ARTIGO ORIGINAL

Non-syndromic sensorineural hearing loss are due to genetic causes, of which approximately one in 500 - 1000 newborns. In this study, we report the frequency of the less common variants of the GJB2 gene in a Portuguese sample and compare these frequencies with those of a group of hearing-impaired patients.

Material and Methods: In order to select the less common GJB2 variants, 147 hearing-impaired patients followed in Centro Hospitalar Universitário de São João were evaluated. Afterwards, the presence of those variants was tested in 360 individuals from Generation 21.

Results: The patient assessment enabled the selection of 11 GJB2 variants. Of those, 10 were investigated in Generation 21 participants, with only four being detected, in heterozygosity: p.Phe83Leu, p.Arg127His, p.Val153Ile and p.Asn206Ser, with the allelic frequencies (95% confidence interval) of 0.14% (0.01% - 0.87%), 0.28% (0.01% - 1.08%), 0.97% (0.43% - 2.04%) and 0.14% (0.01% - 0.88%), respectively. Two variants, p.Val37Ile and p.Val95Met, were more frequent in the patients’ group with statistical significance.

Discussion: Our results allow for the p.Arg127His and p.Val153Ile variants to comply with polymorphism criteria and support the pathogenicity of p.Val37Ile and p.Val95Met variants. Moreover, two cases of moderate hearing loss were explained by the p.Val37Ile/p.Asn206Ser genotype, substantiating both the pathogenicity of such variants and the hypothesis that compound heterozygosity with p.Ans206Ser is associated with mild-moderate hearing impairment.

Conclusion: Understanding the role of the variants is essential in order to provide genetic counselling to patients and their families. We explored a set of uncommon GJB2 variants that comprised 12% of the hearing-impaired patients in this study, supporting the relevance of their description.

Keywords: Connexin 26; Gene Frequency; Genetic Counselling; GJB2 protein, human; Hearing Loss, Sensorineural

INTRODUCTION

Sensorineural hearing loss (SNHL) is one of the most common congenital sensory impairments, affecting approximately one in 500 - 1000 newborns. About 60% of cases of early-onset hearing loss are due to genetic causes, of which 70% are non-syndromic. Non-syndromic sensorineural hearing loss (NS-SNHL) is inherited in an autosomal recessive trait in 80%, but it can also be transmitted in autosomal dominant (15% - 20%), X-linked (2% - 3%), or mitochondrial

RESUMO

Aconselhamento Genético; Conexina 26; Frequência do Gene; GJB2 humano; Perda Auditiva Neurosensorial

INTRODUCTION

Sensorineural hearing loss (SNHL) is one of the most common congenital sensory impairments, affecting approximately one in 500 - 1000 newborns. About 60% of cases of early-onset hearing loss are due to genetic causes, of which 70% are non-syndromic. Non-syndromic sensorineural hearing loss (NS-SNHL) is inherited in an autosomal recessive trait in 80%, but it can also be transmitted in autosomal dominant (15% - 20%), X-linked (2% - 3%), or mitochondrial
More than one hundred genes are known to be involved in NS-SNHL. Despite the genetic heterogeneity, sequence variants in the GJB2 gene account for up to 50% of cases of NS-SNHL in several populations. This gene encodes connexin 26, which is the major component of gap junctions in the cochlea and has been implicated in the maintenance of K⁺ homeostasis in the inner ear. More than two hundred GJB2 variants have been reported, most of them considered pathogenic. The p.Gly12Valfs*2 (also known as c.35delG) variant is the most common GJB2 mutation in several SNHL populations, including Portugal. The p.Met34Thr variant, recently classified as pathogenic, has also been found with a high frequency among SNHL patients. The frequency of the p.Gly12Valfs*2 and p.Met34Thr mutations in the general Portuguese population has already been estimated. As for the remaining GJB2 variants, no published studies in the Portuguese population have estimated their carrier rates.

