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CONTRIBUTIONS OF COMMON SINGLE NUCLEOTIDE POLYMORPHISMS IN NOISE-INDUCED HEARING LOSS

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Abstract

Noise induced hearing loss (NIHL), is common sensory illness especially occur in industrial areas, about 10% population affected annually. NIHL is second occupational and sensori-neural hearing disability all over the world. Since the description between PON2, ATP2B2, CASP gene, Potassium recycling genes (KCNE1, KCNJ10, KCNQ1, KCNMA1, KCNQ4), SLC12A2, SLC26A4, connexins (GJB2, GJB3, GJB6), myosin 14 genes, CAT SNPs/haplotypes, cadherin 23 & protocadherin 15 (CDH23, PCDH15), HSP haplotypes (HSP70-hom, HSP70-1 and HSP70-2) there have been significant advances in the understanding and genetic manipulation of this disease. This review focused on the genes involved in Noise induced hearing loss (NIHL). But all these genes are studied separately in different populations. One large research plan has to be introduced to identify common genes involved in this disease. We should have to know the mechanism of involvement of these genes in this disease.

Keywords: NIHL, PON2, ATP2b2, CASP gene, CAT, cadherin 23, connexins, HSP haplotypes

INTRODUCTION

Hearing loss is a chronic sensory disability of ear which can be of both types, noise induced hearing loss, age related hearing loss or both (1-3). Both can exist at the same time which is difficult to trace and is due to the hair cells loss with spiral ganglion neurons degeneration (4). Center for disease control (CDC) announced hearing loss as third chronic disease in US and second pervasive type hearing loss (5, 6).

At the present time NIHL is worldwide sensori-neural risk disorder which influences socio-economic globally and occurs due to day by day exposure of noise with frequency notch at 4-6 kHz. It depends upon the exposure duration, type and strength of the noise. Two types of NIHL have been defined as temporary (TTS) and permanent (PTS) with the disturbance of mechanical as well as metabolic factors (7, 8). It is proportioned to the exposure of noise and left ear affects more than right one (9). Noise firstly affects the hair cells of which result Cochlear nerve fibers and spiral ganglion cells degenerate (10). WHO reported 1.3 billion people affected by hearing loss due to continuous sound exposure and about 10% world population suffering from NIHL (11). It is reported by the international standard (ISO-1999, 1990) when an individual exceeds the normal threshold hearing level then suffer from the hearing loss correlated also with the age and noise induction depend upon the noise frequency and exposure duration (12).

Genetically it is essential to properly diagnose the noise induce hearing loss which is exponentially increasing as a genetic trait and subject to selective evolution. Heavy instruments and tools are affecting our daily life while producing noise. Although less exposure of such noise leads to temporary loss of hearing ability which can lead to permanent with increasing noise exposure can lead to auditory loss permanently (13). In industrial areas due to the sensory deficiency 10% population affected by Noise induced hearing loss (14). NIHL is second Sensi-neural occupational hearing loss (15, 16). It is alarming that about 500 million people are at risk of hearing defects throughout the world (17). Among different individuals, susceptibility to NIHL differs owing to a permutation of genetic as well as environmental factors (18).

Recently, the detection of Single Nucleotide Polymorphisms (SNPs) has been started as the as the risk of many different genetic diseases (19). These are point mutations found every 100-300 bp apart in the genome and their numbers vary in a specific genome. The use of SNPs is supposed to be an excellent tool to evaluate the genetic and clinical conditions of composite diseases in which many genes are thought to be involved, such as NIHL.

It is a multi-factorial disease in which large numbers of genes are involved and played functional as well as morphological role in inner ear. The involvement of potassium (K⁺) ion and heat shock protein (*HSP*) pathways involving genes was determined as a profound cause of the disease. Potassium (K⁺) recycling genes played role in hearing, as the defect in these genes cause multiple forms of hearing impairment (*KCNE1*, *GJB2*, *KCNQ1*, *KCNQ4*, *GJB3* and *GJB6*). Recent studies on HSP haplotypes (*HSP70-1*, *HSP70-2* and *HSP70-hom*) showed that the mutation in these haplotypes may be related to inclination of NIHL. Recently, the significance of protocadherin 15, myosin 14 genes and many other genes have been found to be associated (20).

