DETECTION OF POLYMORPHISMS IN THE HUMAN MITOCHONDRIAL GENOME OF SUBJECTS AFFLICTED WITH AGE-RELATED HEARING LOSS. ***R. de Vitry,*** *K. Raish and Dr. D. Newman*[*]**,** *Department of Biology, rpd5770@hotmail.com; dina.newman@rit.edu*

Mutations in many genes have been identified that cause congenital deafness. Environmental factors such as noise exposure or ototoxic drugs can also result in hearing loss. Studies have concluded that genetic differences in the 12S rRNA gene in the mitochondrial genome result in differences in sensitivity to certain antibiotics that lead to hearing loss. Age-related hearing loss, or presbycusis, is known to have a strong genetic component, but the actual genes involved are unknown. Family studies have demonstrated that presbycusis shows a higher correlation between mothers and their children than between fathers and their children. One explanation for this phenomenon would be mitochondrial variation. We have begun examining the mitochondrial genome for genetic variation in presbycusic human subjects, beginning with the 12S rRNA gene. Thus far, we have validated numerous polymorphisms, from 20 presbycusic individuals, in the 12S rRNA and 16S rRNA genes as well as in the hypervariable region of the mitochondrial genome. In the future we intend to search for correlations between genotype at these loci and hearing ability in aged subjects.