

Review Article



The Genetic Basis of Auditory Neuropathy Spectrum Disorder

Majid Karimi¹ , Mohsen Ahadi^{1*} , Mohammad Ajalloueyan² , Nader Saki^{3,4} , Saeid Morovvati⁵ , Golshan Mirmomeni⁶

1. Department of Audiology, Rehabilitation Research Centre, School of Rehabilitation Sciences, Iran University of Medical Sciences, Tehran, Iran.
2. Department of Otorhinolaryngology, Baqiyatallah Hospital, Baqiyatallah University of Medical Sciences, Tehran, Iran.
3. Department of Otolaryngology, Head and Neck Surgery, Ahvaz Jundishapur University of Medical Sciences, Ahvaz, Iran.
4. Hearing Research Center, Clinical Sciences Research Institute, Ahvaz Jundishapur University of Medical Sciences, Ahvaz, Iran.
5. Faculty of Advanced Sciences and Technology, TeMS.c., Islamic Azad University, Tehran, Iran.
6. Hearing Research Center, Clinical Sciences Research Institute, Ahvaz Jundishapur University of Medical Sciences, Ahvaz, Iran.



Citation Karimi M, Ahadi M, Ajalloueyan M, Saki N, Morovvati S, Mirmomeni G. The Genetic Basis of Auditory Neuropathy Spectrum Disorder. Journal of Modern Rehabilitation. 2026; 20(1):1-8. <http://dx.doi.org/10.18502/jmr.v20i1.21021>

<http://dx.doi.org/10.18502/jmr.v20i1.21021>

Article info:

Received: 17 Feb 2025

Accepted: 1 Jun 2025

Available Online: 01 Jan 2026

ABSTRACT

Introduction: Despite normal outer hair cell function, auditory neuropathy spectrum disorder (ANSO) disrupts neural coordination and impairs speech comprehension, especially in noisy environments. This review study explores the genetic mechanisms underlying ANSO.

Materials and Methods: PubMed, Scopus, and Web of Science were searched from 2010 to 2023 for studies on ANSO genetics, excluding those focused on non-genetic causes or lacking relevant data.

Results: ANSO is associated with conditions such as Brown-Vialetto-Van Laere syndrome (BVVL) and Charcot-Marie-Tooth (CMT) disease, often resulting from mutations in the auditory nerve. Nonsyndromic ANSO is associated with genes such as OTOF and PJKK, which are essential for neural function.

Conclusion: ANSO is a multifactorial condition resulting from genetic mutations in key genes, which disrupt auditory pathways and impair sound signal transmission. Further research is needed to identify additional genes and understand molecular mechanisms contributing to ANSO. This knowledge will improve diagnosis, prognosis, and therapeutic strategies, and could lead to innovative treatment approaches in the future.

Keywords:

Auditory neuropathy; Genetic mutation; Hearing loss

* Corresponding Author:

Mohsen Ahadi, PhD.

Address: Department of Audiology, School of Rehabilitation Sciences, Iran University of Medical Sciences, Tehran, Iran.

Tel: +98 (12)3969746, +98(21) 77684889

E-mail: ahadi.m@iums.ac.ir



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Introduction

Individuals with auditory neuropathy spectrum disorder often exhibit a notable discrepancy between their hearing thresholds, which may appear normal, and their difficulties with speech comprehension, particularly in noisy environments [1]. Terms like auditory neuropathy (AN) primarily describe this discrepancy, emphasizing the difficulty in understanding speech despite the ability to hear sounds [1]. Auditory desynchrony is another term for the primary issue: timing problems in neural transmission make it challenging to process sound information accurately. Auditory synaptopathy has recently emerged, focusing on potential dysfunctions at connections between inner hair cells and auditory nerve fibers, which can significantly impair auditory processing [2, 3].

Audiological findings in ANSD often reveal a unique pattern. Hearing loss, typically bilateral and sensorineural, can range from mild to severe, with a particular emphasis on lower frequencies. Audiograms may exhibit varied configurations, including peaked or saucer-shaped patterns [4]. Otoacoustic emissions are often preserved despite hearing loss, indicating that outer hair cell function is intact. On the other hand, auditory brainstem responses are usually absent or distorted, suggesting a disruption in neural transmission. The acoustic stapedial reflex is absent in most people with ANSD, further evidence that the brain is not working properly. Cochlear microphonics, which are often present, give more evidence of optimal outer hair cell function [5, 6].

