EUROPEAN MITOCHONDRIAL HAPLOGROUPS EXHIBIT DIFFERENTIAL RISK OF DEVELOPING PRESBYCUSIS.

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The genetic basis of human presbycusis (age-related hearing loss) is unknown. This common disorder is characterized by inability to understand conversation, particularly in noisy backgrounds. Audiograms of presbycusics show sloping hearing loss, with greatest deficiencies at the highest frequencies, and over time an individual's hearing loss progresses into the lower frequencies that are more important for understanding speech. We investigated the hypothesis that the mitochondrial (mt) genome plays a role in presbycusis. Subjects of European ancestry, all over age 58, were tested for both classical and advanced audiometric measures and then genotyped to determine mt haplogroups. Genotyping of the sample population (N=246) was performed using custom TaqMan assays (real-time PCR) for nine SNPs. One SNP, found in the hypervariable region of the mtDNA, was genotyped using a combination of direct sequencing and restriction fragment length polymorphism (RFLP). The genotyping of all ten SNPs allowed us to classify the subjects into the nine major European Haplogroups. We found that subjects belonging to haplogroup H had better hearing than other Europeans, with the greatest differences observed in the right ear at 3K Hz ($p=0.017$) and 10K-14K Hz ($p=0.016$). The difference at 3K correlates with the common noise notch location, and thus may indicate a difference in susceptibility to noise damage. Distortion product otoacoustic emissions (DPOAE) also indicated better hair cell health in haplogroup H subjects, at higher frequencies and in the right ear (average DPOAE for 4K-6K Hz, $p= 0.010$). These results support the hypothesis that a mitochondrial factor influences susceptibility to the development of presbycusis. Future work will investigate the mt genome for causative mutations linked to the haplogroups.