Casting light on the genetics of age-related hearing loss: Insights from the Canadian Longitudinal Study on Aging



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WORLD REPORT ON HEARING



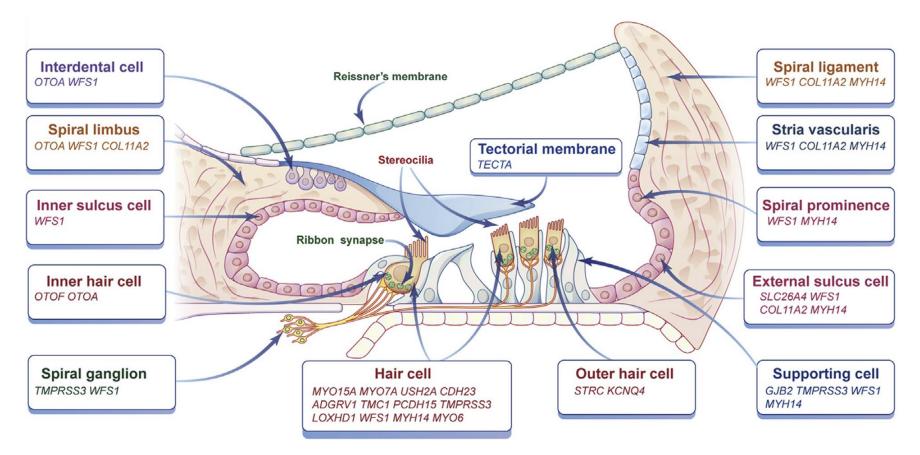
Hearing loss places a large burden on older adults

Most common sensory impairment in older people

~65% of Canadians >70 years experience hearing loss

↑ communication difficulties, social isolation, depression& cognitive decline

Genetics plays an important role in hearing phenotypes



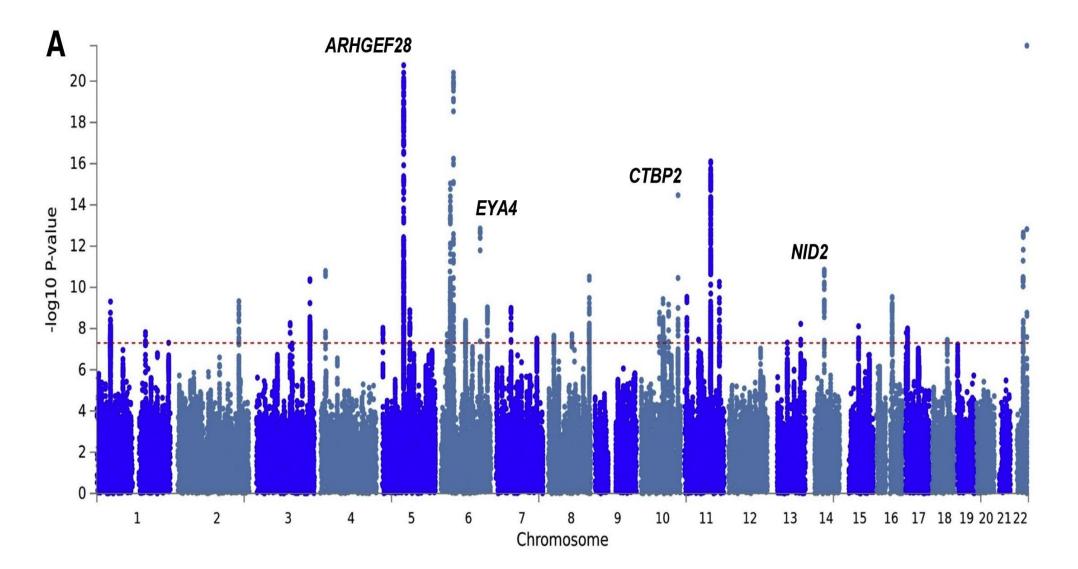
Jiang et al. Mol Ther. 2023;31:934-950.

The majority of hearing loss traits are polygenic

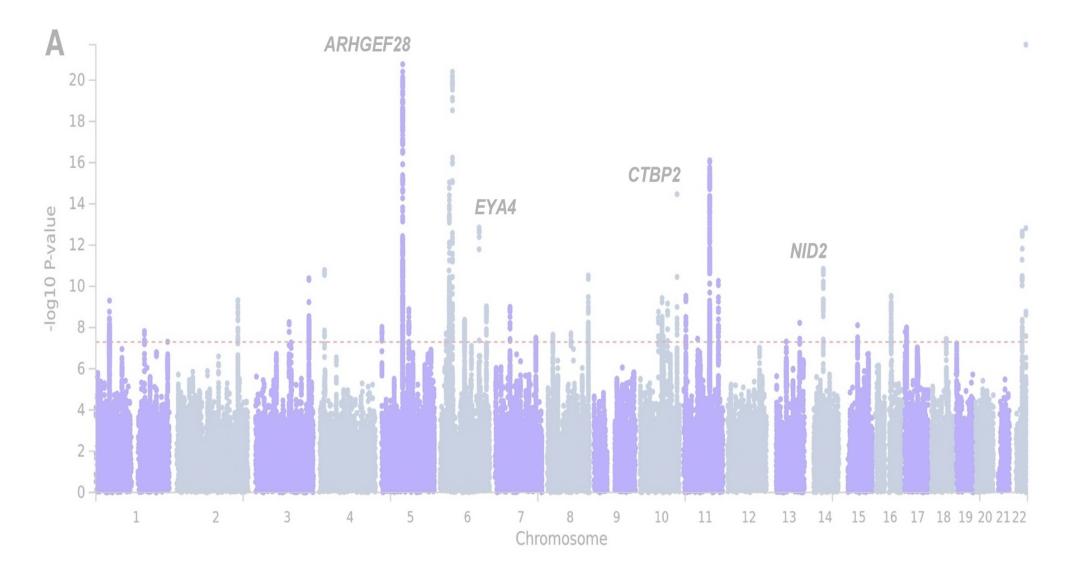
How do we identify genetic variants contributing to hearing loss?

