Frequency of the 35delG Mutation in the GJB2 Gene in Samples of European, Asian, and African Brazilians

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Abstract
Mutations in the GJB2 gene are a major cause of congenital deafness. One specific mutation, the 35delG mutation, has accounted for most of the GJB2 mutations detected in European populations and is one of the most frequent disease mutations identified so far. We evaluated the frequency of the 35delG mutation in DNA samples from Brazilians of European, Asian, and African ancestry. All DNA samples were screened for the 35delG mutation using an allele-specific PCR. This study shows that the frequency of a common mutation (35delG) is significantly lower in non-European populations.

Because of the complexity of the hearing mechanism, deafness can result from a wide variety of genetically determined anomalies as well as from several environmental factors (Simões and Maciel-Guerra 1992). DFNB1 was the first locus implicated in nonsyndromic deafness. The causative GJB2 gene, which encodes the protein connexin 26 (Cx26), leads to hearing impairment. Mutations in the GJB2 gene are involved in roughly 50% of recessively inherited hearing loss in many populations (Kelsell et al. 1997). The most frequent mutation of the GJB2 gene associated with deafness is 35delG, which accounts for up to 70% of the mutations observed in Northern and Southern European populations and in American white populations, with a carrier frequency ranging from 1.3% to 2.8% (Gasparini et al. 2000; Green et al. 1999). In addition, the 35delG mutation also appears to be frequent in Brazil. A study performed in randomly selected newborns from the southern region of Brazil demonstrated a 0.97% carrier rate of the 35delG mutation (Sartorato et al. 2000).

Brazilian families with either familial or sporadic nonsyndromic deafness

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Anthropologists and human geneticists agree that human races do not exist under the traditional concept of a subspecies as a geographically circumscribed population showing sharp genetic differentiation (Templeton 1998). However, many traits and their underlying polymorphic genes show independent patterns of geographic variation. Brazil has a large territory, and because of the admixture of different population groups into diverse parts of the country, there is considerable phylogeographic heterogeneity.

Among the 100 Caucasians there were 2 heterozygotes for the 35delG mutation, giving a carrier frequency of 2% (1 in 50) and an allele frequency $q$ of 0.01. There was only 1 heterozygote among 100 Brazilians of African ancestry (1 in 100; $q = 0.005$), and no carriers of the 35delG mutation were found among the 107 Asian Brazilians.

The data regarding the 35delG carrier frequency in the white population of southeastern Brazil in the present study was similar to that in the overall European population (1 in 51), which clearly indicates that this genetic alteration is a major mutation for autosomal recessive deafness in Caucasians (Gasparini et al. 2000).

Our samples of African Brazilians from Salvador demonstrated an evident influence of European immigration, resulting in a carrier rate of 1 in 100, half of that observed among Caucasians (1 in 50). None of the Asian Brazilians in our sample were positive for the 35delG mutation, confirming that this mutation is absent or exceptionally low in Asian populations.

In conclusion, this study reinforces the notion that the frequency of the common mutation (35delG) of the GJB2 gene decreases significantly outside the white population. Thus strategies for screening for genetic deafness in Brazil must take into account the ethnic heterogeneity of the country.

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