The main purpose of this study was to estimate the frequency of the less common GJB2 variants in a Portuguese community sample – Generation 21 (G21) – and to compare these frequencies with those of SNHL patients. To select the less common GJB2 variants, a cohort of SNHL patients was evaluated.

We also compare the allelic frequencies of the G21 sample with those of the European sample of the GnomAD Exome population database.

MATERIAL AND METHODS

SNHL patients

A total of 147 consecutive patients followed in the Hereditary Hearing Loss Genetics Clinic from June 2011 until February 2019, presenting with mild to profound SNHL, were studied for GJB2 variants. For that purpose, peripheral blood samples were collected. Additionally, the audiological evaluation was performed using auditory brainstem response tests or pure tone audiometry. For each patient, the medical history has been collected to determine the age of onset and hearing loss evolution, family and patient history. Moreover, causes of acquired hearing loss were excluded. The severity of SNHL was classified by the pure tone average (PTA) of 0.5, 1, 2 and 4 kHz thresholds: PTA < 20 dB was defined as normal hearing, 21 - 40 dB as mild SNHL, 41 - 70 dB as moderate SNHL, 71 - 95 dB as severe SNHL and PTA > 95 dB as profound SNHL.

Selection of the less common variants

The evaluation of the SNHL patients’ cohort provided the spectrum and frequency of GJB2 variants in this group. Taking this spectrum as reference, every variant other than p.Gly12Valfs*2 (c.35delG) and p.Met34Thr was included in our set of less common variants - the target variants of this study. Then, the G21 cohort participants were screened for the selected GJB2 variants, in order to assess their frequency in this Portuguese community group.

G21 cohort participants

Generation 21 (G21), is a population-based birth cohort of 8647 newborns recruited in the metropolitan area of Porto, Portugal, in 2005 - 2006. The recruitment occurred at all level III public units providing obstetrical and neonatal care. At four years of age, the total cohort was invited to a re-evaluation that occurred between April 2009 and July 2011. For this specific study, 480 of the participants attending the follow-up evaluation were randomly selected to study the carrier rate of the most common variants of the GJB2 gene. To fit into the general study aim, only children with parents of Portuguese nationality were included. For each child, a sample of buccal mucosa cells was collected with a swab. Of the 480 selected participants, only 360 were included in the study, due to sample quality constraints.

Genetic analysis

In total, 360 DNA samples were completely sequenced and analyzed. Firstly, genomic DNA was extracted from buccal mucosa cells, using a commercial kit (JETQUICK, Genomed). Then GJB2 gene Sanger sequencing was performed. For that purpose, polymerase chain reaction (PCR) of the GJB2 exon 2 was performed, using the following specific primer pair - Cx26F: 5’-TCTTTTCCAGAGCAAACC-GCC-3’ and Cx26R: 5’-TGAGCAGGGTTTGCGCTCATC-3’. PCR products purification using AmpureXP was performed to remove the contaminants. The sequencing analysis of amplified fragments was performed on an automated sequencer (Applied Biosystems 3730xl DNA Analyzer) and the Applied Biosystems Sequencing Analysis v.5.4 software was used. The annotation of GJB2 sequence variants was based on the GenBank cDNA reference sequence NM_004004 and following the standard nomenclature recommended by the Human Genome Variation Society.

All phases of the study complied with the Ethical Principles for Medical Research Involving Human Subjects expressed in the Declaration of Helsinki (World Medical Association, 2013). The study was approved by the Centro Hospitalar Universitário de São João Ethics Committee and a signed informed consent according to the Declaration of Helsinki was obtained from all participants.

Statistical analysis

The statistical analysis was performed using GraphPad® and OpenEpi® software. Confidence intervals (CI) were calculated using the modified Wald method. Differences in the allelic frequencies between the G21 and the SNHL groups were tested by Fisher’s exact test, as expected values in some cells of the contingency table were below five and the sample size was small. The chi-square test was used to assess differences between the allelic frequencies of the G21 group and the data from the European sample of the GnomAD Exome population database. A significance level of 0.05 was considered.
A total of 147 index cases with SNHL were studied for the presence of the less common variants in the G21 group. A total of 360 individuals from the G21 sample, SNHL patients and European Sample of the GnomAD Exome database and statistical comparison between the groups.

