Presbycusis, or age-related hearing loss, is a hearing disability due to deterioration within the ear commonly found among old people. Although no genes are yet known to cause presbycusis in humans, many genes are implicated in various forms of congenital deafness. Mutations in gap junction genes GJB2 (connexin 26) and GJB6 (connexin 30) are the most common cause of nonsyndromic sensorineural hearing impairment; therefore, these genes were chosen as candidate genes for possible role in presbycusis. We have sequenced sections of GJB2 and GJB6 from 20 human subjects with presbycusis. Both exons of GJB2 have been completely sequenced, and 1500 bp upstream of the gene has been partially sequenced in the screening set. For GJB6, all three exons have been entirely sequenced, and 1500 bp upstream of the gene has been partly sequenced in the screening set. To date, 12 single nucleotide polymorphisms (SNPs, i.e. individuals differ in their DNA sequence by a single base) have been found in GJB2 and seven SNPs in GJB6. Three SNPs (two in GJB2 and one in GJB6) were analyzed for association with presbycusis in the entire sample set; however, no correlation between phenotype and genotypes was found. Future work will involve completing the sequencing of the screening set for these two genes as well as genotyping additional SNPs for the entire population in order to determine whether or not variation in these genes is associated with presbycusis.