

Conclusions ARHL is a complex disorder, influenced by genetic, environmental/lifestyle and stochastic factors. Despite its high prevalence and the recent progress in hearing research, few attempts to identify genetic determinants of ARHL have been made. In this post-genome era, with high-throughput genotyping platforms now developed, a HapMap project to guide marker selection, the constructive challenge we face is to find strategies that are best suited to unravel the genetic basis of complex traits such as presbycusis. The reverse genetics approach, where phenotypes are refined in relation to genetic marker data (linkage and linkage-disequilibrium analysis), although statistical challenges remain, may lead to the identification of susceptibility components for ARHL. On the other hand, forward genetics may also be a promising approach. Isolating all the genes in the human genome, as well as identifying and cataloguing the functional variants within them in the human population, will allow assessment of the impact of genotype on phenotypic outcome of interest. Additionally, complementary strategies, based on functional genomics technology involving microarrays and proteomics, can be used to develop predictors of disease susceptibility based on biological pathways physiologically relevant to ARHL. Nevertheless, choices in study designs will still be the major factor in the probability of success. Determination of the genetic variants involved in ARHL should provide new insights into the disorder mechanism, which may uncover new leads for pharmaceutical intervention .and could result in the development of screening kits to identify individuals at increased risk