<table>
<thead>
<tr>
<th>GJB2 variant</th>
<th>G21 group (Alleles no. / n (Frequency, %) (95% CI))</th>
<th>SNHL patients (Alleles no. / n (Frequency, %) (95% CI))</th>
<th>European sample (GnomAD Exome database) (Alleles no. / n (Frequency, %) (95% CI))</th>
<th>Statistical comparison</th>
</tr>
</thead>
<tbody>
<tr>
<td>p.Ile20Met</td>
<td>0 / 656 (0.00% - 0.70%)</td>
<td>1 / 112153 (0.34% - 2.10%)</td>
<td>1 / 112153 (0.0009% - 0.0056%)</td>
<td>Fisher's exact test p-value* = 0.3095</td>
</tr>
<tr>
<td>p.Trp24Ter</td>
<td>0 / 720 (0.00% - 0.64%)</td>
<td>1 / 112798 (0.0044% - 0.0107%)</td>
<td>5 / 113146 (0.0016% - 0.0155%)</td>
<td>Chi-square test p-value* = 0.0020</td>
</tr>
<tr>
<td>p.Ile30Val</td>
<td>0 / 720 (0.00% - 0.64%)</td>
<td>1 / 112798 (0.0044% - 0.0107%)</td>
<td>5 / 113146 (0.0016% - 0.0155%)</td>
<td>0.8592</td>
</tr>
<tr>
<td>p.Val37Ile</td>
<td>0 / 720 (0.00% - 0.60%)</td>
<td>150 / 113566 (0.01326% - 0.1556%)</td>
<td>0.3639 (0.3305% - 0.3668%)</td>
<td>0.2032</td>
</tr>
<tr>
<td>p.Phe83Leu</td>
<td>1 / 720 (0.14% - 0.87%)</td>
<td>377 / 113688 (0.3316% - 0.3668%)</td>
<td>0.3316 (0.2998% - 0.3668%)</td>
<td>0.3690</td>
</tr>
<tr>
<td>p.Val95Met</td>
<td>0 / 720 (0.00% - 0.64%)</td>
<td>4 / 113566 (0.0035% - 0.0094%)</td>
<td>0.0035 (0.0010% - 0.0094%)</td>
<td>0.8735</td>
</tr>
<tr>
<td>p.Arg127His</td>
<td>2 / 720 (0.28% - 1.08%)</td>
<td>350 / 113072 (0.3095% - 0.3437%)</td>
<td>0.3095 (0.2788% - 0.3437%)</td>
<td>0.0622</td>
</tr>
<tr>
<td>p.Arg143Gln</td>
<td>0 / 720 (0.00% - 0.64%)</td>
<td>1 / 720 (0.34% - 2.10%)</td>
<td>0.34% (0.01% - 2.10%)</td>
<td>0.2899</td>
</tr>
<tr>
<td>p.Val153Ile</td>
<td>0 / 720 (0.00% - 0.64%)</td>
<td>413 / 113494 (0.3639% - 0.4007%)</td>
<td>0.3639 (0.3305% - 0.4007%)</td>
<td>0.4501</td>
</tr>
<tr>
<td>p.Arg184Trp</td>
<td>0 / 718 (0.00% - 0.64%)</td>
<td>0 / 113592 (0.0000% - 0.0041%)</td>
<td>0.0000 (0.0000% - 0.0041%)</td>
<td>0.2905</td>
</tr>
<tr>
<td>p.Asn206Ser</td>
<td>1 / 704 (0.14% - 0.88%)</td>
<td>8 / 113466 (0.0071% - 0.0142%)</td>
<td>0.0071 (0.0033% - 0.0142%)</td>
<td>0.2090</td>
</tr>
</tbody>
</table>

CI: confidence interval; n: total number of chromosomes assessed; NA: not available.

