

# Novel genetic loci identified for high-frequency hearing loss

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The genetics responsible for frequency-specific hearing loss have remained elusive until recently, when genetic loci were found that affected high-frequency hearing. Now, a study published today in the open access journal *BMC Genetics* reports, for the first time, genetic loci with effects that are limited to specific portions of the hearing frequency map, particularly those that are most affected in ageing-related hearing loss.

Presbycusis is the loss of hearing for high-pitched sounds that gradually occurs in most individuals as they grow older. Although many [genetic loci](#) have been linked to hearing deficits in humans, many loci that contribute to tonotopy, i.e. the organization of the [auditory system](#) that permits detection and discrimination of sounds of different frequency, remain undiscovered.

A group from the National Institute on [Deafness](#) and Other Communication Disorders (NIDCD) at the National Institutes of Health (NIH), used genome-wide linkage analysis in NIH Swiss mice to successfully identify two quantitative trait loci that affect hearing at [high frequencies](#) – Hfhl1 and Hfhl3. Specifically the effect of the locus Hfhl1 is thought to be confined to hearing frequencies from 25-44kHz of the tonotopic map, whilst Hfhl3 is restricted to the 35-44kHz region.

Lead author James M Keller commented, "Our results support the hypothesis that frequency-specific hearing loss results from variation in gene activity along the cochlear partition and suggest a strategy for

creating a map of genes that influence differences in hearing sensitivity and or vulnerability in restricted portions of the cochlea."

He continued, "The high-frequency hearing loss loci, Hfhl1 and Hfhl3, explain only a portion of the variation in high-frequency [hearing loss](#) observed in these mice. Other loci, and cross talk between genes at different loci, probably account for much of the remainder - in fact we detected a number of additional loci that could account for some of the residual variation. Additional genotyping and analysis could greatly increase our understanding of the genetic architecture of the HFHL phenotype."

**More information:** Genome-wide linkage analyses identify Hfhl1 and Hfhl3 with frequency-specific effects on the hearing spectrum of NIH Swiss mice James M Keller and Konrad Noben-Trauth *BMC Genetics* (in press)

Provided by BioMed Central

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