HISTORY

In the 18th century, the disease of workers of Ramazzini's classic occupational medicine *De Morbis Artificum* first reported the noise induces hearing loss just because of high noise exposure. Ramazzini's discussions shows that hearing loss was related to both occupational and environmental which affects whole population not only individuals. In Egypt same study was done by coppersmiths of Venice (21).

NIHL clinical summary shows Sensi-neural insufficiency was around the 3,000 Hz – 6,000 Hz in the regions of audiograms while higher amount was around 6,000 Hz. In males, majority of the police force males (74.8%) were affected while their mean age was 35.55 ± 9.57 years. A study was performed on Royal Brunei Police Force in Darussalam showed that more cases of males (37.7%) than females (23.9%). This study also update us involvement of hypertension, age, diabetes, service duration and gender along with NIHL. (22).

In Tanzania NIHL prevalence was found of 47% (12% poor hearing loss, 35% mild hearing impairment). NIHL increases exponentially within a year of underground miners

(71%), open pit miners (28%), young age group (60%) between the 20 to 29 years of age (23).

A study in Nepal revealed the prevalence of NIHL in wood industry. From 88 carpenters and 36 sawyers, 16 of joiners (31%) and 27 of sawyers (44%) showed occupational NIHL whereas, levels of sound ranging from 71.2 to 93.9 dBA (24).

FACTORS ASSOCIATED WITH NOISE INDUCED HEARING LOSS (NIHL)

NIHL is a complex disorder mainly originated by a blend of a number of environmental as well as genetic factors (25). In all environmental factors that cause hearing loss, continuous noise exposure is the best known. Environmental factors associated with NIHL such as extreme heat, exposure to solvents especially organic ones, microbial infections, chemicals causing ototoxicity and smoking. In addition, factors like elevated blood pressure and other medical factors also make ear susceptible to noise (18). Propensity to noise injury differed among persons which described the role of genetic grounds in this field (26).

CAUSES

The main root of defect in occupational hearing was found to be cochlear hair cell injury (27). Free radicals discharge as a result of noise can destroy the cochlear epithelium, leading to NIHL(28).

Repeatedly noise exposure is the main reason behind hearing loss among wide range of secondary, non-auditory effects including sleep disorder, intellectual deficiency and cardiac disease (29). Noise-induced hearing loss (NIHL) with tinnitus affects 16% of the population globally (30).

CLINICAL FEATURES

The main feature of the disease is the sensory and neural hearing defect concerning primarily the high audiometric frequencies. An audiometric “notch,” is thought to be indicative of noise-induced damage (31).

PATHOPHYSIOLOGY

Noise contact mainly affects the lateral wall, organ of Corti and afferent neurons in the inner ear which considered as either provisional or endless hearing threshold shifts. Their functions and morphology are clearly different but at the molecular level scientists are unable to find clear difference. It is clear that hearing loss is because of the loss of cochlear hair cells in organ of corti, stria vascularis and afferent neurons. Some reports suggests reactive oxygen species (ROS) the reason behind hearing loss by which hair cells failure to grow. Reactive oxygen species damages mitochondrion which affects pro-apoptotic factors trigger the cellular apoptotic reaction. Loss of hair cells because of noise exposure results in Potassium dys-regulation between Hensen’s cells and hair cells present in organ of corti (30).

Whole genome and genome wide studies showed the association of genetic variations with NIHL. These studies reported polymorphisms in different pathways includes oxidative stress response pathways, involving *HSP70* and *SOD1* proteins; as well as potassium recycling pathways, concerning *KCNQ4* and *KCNE2* proteins (25).

COMMON GENES INVOLVED IN HEARING MECHANISM

Genes involved in NIHL are mainly involved in Structural Integrity of Stereocilia (mechano-sensing organelles of cochlear hair cells), Ion Homeostasis (Pumps, Channels and Connexins), Protective Pathways (Glucocorticoids and Stress Response) Oxidative Stress, and Other Processes (21).

PARAOXONASE2 GENE (PON2)

Paraoxonase2 genes categorized as *PON1*, *PON2* and *PON3* code for esterases, localized on “q” arm of chromosome 7 (q21.3–22.1). *PON2* gene present at the whole body and produce antioxidant effects while any change in its sequence which increase ROS and damage cochlear cell. *PON2* genetic analysis shows polymorphism of ‘rs12026 and rs7785846’ in sample of 94 male workers exposed to noise revealed a significant association with NIHL in Italy (28, 32).