 Large-scale **genome-wide association studies** (GWAS) can identify genetic variants associated with **hearing loss**

GWAS identifies 44 independent associated genomic loci for selfreported adult hearing difficulty in UK Biobank

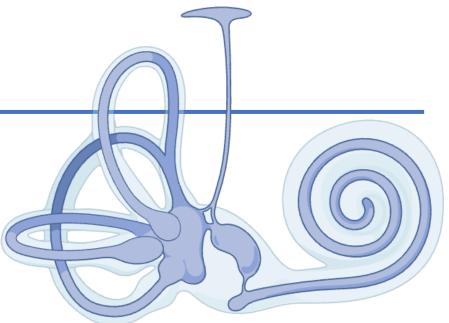


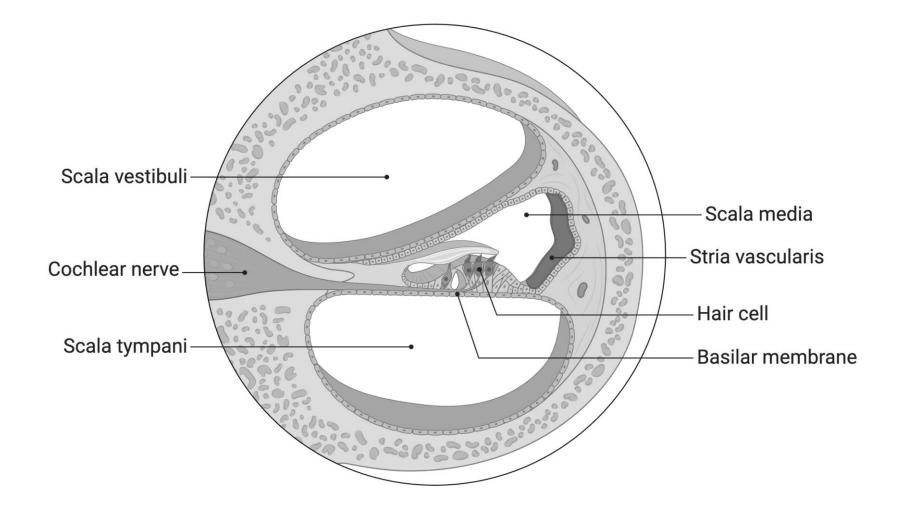
GWAS identifies 44 independent associated genomic loci for selfreported adult hearing difficulty in UK Biobank



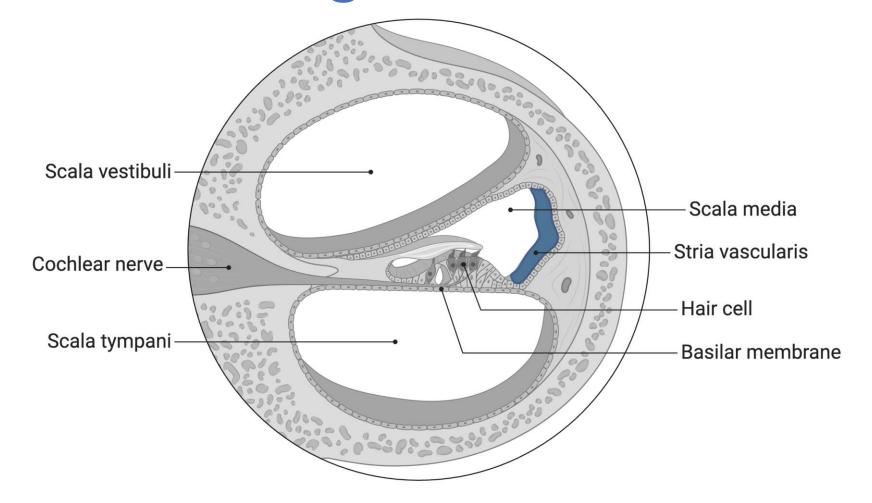
Knowledge gap: No large-scale investigation of genetic variants that contribute to **specific hearing phenotypes**

