVS1+1G-A  
c) Real-time quantitative PCR (qPCR) for deletions in GJB6 | 23 Hom mutations, 57 Het mutations, one double Het (GJB2/GJB6), The propositus in family 1 had three mutations: |
| Leeza-Becerra et al. (2014) | 140 individuals/deafness | West, Northwest, East, Northeast, and Central | GJB2, GJB6 IVS1 + 1G Mutations (m.1555A>G) | Direct sequencing of  
a) GJB2  
b) GJB6  
c) Int.1555A>G | Twenty-seven cases (3.35%) were carriers of the pathogenic variant in GJB2. |
| Martínez-Saucedo et al. (2015) | Two families | Not specified | GJB2 | a) First GJB2 mutations were discarded  
b) Whole-exome sequencing analysis  
c) Pre-screening for GJB2 variants  
d) Whole-exome sequencing identifying SLC26A4 and Sanger sequencing for confirmation | N/A |
| Bademci et al. (2016) | Two Mexican families out of 90 families from several backgrounds | Not specified | GJB2 | Preconception expanded genetic carrier screening; panel test for 283 clinically impactful diseases. Next-generation sequencing was performed for 21 pathogenic variants and the two exons of GJB2, the presence or absence of the two upstream deletions of the GJB2 regulatory region, del(GJB6-D13S1830) and del(GJB6-D13S1854) | N/A |
| Cengiz et al. (2017) | 11 individuals | Not specified | GJB2 | N/A | N/A |
| Hernández-Nieto et al. (2020) | 805 individuals | From 25 out of 32 states. Ancestry: Latin (640), European (72), Middle East (22), other (3) | GJB2, del(GJB6-D13S1830) and del(GJB6-D13S1854). | N/A | N/A |
Table 1. Comparison of information regarding the different mutations related to hearing impairment in Mexican populations (continued)

|---------------|----------------|-----------------------------------|-----------------------------------|-------------------------------|--------------------------------|-------------------|-------------------|-------------------|
| Arenas-Sordo et al. (2012)26 | No deletions were identified in GJB6 or m.1555A>G. Eight cases (10.52%) with biallelic mutations. c.35delG (GJB3) was the most frequent pathogenic variant, with six heterozygous and two homozygous individuals. Five rare pathogenic variants were identified, including the autosomal dominant c.551G>G. c.79G>A was the most frequent benign polymorphic variant. | c.35delG Hom (1); c.35insG (1); c.340>T Het (1); c.79G>A (p.V27I) Het (2) | Mutations in GJB2 were detected in 9.8% of the alleles; c.35delG was the most frequent. Other six mutations were less frequently detected including c.645_S48delTAGA, c.35G>A, and one with a possible Mexican origin (c.34G>T). There were no deletions detected in GJB6 and GJB2 IVS1 + 1G>A and 59 wild-type genotypes in GJB2. Three Hom c.35delG and 26 Het patients. One patient with a GJB6 deletion (including the double Het GJB2/GJB6). m.1555A>G was not identified. | and 59 wild-type genotypes in GJB2. Three Hom c.35delG and 26 Het patients. One patient with a GJB6 deletion (including the double Het GJB2/GJB6). m.1555A>G was not identified. | Tp.S19N/p.R325S/p.E47*, meanwhile, the affected family members had three mutations p.F311p. W447p. V434M. The parents of both families were Het and had a normal auditory function. | Het c.2999 G>A p.D987N One compound Het (consanguinity)* | Hom: 3; compound Het: 4, for SLC26A4 variants. Seven families with ten different variants. in SLC26A4 A new recurrent variant was identified: t (c.1673A>G (p.N558S) in two families** | c.35delG (10 cases [37%]), c.101T>G (5 cases [18.5%]), c.817A>G (4 cases [14.8%]), c.109G>A (2 cases [7.4%]), other variants (deletion GJB6-D13S1830, c.416G>A, p.Leu90Pro, c.365A>T, c.617A>G, m.1555A>G, IVS1+1G>A, DFNB1 c.551G>A, c.79G>A was the most frequent benign polymorphic variant. |}