While reported prevalence estimates range from less than 1% to 10% of individuals with hearing impairment [2], ANSD prevalence varies greatly, clearly depending on the specific population under study. Research indicates a higher prevalence among children with sensorineural hearing loss, especially those with severe-to-profound hearing impairment. The wide range in reported prevalence suggests that ANSD may be underdiagnosed in some populations [6-8].

ANSD can arise from various etiologies, including environmental and acquired factors. Some common non-genetic causes are early birth, high bilirubin levels, lack of oxygen, congenital brain defects, and exposure to drugs that damage the ears. If you have an acquired form of ANSD, you may start losing your hearing earlier than if you have a genetic form [9]. Genetic causes significantly influence the development of ANSD, with about 40% of cases having a genetic basis. There are different

ways these genetic factors can be passed down, including autosomal dominant, autosomal recessive, X-linked, and mitochondrial inheritance [10]. Understanding the genetic basis of ANSD is essential for accurate diagnosis, effective treatment, the development of management strategies, such as gene therapy, and predicting disease progression. Genetic mutations can act as diagnostic markers, and comprehending genotype-phenotype correlations facilitates personalized medicine, ultimately enhancing patient outcomes. This study aims to investigate the role of genetics in the development of both syndromic and nonsyndromic ANSD and to analyze their related clinical and audiological manifestations.

Materials and Methods

A comprehensive search was conducted across PubMed, Scopus, and Web of Science from January 2010 to December 2023, using relevant keywords such as “auditory neuropathy spectrum disorder” and “genetics,” along with suitable variations, to identify studies related to the genetic aspects of ANSD. Boolean operators (AND, OR) refined the search strategy. This review included peer-reviewed articles that specifically addressed the genetic causes of ANSD, described the audiological characteristics associated with genetic conditions, and provided clinical profiles of individuals diagnosed with ANSD. Studies were excluded if they did not primarily focus on the genetic aspects of ANSD, did not include genetic information in their discussion of treatment options, lacked audiological data, or did not provide full-text access.

Results

We identified 52 articles spanning diverse case reports, case series, clinical reviews, genetic investigations, observational studies, and experimental research. These studies explore neurological and auditory disorders, examining genetic mutations, disease progression, clinical characteristics, and therapeutic interventions, providing valuable insights into both hereditary and acquired conditions affecting hearing and neural function. We will give the review results in greater detail by classifying the data into two main groups: syndromic and nonsyndromic variants. Each category will be examined thoroughly, highlighting the unique genetic pathways, crucial linked genes, and the clinical manifestations reported in both syndromic and nonsyndromic AN.

Syndromic

Brown-Vialetto-Van Laere syndrome (BVVL) is a rare neurodegenerative disorder that affects the sensorimotor nerves, the optic nerve, the bulbar nerve, and the lungs. Symptoms can include pontobulbar palsy, muscle weakness, and respiratory compromise. Patients may experience difficulties with feeding, hypotonia, and cranial nerve impairments. Magnetic resonance imaging can reveal abnormalities, such as T2 hyperintensity in the spinal cord. BVVL is primarily inherited in an autosomal recessive manner. Changes in the riboflavin transporter genes solute carrier family 52 member 2 (*SLC52A2*) and *SLC52A3* cause this syndrome. These genes encode riboflavin transporters, namely riboflavin transporter 2 (*RFVT2*) and riboflavin transporter 3 (*RFVT3*). There is evidence of genetic heterogeneity, with some cases suggesting a possible autosomal dominant pattern. Inheritance or involvement of a mutant gene on the X chromosome [11–13]. Audiological investigations in BVVLS patients typically reveal ANSD, with normal otoacoustic emissions but absent ABR, and the hearing loss in BVVLS is likely of postsynaptic origin [14].

Charcot-Marie-tooth (CMT) disease is the most common genetic neuromuscular condition, impacting approximately 1 in 2500 individuals [15]. It is characterized by peripheral nerve degeneration, leading to distal muscular weakness, atrophy, foot deformities, and sensory loss. CMT is genetically heterogeneous, with over 60 genes implicated in its pathogenesis. These genes are crucial for preserving neuronal integrity, facilitating axon transport, and enabling nerve signal transmission [16]. Key genes include peripheral myelin protein 22, myelin protein zero, gap junction protein beta 1, and SH3 domain-containing transcription factor 2 [17]. Research on hearing loss in CMT disease reveals a complex audiologic profile characterized by cochlear and neural deficits. Studies have found varying degrees of hearing loss, ranging from mild to severe, with difficulties in speech perception, especially in noisy environments. Audiological abnormalities include elevated or absent acoustic reflexes, abnormal ABR, and distorted otoacoustic emissions [18]. Hearing impairment in CMT patients is significant, with one study reporting that 28% of cases are affected [19]. AN appears to be present in all CMT type 4C patients, often detectable unilaterally in infancy and progressing with age. The hearing loss in CMT is generally bilateral and may be more severe in male patients [20].