Diverse pathologies implicated in different hearing phenotypes

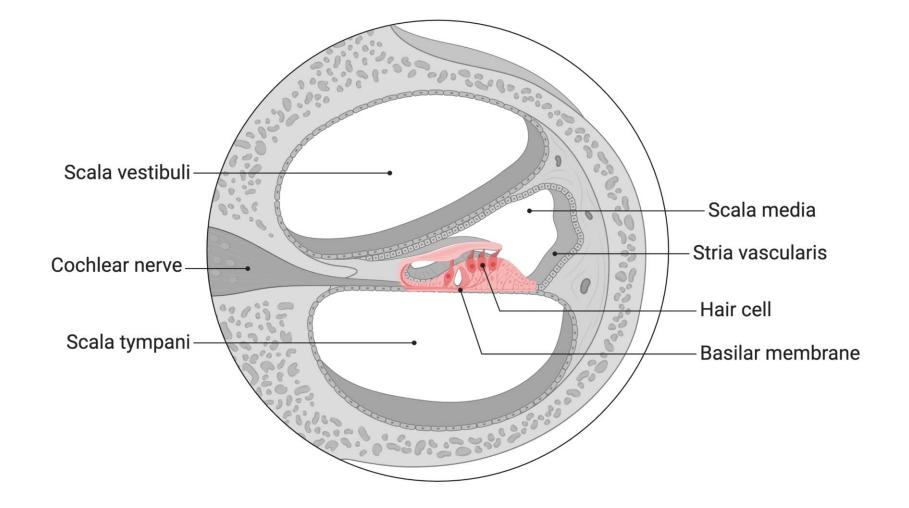




Hearing loss due to age-related sensorineural degeneration

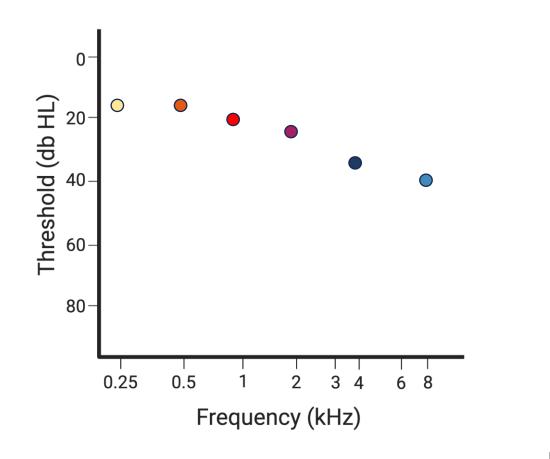


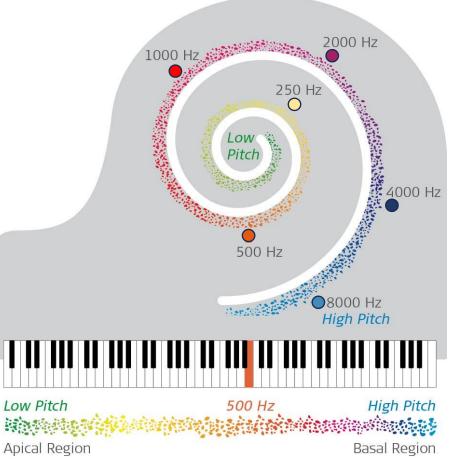
Hearing loss due to noise exposure



Self-report Audiograms provide a tool to more carefully phenotype hearing loss

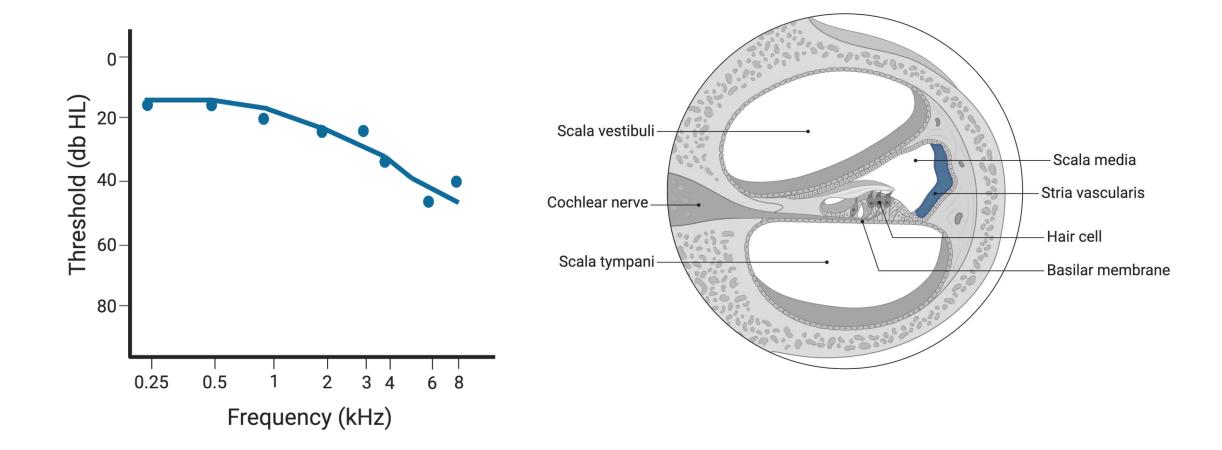
Audiograms measure the softest sounds that individuals can hear at different frequencies



