Journal of Molecular Diagnostics. 2015;17(2):155-161
Doi: 10.106/j.jmoldx.2014.11.003

NADf chip, a two-color microarray for simultaneous screening of multigene mutations associated with hearing impairment in North African Mediterranean countries

Chakchouk I[1], Ben Said M[1], Jbeli F[1], Benmarzoug R[1], Loukil S[1], Smeti I[1], Chakroun A[2], Gibriel AA[3], Ghorbel A[2], Hadjkacem H[1], Masmoudi S[4]

1. Processes Laboratory of Molecular and Cellular Screening, Center of Biotechnology of Sfax, University of Sfax, Sfax, Tunisia.
2. Otorhinolaryngology Service, Habib Bourguiba University Hospital Sfax, Sfax, Tunisia.
3. Department of Biochemistry and Molecular Biology, Faculty of Pharmacy, Ahram Canadian University, Giza, Egypt; Department of Biochemistry and Molecular Biology, Faculty of Pharmacy, British University in Egypt, Cairo, Egypt.
4. Processes Laboratory of Molecular and Cellular Screening, Center of Biotechnology of Sfax, University of Sfax, Sfax, Tunisia.

Abstract:

Hearing impairment (HI) is the most frequent sensory defect. Genetic causes are involved in two thirds of prelingual cases. Moreover, the autosomal recessive HI frequency is increased in countries where there is a high rate of consanguinity, such as in North African Mediterranean countries. This population shares several features, including history and social behavior, that promote the spread of founder mutations. HI is characterized by tremendous heterogeneity in both the genetic and clinical aspects. The identification of the causal mutation is important for early diagnosis, clinical follow-up, and genetic counseling. Addressing the extreme genetic heterogeneity of HI using classic molecular methods would be expensive and time-consuming. We designed a cost-effective North African Deafness chip for rapid and simultaneous analysis of 58 mutations using multiplex PCR coupled with dual-color arrayed primer extension. These mutations are found in North African HI patients and are distributed over 31 exons and five introns in 21 distinct genes. Assay specificity was initially optimized using 103 archived DNA samples of known genotypes. Blind validation of HI-unrelated patients revealed mutant alleles in 13 samples, and these mutations were confirmed by Sanger sequencing. The North African Deafness chip allows for simultaneous genotyping of eight different samples, at a minimal cost and in a single day, and is therefore amenable to large-scale molecular screening of HI in North Africa.

Full text: http://dx.doi.org/10.1016/j.jmoldx.2014.11.003