

Genomic sequencing enhances findings of hearing loss in NICU

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Expanded genomic sequencing may be an effective adjunct hearing

screening to detect hearing loss among patients in the neonatal intensive care unit (NICU), according to a study published online July 11 in *JAMA Network Open*.

Yunqian Zhu, from National Children's Medical Center in Shanghai, and colleagues examined the association between expanded genomic sequencing combined with hearing screening and detection of hearing loss as well as improvement in the NICU. The analysis included 8,078 newborns.

The researchers found that 52 of 240 newborns (21.7 percent) received a diagnosis of hearing loss. When expanded [genomic sequencing](#) was used, there was a 15.6 percent increase in cases of diagnosed hearing loss that were missed by existing newborn hearing screening. Genetic factors were identified for 39 of 52 patients with hearing loss, with *GJB2* and *SLC26A4* emerging as the most common genes identified. Compared with those without genetic findings, those with genetic findings experienced a more severe degree of hearing loss (21 profound, four severe, seven moderate, and seven mild versus two severe, four moderate, and seven mild). Patients with [genetic factors](#) had more bilateral hearing loss (100 versus 69.2 percent).

"Genetic factors associated with hearing loss need to be identified for the proper clinical management of [hearing loss](#) in patients," the authors write.

More information: Yunqian Zhu et al, Association Between Expanded Genomic Sequencing Combined With Hearing Screening and Detection of Hearing Loss Among Newborns in a Neonatal Intensive Care Unit, *JAMA Network Open* (2022). [DOI: 10.1001/jamanetworkopen.2022.20986](#)

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Screening for Hearing Loss in the Neonatal Intensive Care Setting—Is It Time?, *JAMA Network Open* (2022). DOI: [10.1001/jamanetworkopen.2022.20992](https://doi.org/10.1001/jamanetworkopen.2022.20992)

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