* A significance level of 0.05 was considered.
heterozygotes were found for any of the variants. The p.Trp24Ter, p.Ile30Val, p.Val37Ile, p.Val95Met, p.Arg143Gln and p.Arg184Trp variants were not identified in the cohort.

**Comparison between the G21 group and SNHL patients**

We compared the allelic frequencies in the G21 group with those of SNHL patients. The differences in the allelic frequencies between the two groups were statistically significant for the p.Val37Ile and the p.Val95Met variants (p = 0.0020), these variants being present only in the SNHL group. Regarding the other variants, no statistically significant differences were found (p > 0.05). The statistical results are presented in Table 1.

**Comparison between the G21 group and the European sample of the GnomAD Exome**

We compared the G21 group allelic frequencies with those of the GnomAD Exome for a (non-Finnish) European sample. The differences were statistically significant for p.Val153Ile (p = 0.0072) and p.Asn206Ser (p < 0.0001) variants, with these variants being more frequent in the G21 sample. No statistically significant differences were found for any of the other variants (p > 0.05). The allelic frequencies of the GJB2 variants in the GnomAD European sample, as well as the statistical results, are presented in Table 1.


The p.Phe83Leu, p.Arg127His, p.Val153Ile and p.Asn206Ser variants correspond the ones that were identified in the G21 sample. In order to further characterize them, we report on the NSHL patients and respective families in which they were present, corresponding to a total of seven unrelated families. The families’ genograms with the individuals’ genotypes and phenotypes are presented in Fig. 1.

Syndromic hearing loss was evaluated for all hearing-impaired members. Subjects presenting other clinical findings beyond hearing loss were further studied using complementary diagnostics tests and were observed by other medical specialists when required. No individual fulfilled the criteria for syndromic hearing loss. Also, none of them com-

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**Table 1**

<table>
<thead>
<tr>
<th>Variants</th>
<th>G21 group (GnomAD Exome database)</th>
<th>G21-SNHL (Frequency, %) (95% CI)</th>
<th>G21-European sample (Frequency, %) (95% CI)</th>
<th>p-value</th>
</tr>
</thead>
<tbody>
<tr>
<td>p.Ile20Met</td>
<td>0.00</td>
<td>0.00% (0.00-0.70%)</td>
<td>0.34% (0.01-2.10%)</td>
<td>0.34</td>
</tr>
<tr>
<td>p.Trp24Ter</td>
<td>0.00</td>
<td>0.00% (0.00-0.70%)</td>
<td>0.34% (0.01-2.10%)</td>
<td>0.34</td>
</tr>
<tr>
<td>p.Ile30Val</td>
<td>0.00</td>
<td>0.00% (0.00-0.70%)</td>
<td>0.34% (0.01-2.10%)</td>
<td>0.34</td>
</tr>
<tr>
<td>p.Arg143Gln</td>
<td>0.00</td>
<td>0.00% (0.00-0.70%)</td>
<td>0.34% (0.01-2.10%)</td>
<td>0.34</td>
</tr>
<tr>
<td>p.Arg184Trp</td>
<td>0.00</td>
<td>0.00% (0.00-0.70%)</td>
<td>0.34% (0.01-2.10%)</td>
<td>0.34</td>
</tr>
</tbody>
</table>

---

**Figure 1** – Genogram of the seven families. Hearing-impaired symptomatic individuals are indicated by green symbols, unaffected patients by light grey symbols. The severity of SNHL considering the PTA_{<1,2kHz} is presented: normal hearing corresponds to a PTA < 20 dB, mild SNHL to 21 - 40 dB, moderate SNHL to 41 - 70 dB, severe SNHL to 71 - 95 dB and profound SNHL to PTA > 95 dB. The index case is identified by a green arrow.