ATP2B2

ATPase, calcium-transporting, plasma membrane 2 (*ATP2B2*) gene, encodes plasma membrane calcium transporting ATPase isoform2 (PMCA2) is located on “p” arm of the human chromosome 3 (3p25). The characteristic role of *ATP2B2* in hearing was specified by its increased level of communication in cochlear hair cells, where it played significant role in calcium homeostasis. *ATP2B2* is an influencing gene for NIHL and also its absence can direct towards the defects of auditory systems leading to hearing loss. Researchers have worked on rs1719571, rs3209637 and rs4327369 and they found involvement of these genes in NIHL (33).

CASP GENE

Hair cell death way is apoptosis, which is orderly organized by a specific gene. Caspases pathway activation is the essential connection in apoptosis. Caspases enzymes are encoded by *CASP* genes and are activated under the influence of an apoptotic signal by stepwise hydrolysis. When activated, cause structural and functional damage of the cell. According to recent studies, two SNPs in *CASP3* gene (rs1049216. rs6948) have been associated with NIHL risk (34).

POTASSIUM RECYCLING GENES

Electrochemical gradient cross wises the cell cubicle and potassium flow in cochlea which are also vital for hearing and is maintained by the potassium recycling pathway genes. Subsequently, polymorphism in the potassium recycling genes leads to or may be associated with hearing loss. Genes involved are potassium voltage gated canal genes *KCNE1*, *KCNQ1* and *KCNQ4*. Potassium inwardly rectifying channel *KCNJ10* and

potassium calcium activated gated channel subunit *KCNMA1*. Sometimes mutations in these genes cause congenital deafness in humans (35).

STRESS RESPONSE GENES

Mild exposure to noise has been reported that it shields the ear from earsplitting music that is branded as “Sound Conditioning” (36). A number of methods are offered to explain it. Some other best developed natural mechanisms include antioxidant, heat shock and glucocorticoid signaling cascade. An important transcription factor is Heat shock transcription factor 1 (Hsp70) that manages the inducible stress response protecting tissues and cells from numerous cellular as well as environmental stresses which is sometime called shock response (Morimoto et al. 1997). *Hsp70* gene expression in cochlea is up regulated by heat stress participating in protecting hair cells from consequent pressure of noise. It is reported that SNP rs2227956, rs1061581 and rs1043618 in *Hsp70* has significant association with NIHL (6).

CAT

CAT SNPs/haplotypes are identified as the association connecting Noise exposure and these genes (37).

CADHERIN 23 (*CDH23*) & PROTOCADHERIN 15 (*PCDH15*)

CDH23 and *PCDH15* both play role in growth and maintenance of hair cells (38, 39). Proteins variation of *CDH23*, *PCDH15* damages the structure which is important from motorized stimuli to electrical signals. As a result of missense mutation one form converted to another (such as *CDH23* in *DFNB12*; *PCDH15* in *DFNB23*) causes deafness (40, 41). First reported cross sectional study in chinese industrial workers showed *CDH23* associated with NIHL (42). *CDH23* SNPs inspected in 93/101 workers showed hearing loss only two reported as associated with NIHL. SNPs of rs3802711 with T/T genotype were more prevalent than C/T genotype. When examined exon 7 from terminal position it was suggested that individuals with G/G genotype were more prone to noise than A/G genotype. When different parameters such as gender, age, noise history and smoking C/C genotype at the SNPs rs1227049 suggested as linked with G/G genotype. More than 35 SNPs in *CDH23* have been reported in controlled population which was associated with NIHL (43).

CONNEXINS

Connexins are intercellular channels known as gap junctions. The movement of small metabolites and molecules from cell to cell occurs by these gap junctions that form pores among neighboring cells (44, 45). Connexins 26 (Cx26) is encoded by *GJB2* (*DFNB1*) which is a most common gene involved in deafness (46). 25delG mutation is most frequent mutation in Caucasians that eventually leads to the truncation of connexins 26 and hearing loss. Other mutations in *GJB1* (Cx32), *GJA1* (Cx43), *GJB3* (Cx31), *GJB4* (Cx30.3) and *GJB6* (Cx30) have played an important role in non-syndromic hearing loss. In a study of

702 polish GJB 235delG carriers, no correlation was found between GJB2 and vulnerability to noise induced hearing loss (47). An important association was found for single nucleotide polymorphism (SNPs) in *KCNQ1*, *KCNJ10*, *GJB1*, *GJB2* and *GJB4*, that is suggestive of these genes involvement in noise induced hearing loss. Future studies on these SNPs in other populations will be essential for confirmation of these genes role in NIHL (48).