Friedreich ataxia (*FRDA*) is an autosomal recessive neurodegenerative condition that mainly impacts the nervous system and heart. It is defined by decreased coordination and neurologic and cardiac complications [21]. The disease is caused by mutations in the *FRDA* gene, with 98% of cases due to guanine-adenine-adenine (GAA) trinucleotide repeat expansions in intron 1, leading to decreased frataxin protein levels [22]. Frataxin deficiency affects the muscular, nervous, and cardiovascular systems, leading to progressively worsening symptoms over time [23]. The pathogenesis involves mitochondrial iron accumulation, leading to increased free radical production and cellular damage [22]. *FRDA* is associated with auditory dysfunction, characterized by impaired temporal and spectral processing. Patients often exhibit sensorineural hearing loss and abnormal auditory brainstem responses [24]. The degree of auditory dysfunction correlates with the GAA trinucleotide repeat expansion, particularly when GAA1 exceeds 500 repeats. Auditory spatial processing deficits are also observed and may be linked to mild cognitive impairment in *FRDA* patients [25].

X-linked recessive ANSD is a hearing impairment primarily attributed to genetic mutations inherited in an X-linked recessive pattern. These mutations occur in the apoptosis-inducing factor gene (*AIFM1*), located on the X chromosome. *AIFM1* plays crucial roles in cellular processes, including programmed cell death and mitochondrial function. At the same time, while *AIFM1* mutations are associated with various disorders, including mitochondrial diseases with neurological and muscular manifestations, such as Cowchock syndrome, their involvement in X-linked recessive ANSD results explicitly in hearing impairment due to abnormalities within the auditory neural pathways. These mutations, often missense mutations that alter the protein's function, disrupt the normal functioning of *AIFM1*, leading to the characteristic hearing loss associated with this disorder. X-linked recessive ANSD is defined by variable hearing loss, ranging from mild to severe, with some individuals initially exhibiting normal hearing. Despite potentially normal outer hair cell function, as evidenced by standard otoacoustic emissions, abnormal auditory brainstem responses suggest that the primary issue lies in the neural conduction of the auditory signal to the brain. This late-onset condition, typically manifesting during adolescence, often spares female carriers of the *AIFM1* gene mutation, who usually have normal hearing, thus emphasizing this disorder's X-linked recessive inheritance pattern [26–28].

Kallmann syndrome (KS) is a genetic disorder described by hypogonadotropic hypogonadism and anosmia. KS results from impaired hypothalamic gonadotropin-releasing hormone secretion, leading to reduced sex hormone levels and delayed puberty. Recent research has identified five genes associated with KS: *KAL-1*, *FGFR1*, *PROKR2*, *PROK2*, and *NELF*. These genes have essential functions in the migration and maturation of olfactory and GnRH neurons. KS exhibits genetic heterogeneity, with autosomal dominant, autosomal recessive, and X-linked recessive inheritance patterns reported [29]. Studies have reported sensorineural hearing loss in KS patients; the auditory deficits in KS may be part of a broader spectrum of AN disorders. Genetic investigations have revealed mutations in genes such as *KAL1* as potential causes of KS with hearing loss. Additionally, radiological examinations have shown abnormal temporal bone anatomy and labyrinthine morphology in KS patients, which may contribute to both auditory and vestibular dysfunction [30–32].

CHARGE syndrome is a complex genetic disorder identified by a specific pattern of congenital anomalies, including coloboma, heart defects, choanal atresia, growth retardation, genital hypoplasia, and ear abnormalities. The syndrome is primarily due to mutations in the chromodomain helicase DNA-binding protein 7 (*CHD7*) gene on chromosome 8q12.1. Individuals with *CHD7* mutations are more frequently associated with ocular colobomas, temporal bone abnormalities, and facial nerve paralysis than those without [33–35]. CHARGE syndrome is related to various auditory abnormalities, including sensorineural hearing loss and AN. Patients often have hypoplastic or absent auditory nerves, which can affect cochlear implant outcomes. Temporal bone abnormalities, such as ossicular deformities and cochlear malformations, are common [36].