WT: wild type; NSHL: non-syndromic hearing loss; RE: right ear; LE: left ear.
plained of dizziness or tinnitus, nor reported barotrauma or occupational, recreational, or accidental noise exposure. Some individuals had history of otological disease. Clinical features are summarized in Table 2. Parents from families one, two and four were consanguineous. Also, families one and two were of Romani ethnicity.

The p.Phe83Leu variant was present in the heterozygous state in families three and four. Since NS-SNLH is mostly of autosomal recessive inheritance, it is unlikely that this variant is the cause of the condition. Furthermore, in family three, the mother of the index case has the same GJB2 genotype and normal hearing.

The p.Arg127His variant was identified in patients from two different families, both Romani – families one and two – either in heterozygosity or homozygosity or cis configuration of two p.Arg127His variants. The cis configuration was inferred in individuals I-1 and II-1 from family two since the individual II-1 inherited both variants from the male progenitor. The p.Arg127His variant does not seem to segregate with the hearing impairment, as the individual II-2 in family one presented with severe to profound NS-SNLH despite the absence of this variant.

The p.Val153Ile variant was found in heterozygosity in two individuals from family five. Following the same line of reasoning used for the p.Phe83Leu variant, it is unlikely that this variant is the cause of the hearing impairment.

The p.Asn206Ser variant was found in compound heterozygosity with the p.Val37Ile variant in two individuals from families six and seven, both presenting moderate NS-SNHL bilaterally. Families six and seven are not related, but both came from the same region of southern Portugal. As both variants are classified as pathogenic, this compound heterozygosity might be responsible for the hearing loss in these patients.14,15

**DISCUSSION**

In this study, 360 participants from the G21 cohort were screened for the presence of ten less common GJB2