Conclusions

GJB2 mutations are an important cause of prelingual deafness in the Mexican population. Two polymorphisms and three mutations were identified. The frequency of three different mutations was lower than those reported in the literature. The findings suggested that DFNB1 mutations are a rare cause of autosomal recessive deafness in the northeastern Mexican population. The type and distribution of the mutations/alleles varied according to the specific analyzed region: 57.88% of patients had GJB2 or GJB6 mutated alleles, and 42.14% were wild-type. Two cases with three mutations. This situation reflects the complex patterns of mutations regarding GJB2. After excluding pathogenic variants in GJB2, a mutation was identified in 56% of the studied families. One Mexican family had a mutation in CDH23. There is a spectrum of variants in SLC26A4. No common recurrent variation was identified. SLC26A4 is a cause of hearing loss in Turkey, Iran, and Mexico. Sequence changes in GJB2 had a frequency of carriers of 3.35%, and c.35delG (37%) was the most frequently identified. This result is similar to the 2.14% frequency reported in other regions of Mexico27,28, where c.35delG was also the most commonly identified variant.

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*Exome sequencing

Preconceptional analysis with second-generation sequencing identified carriers for several diseases, including congenital hearing loss.

1MEX, State of Mexico; MIDH, Michoacán; GUJ, Guanajuato; CDMX, Mexico City.

2NLE, Nuevo León; SLP, San Luis Potosí; TAM, Tamaulipas.

Het, heterozygous; Hom, homozygous

*The authors identified pathogenic variants in 56% of the families, which involved 31 genes; 54% of these alterations have not been previously reported. In the remaining families of this study, mutations in the GTOOL and FAM65B genes were analyzed as new causes associated with hearing loss with autosomal recessive hearing loss.

**The authors identified 27 unique SLC26A4 variants in 31 probands.
with 10 genes: 22% with GJB2, 16% with STRC, and 7% with SLC26A4. The latter gene encodes a chloride and iodide transporter and, in general, is the second most frequent autosomal recessive presentation and can also cause Pendred syndrome. Pathogenic variants of the ECTA genes corresponded to 5% of cases. When these authors studied the molecular etiology in 77 patients with a cochlear implant, 13 (18%) had mutations in GJB2, and in eight patients, only one mutated allele was identified. Therefore, they were heterozygous for a known autosomal recessive inheritance pattern, although no other variants in other genes were identified, which was a limitation of this study.

It has been reported that patients with congenital hearing loss associated with GJB2 mutations respond adequately to cochlear implants. Also, patients with cochlear implants and pathogenic variants have shown variations in the language evaluation test according to the associated genetic alteration. In this regard, studies of biallelic mutations in GJB2 or SLC26A4 or of patients with no established genetic cause found that patients with GJB2 mutations would have better auditory nerve functional status than those with SLC26A4 mutations when compared to either patients with Mondini malformations and dilated vestibular ducts or patients with idiopathic hearing loss.

Regarding hearing loss with a non-syndromic autosomal dominant inheritance pattern, it has been noted that the hearing abnormality is often less severe than that present in autosomal recessive conditions and manifests between the ages of 10 and 40 years. Some presentations of hearing loss show a unique profile associated with high-frequency hearing loss, such as some pathogenic variants in KCNQ4, a gene encoding a potassium channel. Pathogenic variants in the WFS1 gene cause low-frequency hearing loss (< 2 kHz), and biallelic mutations in WFS1 cause Wolfram syndrome, with an autosomal recessive inheritance pattern. The characteristic anomalies of this syndrome are described with the acronym DIDMOAD (diabetes insipidus, diabetes mellitus, optic atrophy, and deafness). Van Beeck et al. performed a study including image analysis and the clinical and genetic characteristics of 423 children with hearing loss. These authors described that the most common etiology of bilateral hearing loss in 67% of children was a genetic disorder, corresponding to 26% of the cases. In children under one year of age with severe hearing loss, 47% of the cases corresponded to a syndromic presentation, and the rest (53%) presented hearing loss as an isolated alteration.

Moreover, in patients with unilateral hearing loss, a temporal bone anomaly was identified in 27%. When considering children with hearing loss due to genetic etiology, 43% had a family history, 39% had a syndrome associated with sensorineural hearing loss, and 18% showed a known pathogenic variant or mutation; among them, a specific mutation for SLC26A4 (with an autosomal recessive inheritance pattern) was identified. Finally, a unilateral alteration was identified in 20% of patients and a bilateral alteration in 80%.

