The contribution of genetic variations to the individual susceptibility to noise

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Hearing impairment associated with exposure to noise (noise-induced hearing loss – NIHL) is an important occupational hazard that results from an interaction between environmental and genetic factors. Although the former has been extensively studied, little is currently known about the genetic basis of NIHL.

Genes that may influence the development of NIHL have been grouped in several categories: oxidative stress genes, potassium recycling pathway genes, mitochondrial genes and human monogenic hearing impairment genes. So far, only a limited number of association studies has been performed and only three have led to a possible identification of NIHL susceptibility genes: KCNE1, GSTM1 and CAT.

However, promising results have been obtained for genes associated with potassium recycling pathway in the inner ear. Single Nucleotide Polymorphisms (SNPs) in 10 genes (GJB1, GJB2, GJB3, GJB4, GJB6, KCNE1, KCNQ1, KCNQ4, KCNJ10 and SLC12A2) were investigated whether they influence noise susceptibility. Audiometric data from over 2000 noise-exposed Polish workers was analyzed. Based on ISO 1999:1990 up to 20 % most susceptible and 20 % most resistant individuals were chosen for analysis. In total 99 SNPs were selected and genotyped. The results of this study indicate statistically significant differences of genotype and haplotype frequencies between susceptible and resistant to noise individuals, particularly for GJB2 and GJB6 genes.

To discover the complete picture of NIHL it is necessary to combine the power of molecular genetics with the development of a complex statistical model that includes additional potential risk factors, e.g. smoking, elevated blood pressure or cholesterol levels.

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