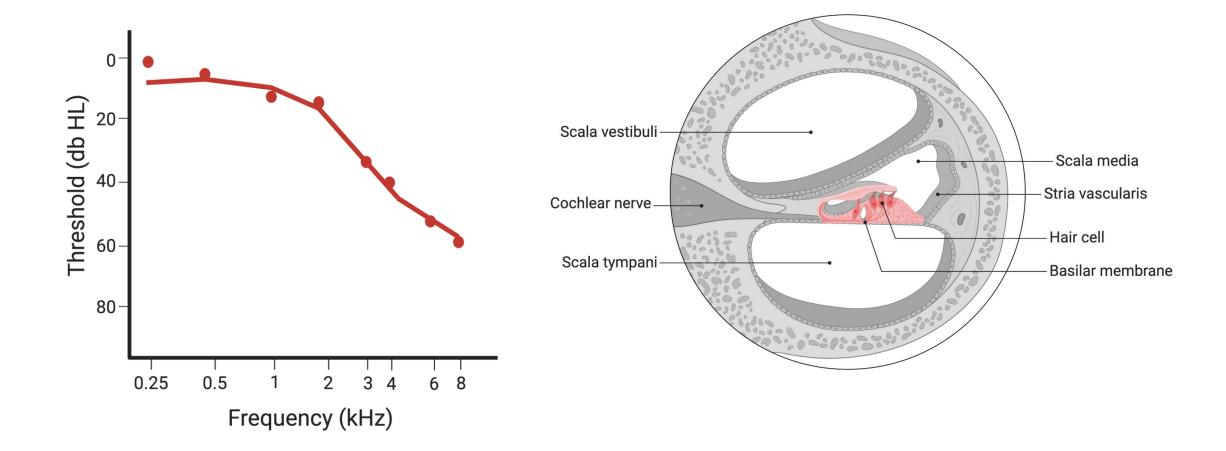


blog.medel.com/technology/hear-the-lowest-sounds-with-a-cochlear-implant/

Hearing loss that occurs due to aging processes exhibits a gradual slope in the audiogram



Hearing loss that occurs due to noise exposure exhibits a steep slope in the audiogram



<u>Challenge</u>: Characterization of hearing loss using audiograms is time consuming



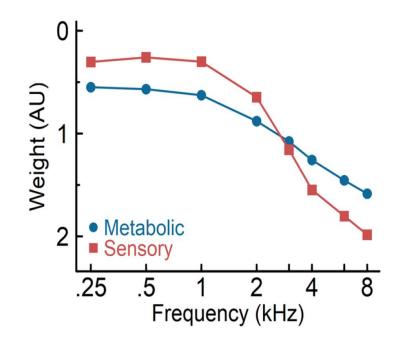
Samah Ahmed PhD student Solution: Use audiograms in combination with automated phenotyping strategies to characterize hearing loss for genomewide association studies

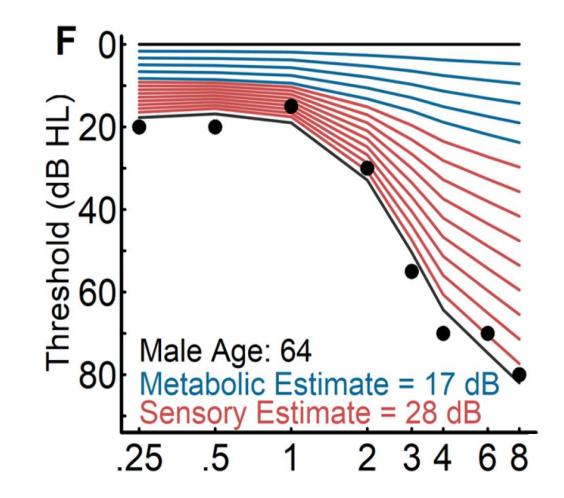
Automated approach used to quantify metabolic and sensory components for each audiogram

Metabolic and Sensory Components of Age-Related Hearing Loss

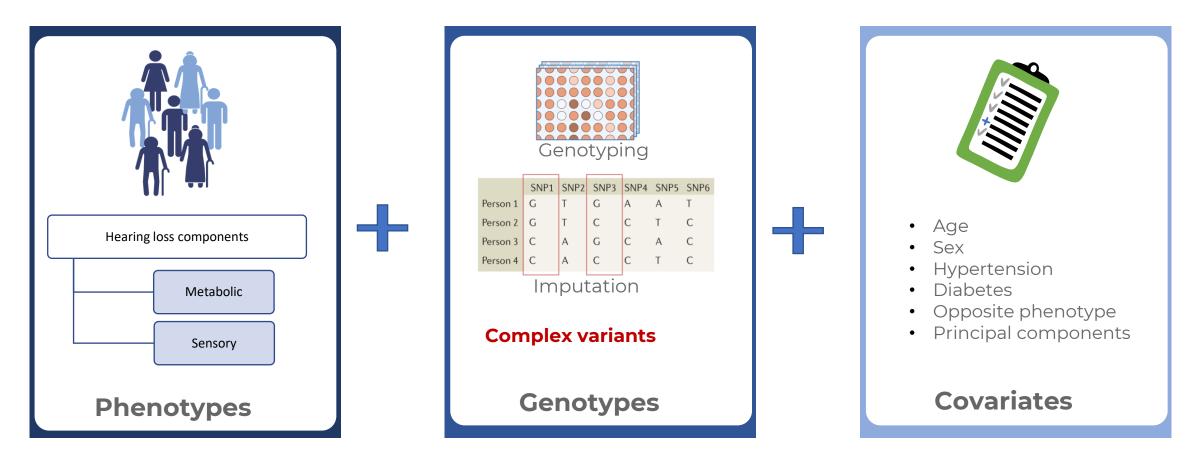
Kenneth I. Vaden Jr.¹⁽⁶⁾, Mark A. Eckert¹⁽⁶⁾, Lois J. Matthews¹, Richard A. Schmiedt¹, and Judy R. Dubno¹⁽⁶⁾

¹ Hearing Research Program, Department of Otolaryngology-Head and Neck Surgery, Medical University of South Carolina, 135 Rutledge Avenue, MSC 550, Charleston, SC 29425-5500, USA





