GJB2, SLC26A4 and KCNQ4 genes polymorphism associated with Non Syndromic Hearing Loss (NSHL) in the population of West Bengal

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Hearing impairment is one of the most common birth defects and one of every 500 new born has bilateral permanent sensorineural hearing loss (SNHL). About 50% of SNHL involves genetic factors. Till date, 46 genes have been identified as causally related to nonsyndromic SNHL. Inspite of this large genetic heterogeneity, mutations in *GJB2* and *SLC26A4* genes are primarily responsible for the major etiologies of genetic hearing loss. Earlier studies have revealed that the forms and frequencies of mutations in these genes are largely dependent on the ethnic and geographic origins. The present study aims to investigate the genetic cause of deafness in the population of West Bengal by genetic screening of the *SLC26A4* and *GJB2* genes.

Methods
The study included 120 unrelated patients with nonsyndromic SNHL and 120 age and sex-matched healthy control without any history of hearing loss from IPGME & R, Kolkata. All patients had severe to profound, bilateral hearing loss. Direct sequencing was done using a Taq Dye Deoxy Terminator sequencing Kit (PE Applied Biosystems, City, USA) to identify sequence variations.

Results
Results showed that among 120 patients, 55(45.83%) carried either biallelic or monoallelic sequence variations in GJB2 gene. These variants included, M1V, T8M, W24X, V27I, W77X, V84L, E114G, R127H and V153I. Among these variants, W24X was the most common (6.67%) pathogenic mutation and R127H was the most frequent polymorphism found in 29(24.17%) patients. In case of SLC26A4 gene, 17 (14.17%) patients were identified to carry sequence variations, among them I455F was most frequent (8.33%). Surprisingly it was found that none of these patients carried biallelic SLC26A4 mutations.

Conclusion
It was observed that GJB2 gene accounts for a large proportion of congenital non-syndromic sensorineural deafness. Therefore, extended molecular screening of individuals with even mild or moderate prelingual hearing impairment seems indispensible for a proper cochlear transplant programme. The mutation spectrum of hearing loss in case of SLC26A4 gene differs significantly from other South East Asian populations. Hence, further study is needed to identify the genes other than GJB2 that are associated with congenital deafness in our population.