Sotos syndrome is a rare genetic disorder defined by abnormal growth, distinctive facial features, macrocephaly, and varying degrees of learning difficulties. The condition is primarily due to mutations or deletions in the nuclear receptor-binding SET domain protein 1 (*SETD1*), located on chromosome 5q35, which encodes a histone methyltransferase involved in transcriptional regulation. Associated features may include hypotonia, feeding difficulties, seizures, and an increased risk of tumors [37, 38]. It is related to various otolaryngologic manifestations. At the same time, conductive hearing loss and chronic otitis media are commonly reported. ANSD has been observed in conjunction with Sotos syndrome [19, 39].

CAPOS syndrome is an uncommon inherited neurological condition resulting from mutations in the *ATPIA3* gene, specifically the c.2452G>A (p.Glu818Lys) variant. The syndrome is defined by cerebellar ataxia, areflexia, pes cavus, optic atrophy, and sensorineural hearing loss, typically triggered by febrile episodes in childhood. Patients may experience recurrent acute ataxic encephalopathy, with symptoms improving within days but showing slow progression afterward [40, 41]. CAPOS syndrome is associated with AN spectrum disorder. This rare condition presents with intact outer hair cell activity with impaired neural synchronization along the auditory pathway. Audiological evaluations typically show preserved otoacoustic emissions and cochlear microphonics but abnormal auditory brainstem responses. Patients often experience poor speech perception, especially in noisy environments [42, 43].

Nonsyndromic

Some mutations in the *OTOF* gene are linked to a condition called nonsyndromic recessive AN, which affects the auditory pathway but not the outer hair cells. This condition results in varying degrees of hearing impairment, as evidenced by the presence of otoacoustic emissions in some patients, indicating intact OHC function and distinguishing it from other forms of hearing loss. The *OTOF* gene is important for AN because it encodes a protein required for the function of inner hair cells in the cochlea. This protein affects the release of neurotransmitters and the transmission of auditory signals [45]. New *OTOF* mutations and their varying frequencies in AN have been found in studies involving a wide range of populations. In Taiwan, a new *p.E1700Q* mutation was found in 23% of AN families, suggesting a possible founder effect [45]. Six new pathogenic variants were found in research from Brazil. *OTOF* mutations were found in 7.7% of cases of autosomal recessive hearing loss and were more common in the AN cases [46]. Italian studies identified 5 new *OTOF* mutations in children with AN, further solidifying the gene's role in this condition [47]. A new homozygous frameshift mutation (*c.1981dupG*) in the *OTOF* gene was also found to be the reason why one Iranian family had trouble hearing [48].

Changes in the *PJVK* gene, which encodes pejvakain, cause DFNB59, an autosomal recessive nonsyndromic hearing loss with variable symptoms. A Pakistani family with *p.C343S* [49] and a Chinese family with *c.930_931del AC* both have new mutations [50]. Other mutations found in Spanish cases are *p.Leu224Arg*, *p.His294Ilefs*43*, *p.His294Asp*, and *p.Phe317Serfs*20*. *PJVK* mutations can result in both cochlear dysfunction and ANSD. Patients with *PJVK* mutations typically demonstrated severe to profound hearing impairment [51].

Changes in the *TMCI* gene are associated with two types of hearing loss that do not exhibit any other symptoms: Autosomal recessive (DFNB7/11) and autosomal dominant (DFNA36). DFNB7/11 typically results in congenital or prelingual severe-to-profound hearing loss, while DFNA36 causes post-lingual, progressive hearing loss. *TMCI* mutations disrupt mechanical-to-electrical conversion in inner ear hair cells. Studies have identified novel mutations in different populations, including 4 in Turkish families and 5 in other families. Interestingly, some *TMCI* mutations can cause moderate to severe hearing loss rather than profound deafness, which suggests that the protein still functions [52–54].

The *DIAPH3* gene has been recognized as the cause of autosomal dominant nonsyndromic AN. A change in *DIAPH3*'s 5' UTR leads to the overexpression of the protein, resulting in hearing loss in humans and *Drosophila* [55]. A new frameshift variant, *c.3551_3552del* (*p.Glu1184AlafsTer11*), was identified in the *DIAPH1* gene in a separate study. This change, located in exon 26 within a linkage region with a high LOD score, is associated with AN in the studied family, strongly suggesting that it contributes to the observed hearing impairment phenotype [56].