<table>
<thead>
<tr>
<th>Family</th>
<th>Case</th>
<th>Age (years)</th>
<th>Age at SNHL onset</th>
<th>Hearing impairment</th>
<th>Genotype</th>
<th>Observation</th>
</tr>
</thead>
<tbody>
<tr>
<td>1*‡</td>
<td>I-1</td>
<td>54</td>
<td>-</td>
<td>Bilateral mild</td>
<td>p.Arg127His/p.Arg127His</td>
<td>-</td>
</tr>
<tr>
<td></td>
<td>I-2</td>
<td>47</td>
<td>-</td>
<td>Normal audition</td>
<td>p.Arg127His/WT</td>
<td>-</td>
</tr>
<tr>
<td></td>
<td>II-1</td>
<td>24</td>
<td>18 months</td>
<td>Bilateral profound</td>
<td>p.Arg127His/p.Arg127His</td>
<td>Bilateral prosthesis</td>
</tr>
<tr>
<td></td>
<td>II-2</td>
<td>17</td>
<td>16 months</td>
<td>RE mixed moderate and LE severe</td>
<td>WT/WT</td>
<td>RE cochlear implant</td>
</tr>
<tr>
<td></td>
<td>I-1</td>
<td>58</td>
<td>-</td>
<td>RE mixed moderate and LE normal</td>
<td>p.Arg127His/p.Arg127His/WT</td>
<td>RE chronic otitis media</td>
</tr>
<tr>
<td></td>
<td>I-2</td>
<td>50</td>
<td>-</td>
<td>RE mild and mixed moderate LE</td>
<td>WT/WT</td>
<td>LE tympanosclerosis</td>
</tr>
<tr>
<td>2*‡</td>
<td>II-1</td>
<td>20</td>
<td>6 years</td>
<td>Bilateral mixed moderate</td>
<td>p.Arg127His/p.Arg127His/WT</td>
<td>Bilateral prosthesis; LE chronic otitis media; RE tympanoplasty; Bilateral myringotomy and tubes at 4 - 5 yo.</td>
</tr>
<tr>
<td>3</td>
<td>I-1</td>
<td>56</td>
<td>-</td>
<td>Normal audition</td>
<td>WT/WT</td>
<td>-</td>
</tr>
<tr>
<td></td>
<td>I-2</td>
<td>54</td>
<td>-</td>
<td>Normal audition</td>
<td>p.Phe83Leu/WT</td>
<td>-</td>
</tr>
<tr>
<td></td>
<td>I-1</td>
<td>69</td>
<td>-</td>
<td>Normal audition</td>
<td>WT/WT</td>
<td>-</td>
</tr>
<tr>
<td></td>
<td>I-2</td>
<td>64</td>
<td>-</td>
<td>Normal audition</td>
<td>p.Val153Ile/WT</td>
<td>-</td>
</tr>
<tr>
<td></td>
<td>II-1</td>
<td>41</td>
<td>1 year</td>
<td>RE severe and LE profound</td>
<td>p.Val153Ile/WT</td>
<td>-</td>
</tr>
<tr>
<td></td>
<td>I-1</td>
<td>34</td>
<td>-</td>
<td>Normal audition</td>
<td>p.Val37Ile/WT</td>
<td>-</td>
</tr>
<tr>
<td></td>
<td>I-2</td>
<td>35</td>
<td>-</td>
<td>Normal audition</td>
<td>p.Asn206Ser/WT</td>
<td>-</td>
</tr>
<tr>
<td>4*</td>
<td>–</td>
<td>5</td>
<td>Congenital</td>
<td>RE mild and LE moderate</td>
<td>p.Phe83Leu/WT</td>
<td>Bilateral prosthesis</td>
</tr>
<tr>
<td>5</td>
<td>I-1</td>
<td>69</td>
<td>-</td>
<td>Normal audition</td>
<td>WT/WT</td>
<td>-</td>
</tr>
<tr>
<td></td>
<td>I-2</td>
<td>64</td>
<td>-</td>
<td>Normal audition</td>
<td>p.Val153Ile/WT</td>
<td>-</td>
</tr>
<tr>
<td></td>
<td>II-1</td>
<td>41</td>
<td>1 year</td>
<td>RE severe and LE profound</td>
<td>p.Val153Ile/WT</td>
<td>-</td>
</tr>
<tr>
<td></td>
<td>I-1</td>
<td>34</td>
<td>-</td>
<td>Normal audition</td>
<td>p.Val37Ile/WT</td>
<td>-</td>
</tr>
<tr>
<td></td>
<td>I-2</td>
<td>35</td>
<td>-</td>
<td>Normal audition</td>
<td>p.Asn206Ser/WT</td>
<td>-</td>
</tr>
<tr>
<td>6</td>
<td>I-1</td>
<td>3</td>
<td>Congenital</td>
<td>Bilateral moderate</td>
<td>p.Val37Ile/p.Asn206Ser/WT</td>
<td>Bilateral prosthesis</td>
</tr>
<tr>
<td></td>
<td>I-2</td>
<td>42</td>
<td>-</td>
<td>Normal audition</td>
<td>p.Val37Ile/WT</td>
<td>-</td>
</tr>
<tr>
<td></td>
<td>II-1</td>
<td>7</td>
<td>18 months</td>
<td>Bilateral moderate</td>
<td>p.Val37Ile/p.Asn206Ser/WT</td>
<td>Bilateral prosthesis</td>
</tr>
</tbody>
</table>

ABG: air-bone gap; RE: right ear; LE: left ear; WT: wild type
* Consanguineous parents; ‡ Romani ethnicity.