Table I. Detail of genes involved in NIHL with reference to their different parameters

Pathways	Genes	Protein	Function	SNPs Involved	Location	References
Antioxidant Pathway	PON1,	Paraoxanase	Antioxidant	rs1202, rs	7q (21.3-22.1)	(2, 28-32)
	PON2 and PON3 ATP2B2	PMCA2	Calcium Homeostasis	Rs1719571, rs3209637, rs4327369	3p25	(2)
Apoptotic Pathway	SOD1 & SOD2	SOD	Superoxide metabolism	IVS3-23T/G and IVS3-60T/G	chromosomal region 21q22	(33, 34)
	CASP 3	Caspase 3	Apoptosis	Rs1049216, rs6948	4q35.1	(10)
Potassium Recycling Genes	KCNE1	-	strength of the cochlear amplifier	rs2070358, rs1805127, rs1805128	21q22.12	(32)
	KCNQ1	-	-	rs163171	11p15.5-15.4	(32)
	KCNQ4	-	-	rs34287852	1p34.2	(32)
	KCNJ10	-	-	rs1130183	1q23.2	(32)
	KCNMA1	-	-	-	10q22.3	(11)
Heat Shock	Hsp70	Hsp70	Sound conditioning	Rs2227956, rs1043618	Human chromosomes 6,14,21	(28, 32, 35)
	Cdh23 gene	Cadherin	congenital deafness(stere ocilia at the top of sensory hair cells)	rs1227049, rs1227051, rs3802711	10q21-q22	(32, 36-39)
Gap junction protein	GJB2	Connexin 26	Deafness	235delG	13q12	(23, 40)
	MYH14	Myosin Heavy chain	-	Rs667907, rs588035	19q13.33	(28)

MYOSIN HEAVY CHAIN

People with *DFNA4* gene mutations can suffer from sensori-neural hearing loss. Non-muscle heavy chain that is encoded by gene *MYH14* is common mutation in *DFNA4* (49). Inside a newborn mouse cochlea, *MYH14* expresses in organ of corti in cochlea, stria vascularis and other cells like Hansen cells, Claudius cells and epithelium layer of spiral prominence. Regardless of its roll in hearing loss and vital rolls in ear by other unconventional myosin, *MYH14* function is not known entirely. SNPs in the *MYH14* gene were among those 53 genes that were screened for NIHL in Poland and Sweden people.

rs667907 and rs588035 are the two SNPs that were found to have an association with NIHL susceptibility (48).

SOD1 & SOD2

The joint effect of SOD, catalase and other enzymes involved in glutaredoxin, anti-oxidative glutathione and thioredoxin systems is required for metabolism of the superoxide and their derived peroxides. Diminished activity in one the above components can lead to the decreased anti oxidative ability of component and enhanced ROS/RNS damage. From five single nucleotide polymorphisms, two intronic polymorphisms (SOD IVS3-23T/G and IVS3-60T/G) were found to be paralleled with noise induced hearing loss. However functional consequences that occur due to these polymorphisms are not clear due to the presence of polymorphism in intronic region (50).

CONCLUSION

By using prevention approaches and today's technology, occupational hearing loss can be prevented (63). Regular audiometric testing every year for the hearing loss detection along with preventive measures to bar any further loss is important (63, 64). Lost hearing of workers suffering from occupational hearing loss can't be reversed however can be optimized by clinical therapy including hearing aids fitting, lip-read learning and other compensative strategies. Precautionary measures, timely diagnosis of the disease, adopting intervention and clinical therapies, might help to greatly recover patients. Up till now, there is no test available at the genetic level to diagnose NIHL. Ongoing genetic studies on mice for underlying mutations will help in future for genetic susceptibility of noise induced hearing loss in humans. At present time it is not possible to sequence all those genes which play a dynamic role in resistance or susceptibility to noise for finding the variation in one individual. However, with advancements in the genome sequencing and expected decrease in cost, it may be possible one day in future to sequence a person's entire genome in a cost effective way aimed at understanding collective effects of the multiple genes that make a person subject to noise induced hearing loss.

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