Mutations in the *OPAI* gene, primarily associated with dominant optic atrophy, can also cause AN and vestibular dysfunction. Studies have identified specific mutations, such as *R445H*, that cause deafness by impairing the function of auditory nerve terminals. The *Opal1del-TTAG* mouse model exhibited adult-onset progressive AN, characterized by the breakdown of spiral ganglion neuron fibers and loss of inner hair cells. A review of 327 patients with *OPAI* mutations revealed that 6.4% experienced sensorineural hearing loss, with varying onset ranging from childhood to adulthood. Audiological tests often support the diagnosis of AN in these cases [57–59].

A new type of autosomal-dominant auditory synaptopathy/neuropathy called AUNA2 has been found in a German family. It was first linked to chromosomes 12q24 and 13q34. AUNA2 is characterized by slowly progressive post-lingual hearing loss, accompanied by no additional symptoms [60].

GJB2 gene mutations are the main cause of nonsyndromic sensorineural hearing loss (NSHL) across various populations. Studies in Chinese patients have identified several mutations, with *235delC* being the most prevalent. The mutation spectrum differs between ethnic groups, with *235delC* more common in East Asian populations than *35delG*, which is prevalent in Caucasians

[61]. *GJB2* mutations can cause both autosomal recessive and dominant forms of NSHL. Some *GJB2* mutations also lead to persistent skin and hearing problems, which typically follow a dominant inheritance pattern [62]. A study found no significant correlation between ANSD and *GJB2* mutations, with only 7.5% of ANSD patients harboring *GJB2* mutations [63]. Recently, however, 16 of the 117 people with ANSD studied had *GJB2* mutations. This finding suggests that *GJB2* variants may be deleterious in ANSD [64].

Treatment options for ANSD

This section provides a brief overview of current treatment strategies, and a more comprehensive discussion of treatment options for ANSD is beyond the scope of this review. The treatment of ANSD currently focuses on maximizing auditory function through a multidisciplinary approach. Hearing aids are the primary treatment for mild to moderate hearing loss. Also, people with severe to profound hearing loss are thought to be getting cochlear implants. This condition is especially true if the inner hair cells do not function correctly or if hearing aids do not provide significant relief. Careful patient counseling, considering individual needs and expectations, is essential in selecting the most appropriate amplification strategy. FM-listening systems can significantly improve signal-to-noise ratios in challenging listening environments, enhancing speech understanding. Gene therapy holds tremendous promise for the future of ANSD treatment. New methods, such as CRISPR-Cas9, SMaRT, and AAV-mediated gene therapy, are being used to correct underlying genetic changes, stimulate the growth of new auditory synapses, and restore the nerves that control hearing. Early preclinical and clinical trials have yielded promising results, but further research is needed to address challenges, including developing accurate animal models, refining diagnostic tools, and assessing the drug's long-term safety and efficacy. Gene therapy products, such as DB-OTO and OTOF-GT, approved by the FDA, represent a significant step forward in the search for effective, targeted treatments for genetic forms of ANSD [65, 66].

Discussion

ANSD is a complex, multifactorial condition arising from various genetic causes and occurring in both syndromic and nonsyndromic forms. Recent genetic studies have highlighted mutations in several key genes, including *OTOF*, *PJVK*, *TMCI*, *DIAPH3*, and *OPAI*, which significantly contribute to the development of this disorder. These genetic changes can disrupt the normal

functioning of auditory pathways, resulting in impaired transmission of sound signals from the inner ear to the brain, even when the outer hair cells remain intact.

Given the diversity and complexity of these genetic disorders, further research is needed to identify additional genes and deepen understanding of the molecular mechanisms underlying AN. This understanding will lay the groundwork for improvements in diagnosis and prognosis, as well as the development of individualized therapeutic strategies. Additionally, exploring gene interactions and their impact on the structure and function of the auditory system could yield valuable insights and inform the development of innovative treatment approaches in the future.

Ethical Considerations

Compliance with ethical guidelines

No ethical approval was required as this study is a review of previously published literature and involved no human or animal subjects.

Funding

There is no external funding for this study.

Authors' contributions

Conceptualization and drafting of the manuscript: Majid Karimi; Critical revisions: Mohsen Ahadi; Literature selection: Mohammad Ajalloueyan; Refining the scientific content: Nader Saki; Organization and synthesis of key findings: Saeid Morovvati; Reviewing and improving the final manuscript before submission: Golshan Mirmomeni; Reading and approval of the final version of the manuscript: All authors.

Conflict of interest

The authors declared no conflicts of interest.

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