Table 2 – Clinical characteristics of individuals from the SNHL families harbouring the variants p.Phe83Leu, p.Arg127His, p.Val153Ile and p.Asn206Ser. The severity of SNHL considering the PTA of 0.5, 1, 2, 4kHz is presented: normal hearing corresponds to a PTA < 20 dB, mild SNHL to 21 - 40 dB, moderate SNHL to 41 - 70 dB, severe SNHL to 71 - 95 dB and profound SNHL to PTA > 95 dB.
variants: p.Ile20Met, p.Trp24X, p.Ile30Val, p.Val37Ile, p.Phe83Leu, p.Val95Met, p.Arg127His, p.Arg143Gln, p.Val153Ile, p.Arg184Trp and p.Asn206Ser. These variants were selected through the evaluation of a cohort of 147 SNHL patients who had been screened for GJB2 variants; every detected variant other than p.Gly12Valfs*2 (c.35delG) and p.Met34Thr was included in our set of less common variants. Even though each less common variant was present in few patients, together they comprised approximately 12% of the SNHL patients included in this study, denoting the relevance in approaching them. An important tool for the classification of the variants regarding pathogenicity is the assessment of their frequency in a healthy population. To our knowledge, this is the first study to estimate the frequency of these variants in a Portuguese community sample.

Four out of ten less common variants were found in individuals from the G21 cohort: p.Phe83Leu, p.Arg127His, p.Val153Ile and p.Asn206Ser. All four are missense variants and are classified as benign/likely benign,16 benign/likely benign/uncertain significance,17 likely benign,18 and pathogenic,14 respectively. Differences between the allelic frequencies of these variants in the G21 sample and the SNHL group were not statistically significant - a finding which was expected for p.Phe83Leu, p.Arg127His and p.Val153Ile, considering their tendentially benign classifications, but not for p.Asn206Ser, whose pathogenicity would be better described by a higher frequency in the SNHL group compared to the G21 sample. For the p.Arg127His variant, however, a right deviation of the CI of the SNHL group was observed, suggesting a higher frequency in this group. An explanation can be the fact that the SNHL group also included Romani people, while the G21 group included only participants with Portuguese ancestry. In fact, both index cases identified with the p.Arg127His variant were Romani. Similarly, in another Portuguese study consisting of a report on three Portuguese families carrying this variant, two of the families were also Romani. Romani people have Indian ancestry and this variant was found at a high frequency in Indian individuals.20 Also, in a study with Slovak Romani hearing impaired people, p.Arg127His was the most common GJB2 variant, occurring in 19.4% of the chromosomes screened. So, the inclusion of Romani people may explain the trend for a higher allelic frequency in the SNHL group.

A key point to mention is that the highest estimate for the allelic frequencies of p.Arg127His and p.Val153Ile variants in the G21 sample is higher than 1%, allowing for these variants to comply with polymorphism criteria. The role of the p.Arg127His variant in SNHL is contentious as functional studies are inconsistent.25-28 Evidence of its possible non-pathogenic nature relies on its common occurrence in the Indian population and the similar frequencies between hearing and non-hearing subjects found in France. Moreover, the p.Arg127His variant has been detected in normal hearing subjects both at homozygous state and in compound heterozygosity with the p.Gly12Valfs*2 (35delG) mutation. Finally, in vitro expression studies in transfected HeLa cells demonstrated that the mutated p.Val153Ile protein was correctly synthesized and targeted to the plasma membrane and its function was not altered. It is noteworthy that some studies do not rule out the possible role of the p.Val153Ile variant as a modifier of the final phenotype in the presence of other mutations in genes involved in hearing function.29,30

The p.Phe83Leu variant was first described in 1998 and since then, it has been reported by several authors as a polymorphism, as similar frequencies in affected individuals and controls have been observed - likewise in the present study - and, in familial studies, it was not segregating with SNHL. Furthermore, functional evidence supports its non-pathogenic nature.43 In this study, the p.Ans206Ser variant was detected in two index cases and, interestingly, both presented compound heterozygosity with the pathogenic variant p.Val37Ile. Also, both children had bilateral moderate NS-SNHL (PTA in the range of 41 - 70 dB). Compound heterozygous genotypes with p.Ans206Ser have received special attention in previous studies, as they have been associated with less severe audiological characteristics. In fact, the genotype p.Val37Ile/p.Ans206Ser was previously identified in a patient with congenital bilateral mild NS-SNHL (PTA in the range of 41 - 55 dB)45 Furthermore, the genotype p.Gly12Valfs*2/p.Ans206Ser was associated with bilateral moderate SNHL in three patients (PTA in the range of 41 - 70 dB); p.Ans206Ser variant was detected in four patients (PTA in the range of 41 - 55 dB)46 and p.Ans206Ser variant was detected in four patients (PTA in the range of 41 - 55 dB)44 These findings led the authors to speculate that the p.Ans206Ser variant may not severely compromise the gap junctional communication system in the inner ear, which was later corroborated by functional studies - some even revealing that the permeability to anionic fluorescent tracers was maintained, but the permeability to larger molecules was compromised.47,48