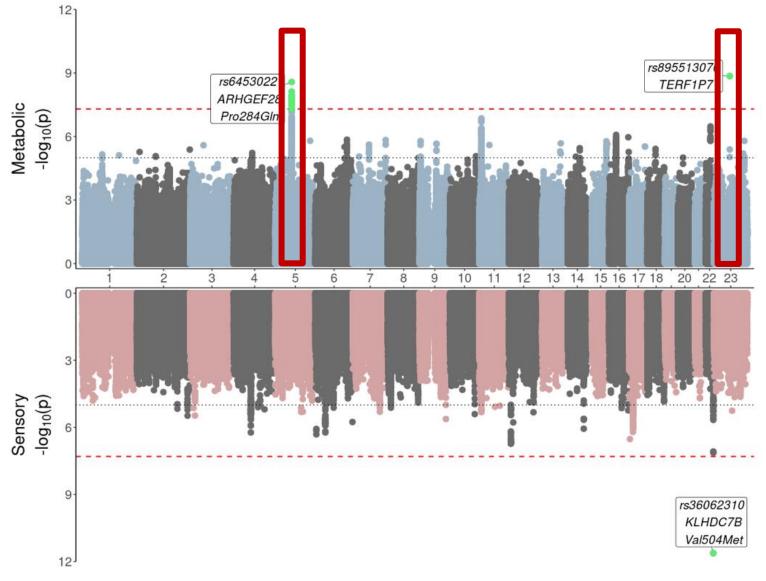
Genome-wide association analyses in the Canadian Longitudinal Study on Aging cohort



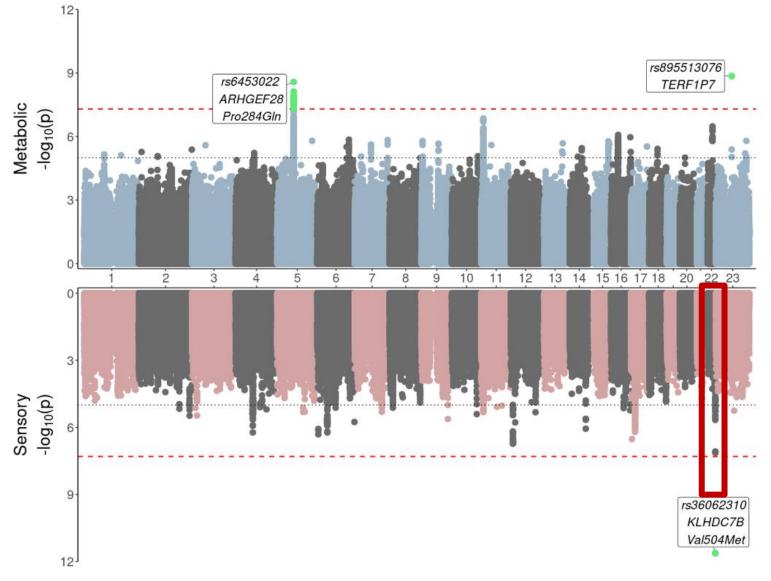
CLSA catalyst grant (Co-PI: Galen Wright): Bioinformatic investigation of previously neglected regions of the genome and their association with age-related hearing loss

