EXAMINATION OF THE MITOCHONDRIAL GENOME FOR PRESBYCUSIS MARKERS. ***B. Brady*** *, K. Raish, Dr. D. R. Frisina, Dr. D. L. Newman*, International Center for Hearing and Speech Research and Department of Biological Sciences, blb05742rit.edu, dina.newman@rit.edu*

Presbycusis is a disease resulting in hearing loss later in life. People suffering from presbycusis are unable to properly hear many frequencies of sound and have difficulty understanding everyday speech, especially in noisy backgrounds. A stronger mother to child correlation, as opposed to father to child correlation, has been established for heredity of presbycusis. As the mitochondrial (mt) genome is passed on exclusively from the mother, we hypothesize that genetic variation determining susceptibility to presbycusis is found on the mt genome. Mutations occur extremely frequently in the D-loop or hypervariable region (HVR), and this sequence information can be used to determine relationships between individuals or human populations. DNA samples are obtained from the ICHSR lab at NTID after subjects have been throughly phenotyped for hearing ability. We are sequencing the HVRs of these subjects and looking for correlations of phenotypic measures with position on the phylogenetic tree using the Cluster Rank Analysis algorithm. Clustering of good or poor hearing on the tree would indicate a causative mutation on the mt lineage. Future work will investigate the mt genome in these subjects for genes that play a role in hereditary presbycusis.