The response to cochlear implantation is a particularly relevant aspect concerning the management and treatment of congenital hearing loss of genetic etiology. Only a few studies have been performed in pediatric populations on this feature. In a study to determine the etiological profile of 122 Lithuanian children with cochlear implants, 65 cases (53.3%) were diagnosed as non-syndromic hearing loss; in 58 of them, hearing loss was associated with GJB2. In contrast, syndromic alterations were identified in eight children (6.6%). Perinatal risk factors for hearing loss, such as prematurity, low birth weight, hypoxia, hyperbilirubinemia, sepsis, ototoxic agents, and meningitis, were associated with hearing loss in 16 (13.1%) and four (3.3%) patients, respectively. Importantly, cytomegalovirus was detected in 12 samples (9.8%). However, even with these results, the origin of hearing loss could not be identified in 17 children. This analysis concluded that GJB2 alterations were the most frequent cause of hearing loss and that only 14% of patients in this cohort had hearing loss of unknown etiology.

In a similar analysis in Polish children, 196 patients with severe prelingual hearing loss were evaluated. The study described a good response to cochlear implants in 149 children with DFN1-related hearing loss. Furthermore, better hearing development was described in children who underwent implantation before 12 months of age. This analysis also demonstrated that cochlear implantation was the most successful treatment in patients with hearing loss associated with the DFN1 locus. These findings underscore the importance of determining the molecular genetic etiology in congenital hearing loss.

**Molecular profile of hearing loss in Mexico**

Few studies have been conducted in Mexico to determine the etiology of congenital hearing loss in the Mexican mestizo population (Table 1). In research...
conducted at the Hospital Infantil de México Federico Gómez (HIMFG) in children with hearing loss (Table 1), a population of almost 100 patients was evaluated to establish the cause of the hearing loss \(^6\). Molecular analysis was performed in 11 patients with a c.35delG homozygous, a c.35insG heterozygous, a c.34G>T heterozygous, and heterozygous patients for the c.79G>A polymorphism, all in \(GJB2\), were identified. Interestingly, several factors suggesting non-genetic causes were identified, including a positive TORCH test in 1% and infections or the use of ototoxic drugs in 3% of patients. Regarding this aspect, it is essential to mention that ototoxic drugs only cause hearing damage in patients with specific genotypes \(^3^4\). This aspect has been studied in patients requiring the use of aminoglycosides as a treatment for infectious diseases; it has been shown that some genetic alterations in mitochondrial DNA confer greater sensitivity to these drugs and, therefore, to the risk of presenting non-syndromic deafness associated with their use. Several mutations in the 12S rRNA region of mitochondrial DNA have been described in various populations \(^3^4,3^5\), including T961insC, T961C, T961+C(n)ins, T1095C, C1494T, and A1555G. However, these pathogenic mitochondrial variants are rare, and their frequency may even vary among different ethnic groups, as has been studied in the Mexican population by Meza et al. (2011) \(^3^1\). In their study of 65 subjects, the authors did not identify any previously reported mutation related to aminoglycoside hypersensitivity, and only two of the patients treated with the aminoglycoside streptomycin had a T1189C variant of the previously mentioned 12S rRNA region, which was considered a possible mutation related to the aminoglycoside hypersensitivity.

Molecular genetics research has been conducted on hearing loss etiology in Mexican mestizo populations (Table 1). For example, in a study conducted in north-eastern Mexico, a pathogenic variant of \(GJB2\) was identified in 78 patients. A mutation in \(GJB2\) was identified in 9.6% of the alleles; c.35delG was the most frequently identified, and six other mutations were also detected. Interestingly, the IVS1+1G>A \(GJB2\) variant was not detected. This study determined that mutations in the \(DFNB1\) locus are a rare cause of autosomal recessive non-syndromic sensorineural hearing loss in this population \(^2^1\).

In a cohort of patients attending the Hospital General de México Dr. Eduardo Liceaga, mutations in \(GJB2\), \(GJB6\), and mt.1555A>G were studied, and a double heterozygous (\(GJB2/GJB6\)) was detected in this group, as well as three patients homozygous for c.del35 in \(GJB2\), while 26 patients were heterozygous for this gene. Conversely, the mt.1555A>G mutation was not detected. In this cohort, 57.86% of patients showed one or two affected alleles of \(GJB2\) or \(GJB6\) \(^2^2\).