Variant-based analyses, including the X chromosome

Unique loci associated with metabolic hearing loss

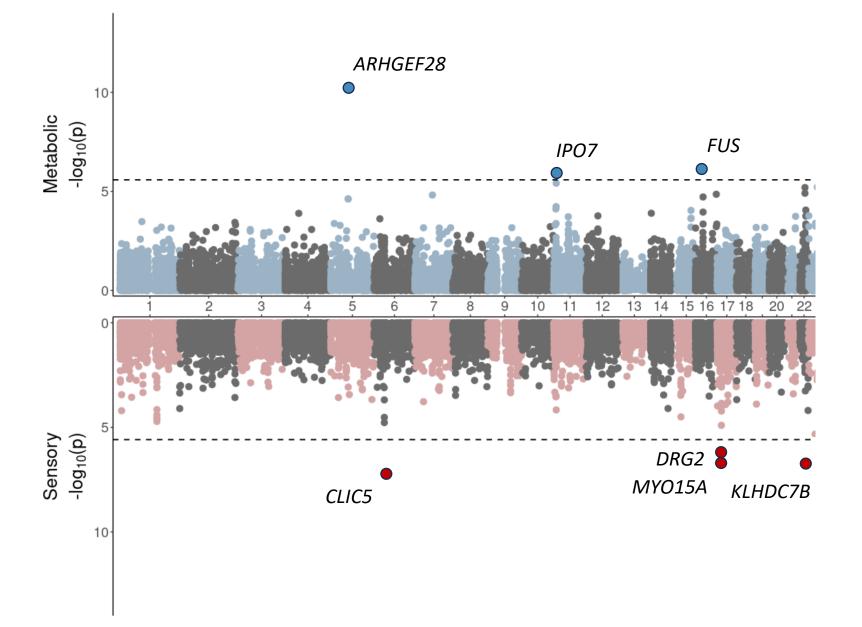


Unique locus associated with sensory hearing loss

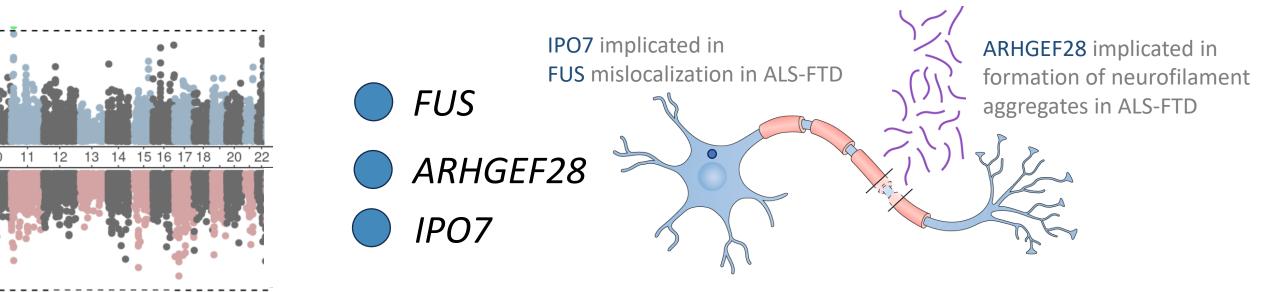


Gene-based analyses

Unique genes associated with metabolic hearing loss



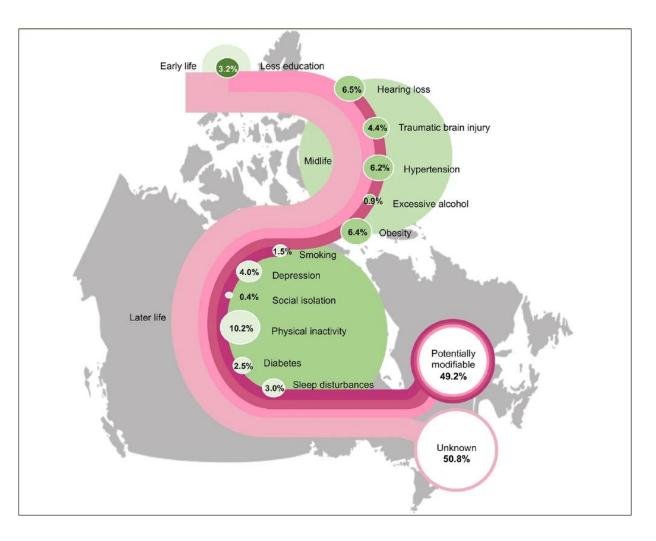
Genes associated with metabolic hearing loss are implicated in ALS frontotemporal dementia



Mead, et al. Nat Rev Drug Discov. 2023;22:185-212 Khalil, et al. Nat Rev Neurol. 2018;14:577-589

Hearing loss is the largest modifiable risk factor for dementia!

Livingston, et al. Lancet. 2020;396:413-446

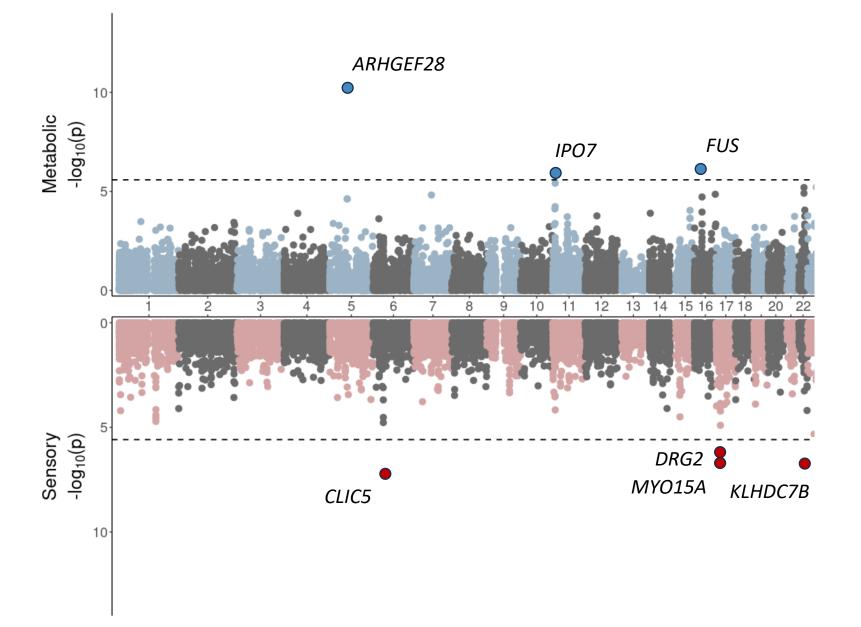


Sun, et al. Potentially Modifiable Dementia Risk Factors in Canada: An Analysis of Canadian Longitudinal Study on Aging with a Multi-Country Comparison. *The Journal of Prevention of Alzheimer's Disease.* 2024

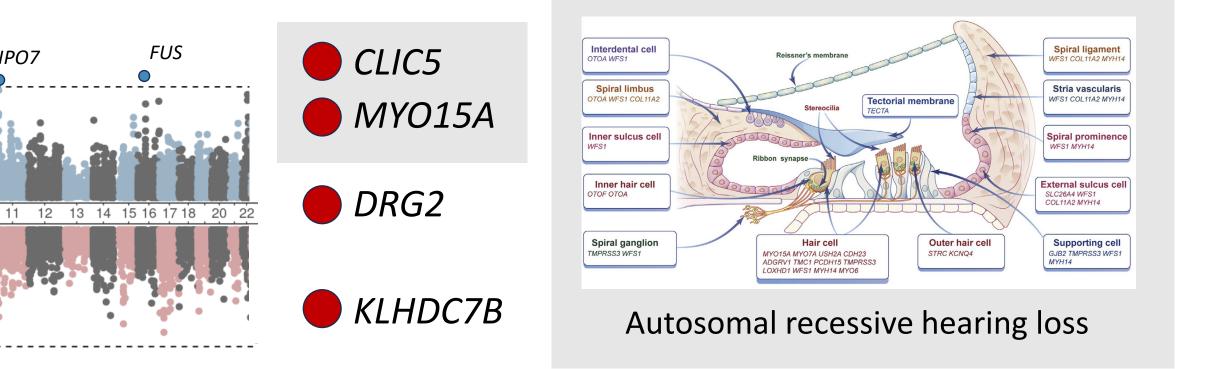


Andy Van Domelen MSc student Investigation of the shared genetic pathways underlying metabolic hearing loss and dementia

