Prevalence of congenital non syndromic hearing loss among offspring of consanguineous marriage: a pilot study

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INTRODUCTION

An estimated prevalence of one in 1000 new born is seen among the hearing loss because of which normal communication, speech acquisition is hindered. Palliative treatment with special education is needed as early as possible. Researchers have shown that the reason for hearing impairment among the children with prelingual hearing impairment is inherited and is autosomal recessive type. Though there are about 100 loci linked to congenital deafness, one among them is the gap junction beta 2 or the GJB2 gene, which is located at chromosome 13q12. This gene encodes for the protein connexin 26 which is mostly present in the cochlea and in the epidermis.

Connexin 26 a small molecule which is actually a gap-junction protein, functioning in cell-to-cell diffusion of small molecules which is necessary for recycling of potassium in the cochlea is required for sensori neural hearing function. This was the first gene to be associated with autosomal recessive form of hearing loss. Connexin 26 mutations are responsible for at least 20% of all gene tic hearing loss and 10% of all childhood hearing loss. In Indian population, more than 80 percent of cases of non-syndromic recessive deafness result from a mutated connexin 26 gene (pW24X).

Studies have reported that the genetic and environmental issues are the causes of congenital deafness and early onset hearing impairment.

ABSTRACT

Background: Mutations in the gene encoding the gap-junction protein connexin-26, is understood to be the most important cause of non-syndromic hearing loss (NSHL). An attempt to identify the single nucleotide polymorphism (SNP) for W24X mutation was done. Consanguineous marriage was seen among the NSHL subjects.

Methods: SNP was identified using restriction fragment length polymorphism-polymerase chain reaction (RFLP-PCR). Forty-five subjects were screened for congenital hearing loss. Twenty subjects matched the inclusion criteria and were included in the study.

Results: 5 out of 20 subjects were found to have mutation i.e., 25%. Though consanguinity is known to cause autosomal recessive defect, the same could not be depicted in this study.

Conclusions: 25% of the study population had a mutation in their gene and the rest though had consanguineous marriage had not been affected genotypically.

Keywords: Hearing impairment, GJB2 mutation, W24X gene, RFLP
gene. Theoretically in consanguine marriage the initial phenotypic expression of genes is seen in these population hence the need of the study.

METHODS

After the approval of the study by institutional ethical clearance board of our institute, screening for non-syndromic congenital sensorineural hearing loss (SNHL) for GJB2 mutations was done at speech and hearing center of Mc Ganns teaching district hospital. This was a prospective study, where in subjects were selected as per the inclusion criteria. The study data represents information conducted over a period of one year (January to December 2019). We screened 45 unrelated Indian subjects with an age group within 21 years. Subjects from Taranga school, Shimoga were included for this study. Most of the subjects were presented with severe-to-profound congenital hearing loss on pure-tone audiography, immittance audiometry, oto-acoustic emissions and evoked auditory brainstem response evaluation. These audiological tools were utilized for screening of all patients and to exclude those who do not match our criteria.

Patients who had conductive hearing loss, syndromic hearing loss, had taken ototoxic drugs, history of otorrhea, head trauma, meningitis, NICU admissions, kernicterus, any other perinatal pathology, maternal complications during pregnancy, or history of maternal consumption of ototoxic drugs during pregnancy; or any other known causes of hearing loss were not included in this study.

Two milliliters of blood samples were collected from each of the 20 patients, in EDTA vacutainers, after obtaining written informed consent from their respective parents (if minor). 25 subjects were excluded since they did not fulfill the inclusion criteria. DNA was isolated from these blood samples using Himedia blood genomic isolation kit. The DNA was aliquoted and stored at -80°C.

Table 1: Genotype of the probands selected.

<table>
<thead>
<tr>
<th>Gender</th>
<th>Total screened for SNP</th>
<th>Single band</th>
<th>Heterozygous</th>
<th>Homozygous</th>
</tr>
</thead>
<tbody>
<tr>
<td>Male</td>
<td>14</td>
<td>11</td>
<td>1</td>
<td>2</td>
</tr>
<tr>
<td>Female</td>
<td>6</td>
<td>4</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>Total</td>
<td>100</td>
<td>75</td>
<td>10</td>
<td>15</td>
</tr>
</tbody>
</table>

Table 2: Description of genotype for offsprings of consanguineous union.

<table>
<thead>
<tr>
<th></th>
<th>Not affected</th>
<th>Heterozygous</th>
<th>Homozygous</th>
</tr>
</thead>
<tbody>
<tr>
<td>First degree</td>
<td>8</td>
<td>1</td>
<td>9 (4 males, 4 females and 1 female)</td>
</tr>
<tr>
<td>Second degree</td>
<td>1</td>
<td>1</td>
<td>2 (1 male, 1 female)</td>
</tr>
<tr>
<td>Third degree</td>
<td>6</td>
<td>1</td>
<td>7 (7 male)</td>
</tr>
<tr>
<td>Non consanguineous</td>
<td>2</td>
<td>1</td>
<td>2 (2 males and 1 female)</td>
</tr>
</tbody>
</table>

As shown in the PCR gel figure, we observed that the subjects with single band are not affected by the mutation. Whereas the subjects with three bands are considered to be heterozygous (sample number 3) and subjects with two bands are homozygous (sample number 9 and 10). Since mutation in the gene creates a restriction site in the DNA, ALU I restriction enzyme cuts only those fragments of DNA where in a restriction site is generated. In the heterozygous subjects only one of the alleles are affected whereas in homozygous subjects both the alleles are affected (Figure 1).

The offspring of consanguineous unions are known to be at increased risk to genetic disorders. Since this research is about congenital sensorineural hearing loss which is an autosomal recessive disorder, an insight into their presence or absence of consanguineous marriage is shown in (Table 2).
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Though subjects found (25%) to be mutated for W24X gene, in which 10% were heterozygous, the exact cause for deafness though had been ruled out, may be due to the result of mutation in another connexin gene.

Since the study population showed varied degree of consanguinity and since consanguinity is known to cause the spread of the autosomal recessive defect in our study 5% of the homozygous proband was a non consanguineous marriage. Hence the strength of consanguinity cannot be depicted.

CONCLUSION

Our results suggest that the frequency of mutation in W24X gene is considerably large and mutation in this gene is one of the major causes of congenital non-syndromic recessive deafness. The tendency towards the detectable progression in this fraction of children associated with this allele suggests that more awareness is needed. Detecting this mutation in early stages of life would facilitate in identifying the early diagnosis of deafness. This will help the subjects in implementing the intervention strategies like learning sign language, using hearing aids will help in acquiring formal education and betterment of life. Also, detection of deafness at an early stage will also help in identifying deserving candidates for cochlear implant surgery which is very essential in overcoming childhood hearing disability.

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