As described in the previously mentioned studies performed in Mexico in specific populations with hearing loss, the most frequent pathogenic variants have been identified in well-known genes such as \(GJB2\) and \(GJB6\). However, it was impossible to identify a genetic alteration in a significant percentage of patients. Therefore, genomic analyses should be performed using next-generation sequencing (NGS) techniques, including gene panels or whole exome, or genome studies \(^3^0\). Implementing this technology will allow efficient simultaneous screening of multiple genes \(^2^5\).

An example of the scope of NGS is that with exome sequence analysis was possible to establish the etiology in 27% of patients in a group of children with development anomalies with no previous diagnosis. Also, genomic studies can provide a timely diagnosis in managing infants in neonatal intensive care units \(^3^6\). This situation underlines the importance of using these molecular techniques in diagnosing diseases such as congenital hearing loss in patients without a definitive etiology.

Several populations with congenital hearing loss in different parts of the world have been studied by NGS, including a small group of Mexican patients with congenital hearing loss in whom an alteration in \(GJB2\) was excluded before NGS. Bademci G et al. studied 160 families (including two of Mexican origin) by exome analysis for all known genes associated with non-syndromic congenital hearing loss \(^2^3\). In this research, the authors identified a novel variant c.2959G>A, p.D987N in the \(CDH23\) gene in one of the Mexican families. Cengiz et al. identified mutations in \(SLC26A4\) in Mexican patients (Table 1), corresponding to three homozygous and four compound-heterozygous patients \(^2^4\).

Hernández-Nieto et al. \(^2^5\) conducted an interesting analysis in which they analyzed data from 805 individuals with NGS (Table 1). The population examined differed from those described in other hearing loss studies since the patients requested a preconception NGS analysis due to genetic counseling. The population analyzed included patients born in Mexico. Different population origins were identified by ancestry analysis, most of them corresponding to the Latino population, and several carriers of other diseases were identified. Among these abnormalities, congenital hearing loss genes were found in 27 cases (3.35%), corresponding to carriers of \(GJB2\) gene pathogenic variants. This frequency is similar to those reported by other authors in
Congenital hearing loss is a public health problem in Mexico. As in other populations, its etiology is diverse. Although few studies have been conducted in Mexico, they have shown GJB2 pathogenic variants, compound heterozygous, and the presence of pathogenic variants in other genes such as GJB6 or SLC26A4 in this population; there are also some families with particular characteristics due to the genes involved. Interestingly, the frequency (3.35%) of the c.35delG variant in GJB2 was found in a population analyzed by exome who consulted for preconception genetic diagnosis. The studies reviewed here indicate the genetic heterogeneity of congenital hearing loss in the Mexican population and the importance of establishing the diagnosis, etiology, and genetic counseling when the most frequent causes have been excluded. Also, the studies showed the implications of genetic diagnosis for patient management, such as that related to cochlear implants. As discussed in this review and summarized in Table 1, the most frequent pathogenic variants associated with hearing loss in the Mexican population are related to the GJB2 gene, although in a low percentage, followed in frequency by pathogenic mutations in SLC26A4 and mutations in CHD23 in third place. Based on these data, a possible diagnostic strategy would be screening for these three genes in Mexican patients. If the result is negative for pathogenic variants at these loci, the following step would be a second-generation sequencing analysis focused on panels of genes already associated with isolated and syndromic hearing loss. If these analyses are not informative, second-generation sequencing should be considered, first by whole-exome analysis, and, in the case of negative results, whole-genome sequencing should be performed.

As proposed for other populations, these data reflect the importance of genetic evaluation with molecular studies to establish the genetic etiology of congenital hearing loss in Mexican patients.

In conclusion, establishing an etiological cause is critical in the clinical evaluation of infants and children with congenital hearing loss and their families, as has been emphasized by many authors. Identifying underlying causes could help choose rehabilitation strategies, such as hearing aids or cochlear implants. This will provide insights into disease progression, facilitate monitoring of clinical manifestations and associated complications, and provide parents information on the risk of recurrence. Finally, this review is critical because it summarizes all the research conducted in Mexico on the genetic etiology of hearing loss.

**Ethical disclosures**

**Protection of human and animal subjects.** The authors declare that no experiments were performed on humans or animals for this study.

**Confidentiality of data.** The authors declare that they have followed the protocols of their work center on the publication of patient data.

**Right to privacy and informed consent.** The authors declare that no patient data appear in this article.

**Conflicts of interest**

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**References**