Unique genes associated with sensory hearing loss

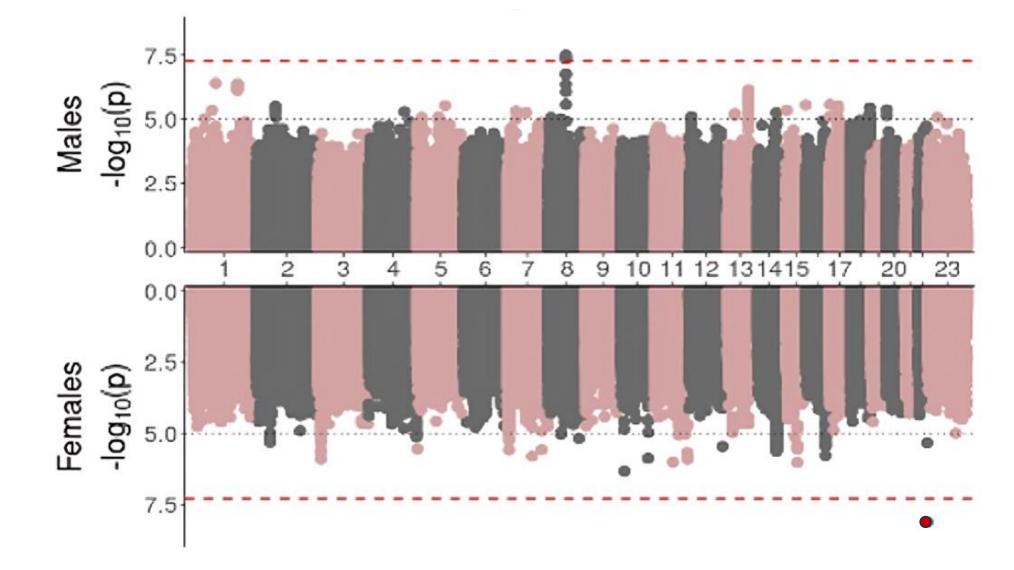


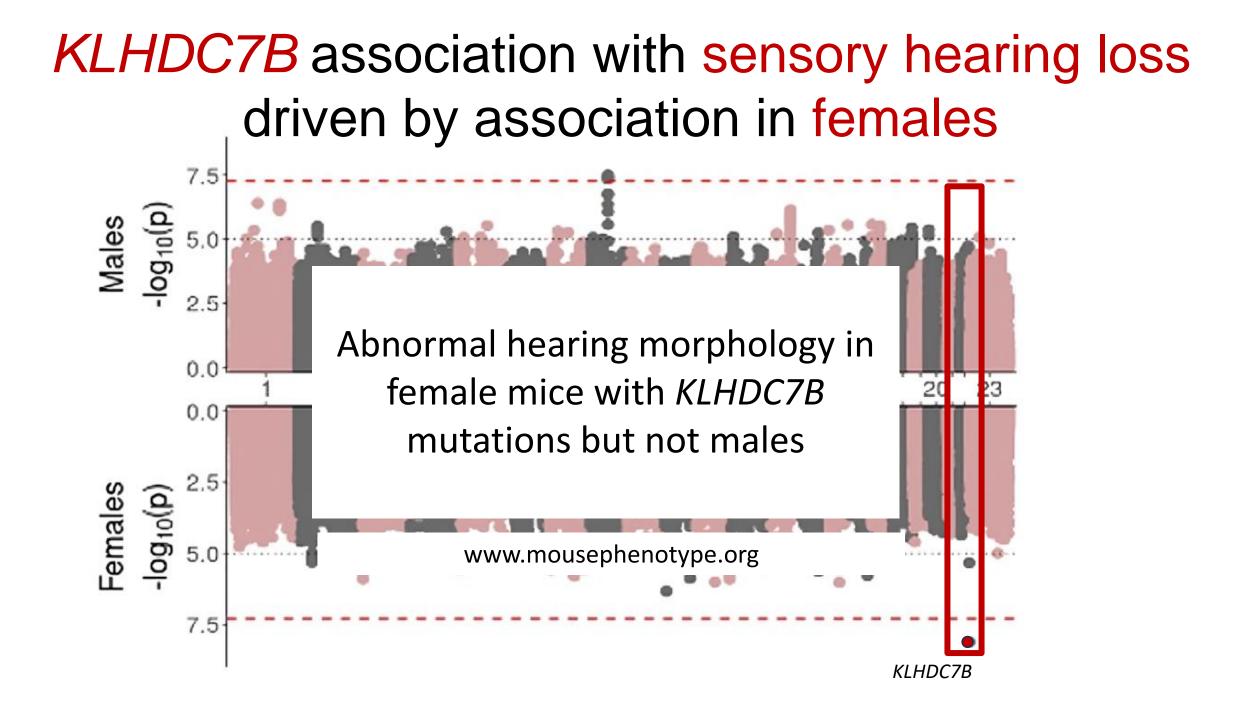
Genes associated with sensory hearing loss cause Mendelian deafness

