First report of prenatal diagnosis of genetic congenital deafness in a routine prenatal genetic test.

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OBJECTIVE: We aimed to screen for connexin26 gene (GJB2) mutations associated with autosomal recessive non-syndromic neurosensory deafness (NSRD) in a general risk population. METHODS: Screening for the most common connexin26 gene mutations was offered to all women undergoing a second-trimester amniocentesis for fetal karyotype analysis in our Center. After rapid DNA extraction from amniotic fluid, PCR amplification was performed and products analysed to detect mutations of GJB2 gene by a sequencing technique. In particular, we searched for the 20 most frequently reported mutations (out of the approximately 90 so far described) and for which there are commercially available tests. RESULTS: From a total of 4819 consecutive amniotic fluids examined, the following five different heterozygous mutations were detected: 35delG in 80 cases, 167delT in 3 cases and 1 occurrence of each of the following mutations: M34T, 35insG and W77R. From these data, a prevalence of 1 : 56 (1.78%) for the heterozygous condition can be estimated in the Mediterranean general risk population. The striking predominance of 35delG mutation is confirmed. In addition, we detected a homozygous 35delG mutation condition in a foetus of no risk parents. In this case, the early diagnosis permitted prompt application of an acoustic prosthesis allowing for cochlear implantation in due time, with significant improvement of the prognosis. CONCLUSIONS: In a general risk population, a carrier status for congenital deafness can be observed in 1 : 56 (1.78%) amniotic fluids; this is mostly due to the presence of a 35delG mutation of the connexin26 gene. Occasional identification of homozygous states, although rare, allows the best therapeutic approach. Copyright 2003 John Wiley & Sons, Ltd.