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Goal of identifying nearly all genetic causes of deafness is within reach

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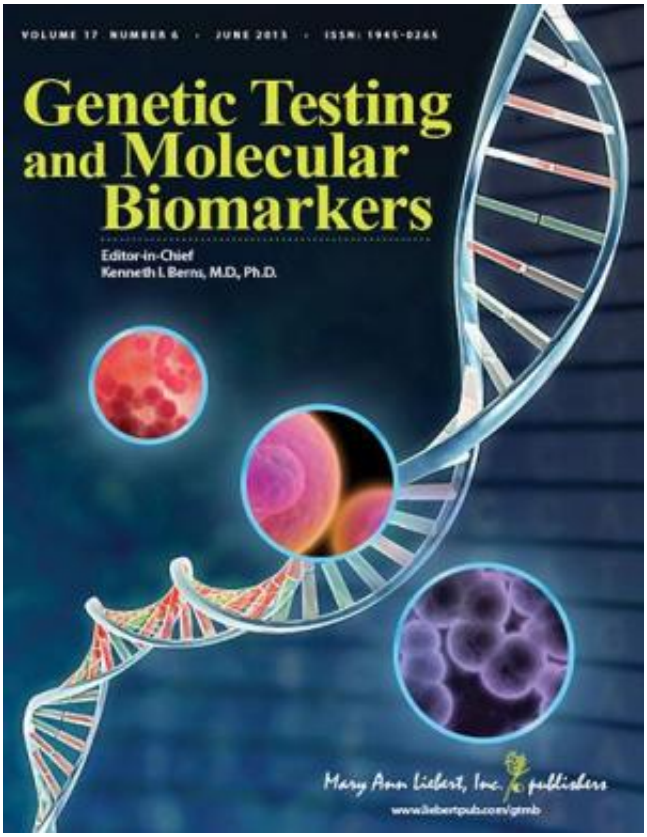

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At least half of all cases of deafness that develop from birth through infancy in developed countries have a genetic basis, as do many cases of later onset progressive hearing loss. To date, at least 1,000 mutations occurring in 64 genes in the human genome have been linked to hearing

loss. Next-generation DNA sequencing technologies are enabling the identification of these deafness-causing genetic variants, as described in a Review article in *Genetic Testing and Molecular Biomarkers*, a peer-reviewed journal from Mary Ann Liebert, Inc., publishers. The article is available on the *Genetic Testing and Molecular Biomarkers* website.

In "Next-Generation Sequencing in Genetic Hearing Loss," Denise Yan and Xue Zhong Liu, University of Miami (Florida), and Mustafa Tekin and Susan Blanton, University of Miami Miller School of Medicine, review the advances in high-throughput, massively parallel DNA sequencing that amplify and repeatedly sequence only specific regions of the human genome in which genes linked to deafness are likely to be found. This strategy, known as "targeted resequencing," allows researchers to find disease-related gene mutations much more quickly than searching through the entire genome. To date at least 1,000 DNA variants at more than 130 sites in the human genome have been identified that can cause hearing loss not associated with other symptoms or syndromes.

"Over the next decade, most of the variant genes responsible for deafness will be identified and such knowledge will lead to the development of practical treatments," conclude the authors.

"Knowledge of the genetic lesions underlying deafness will greatly assist development of targeted therapy," says Kenneth I. Berns, MD, PhD, Editor-in-Chief of *Genetic Testing and Molecular Biomarkers*, and Director of the University of Florida's Genetics Institute, College of Medicine, Gainesville, FL.

Provided by Mary Ann Liebert, Inc

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