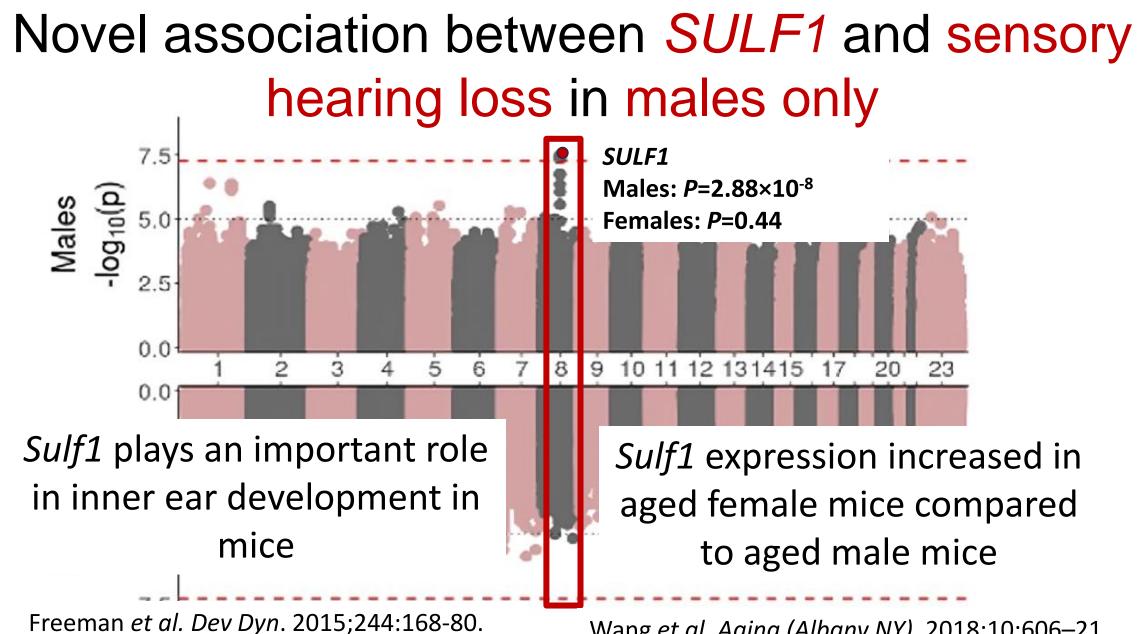


Sex-stratified analyses

Sex-specific associations for sensory hearing loss







Wang et al. Aging (Albany NY). 2018;10:606–21.

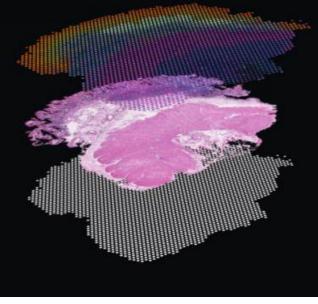
Remaining knowledge gaps: What are the cellular origins and cell specific processes involved in these distinct hearing phenotypes?

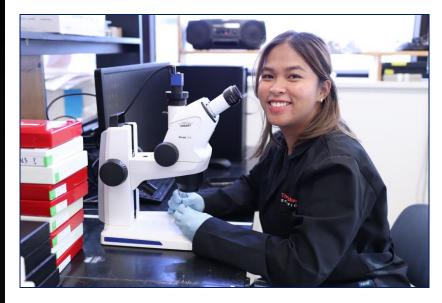
scRNA-seq can provide single cell level insights into the biology of hearing phenotypes



nature methods

Method of the Year 2020: Spatially resolved transcriptomics





Deanne Nixie Miao PhD student

Precision Genomics Suite (Drögemöller, Kowalec, Wright) INNOVATION

Canada Foundation for Innovation

CytAssis

Fondation canadienne pour l'innovation

> **Chromium Xi** Single-cell sequencing Single-cell library prep Gene expression, ATAC, etc.

CytAssist

Spatial information Visium slide set up Includes new HD slides Whole transcriptome

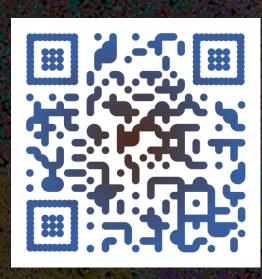
Xenium Analyzer Spatial information In situ/imaging-based platform Subcellular resolution Panel-based (can add custom) Tools for single-cell and spatial genomics

More info available via QR code

Experimental / analysis support

John

Pham



Alana Lamont Confirmed heterogeneous nature of age-related hearing loss

Uncovered specific genetic pathways that are of relevance to distinct hearing loss phenotypes

Revealed striking sex-specific differences

Improved understanding of the genetics underlying sensory and metabolic hearing loss

Opened new avenues for future research aimed at improving early diagnosis and precise treatment of hearing loss in older adults **Drögemöller Lab** Samah Ahmed Deanne Nixie Miao Andy Van Domelen John Pham Alana Lamont Aiya Beken

Mackenzie Wilke Emily Allan Feryal Ladha Avital Kuznecov Mary McAuley

Medical University of South Carolina Judy Dubno Kenneth Vaden

Sunnybrook Research Institute Alain Dabdoub Emilia Luca

University of Manitoba Janilyn Arsenio Darren Leitao Brian Blakley Galen Wright





Recruiting!

Graduate students/postdocs with expertise or an interest in genomics, bioinformatics, and precision medicine