The comparison between the allelic frequencies of the G21 group and the GnomAD European sample revealed statistically significant differences for the p.Val153Ile and p.Ans206Ser variants, suggesting that these variants might
be more frequent in the Portuguese population. In fact, our allelic rate for p.Val153lle (0.97%) is higher than the frequencies described for Italy (0.49%)
and France (0.38%).
but lower than that for the Czech Republic (1.92%). Variants p.Phe83Leu and p.Arg127His variant did not show statistically significant differences, even though our G21 allelic frequencies (0.14% for p.Phe83Leu and 0.28% for p.Arg127His) were lower than frequencies described for France (0.28% and 0.66%, respectively).

Another important consideration of our study is the detection of the Arg127His variant in a cis configuration (family 2, Fig.1) since it has never been described in previous research, as far as we know.

The variants p.Trp244Ter, p.Val37lle and p.Arg184Trp, classified as pathogenic,
and the variants p.Val95Met and p.Arg143Gln, classified as pathogenic/likely pathogenic,
were not identified in individuals from the G21 cohort, which is consistent with their classifications. The p.Ile30Val, a variant of uncertain significance,
was not detected either. The differences in allelic frequencies between the G21 and the SNHL groups for the p.Val37lle and the p.Val95Met variants were statistically significant, strengthening the hypothesis of their pathogenic role in SNHL. No statistically significant differences were observed for the other variants.

CONCLUSION

The present study is the first report of the frequency of the less common GJB2 variants in a Portuguese sample. The p.Phe83Leu, p.Arg127His, p.Val153lle and p.Asn206Ser variants were identified in G21 participants, in heterozygosity, with the allelic frequencies of 0.14%, 0.28%, 0.97% and 0.14%, respectively. The p.Trp244Ter, p.Ile30Val, p.Val37lle, p.Val95Met, p.Arg143Gln and p.Arg184Trp variants were not found in the G21 group. Our estimate of the allelic frequencies allows for the p.Arg127His and p.Val153lle variants to comply with polymorphism criteria. Furthermore, our comparison of the allelic frequencies of the variants between G21 and the patients’ group strengthens the hypothesis of p.Val37lle and the p.Val95Met variants having a pathogenic role in NS-SNHL. Moreover, these results raise the hypothesis that p.Val153lle and p.Asn206Ser variants are more frequent in the northern Portuguese population than in the general European population. Estimating the carrier rates of the variants in a healthy population is an important tool for the classification of their pathogenicity. The clarification of the pathogenic role of each variant is of paramount importance in familial genetic counselling.

REFERENCES


AUTHORS CONTRIBUTION

CSR: Data analysis and interpretation; draft of the manuscript.

ACS, HB: Cohort design and management; critical review of the paper.

SF: Design of the work; data interpretation; critical review of the paper.

CPM: Design of the work; data interpretation; critical review of the paper; approval of the final version.

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PROTECTION OF HUMANS AND ANIMALS

The authors declare that the procedures were followed according to the regulations established by the Clinical Research and Ethics Committee and to the 2013 Helsinki Declaration of the World Medical Association.

DATA CONFIDENTIALITY

The authors declare having followed the protocols in use at their working center regarding patients’ data publication.

COMPETING INTERESTS

The authors have declared that no competing interests exist.

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