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Quantitative trait loci on chromosome 5 for susceptibility to frequency-specific effects on hearing in DBA/2J mice

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Abstarc :

The DBA/2J strain is a model for early-onset, progressive hearing loss in humans, as confirmed in the present study. DBA/2J mice showed progression of hearing loss to low-frequency sounds from ultrasonic-frequency sounds and profound hearing loss at all frequencies before 7 months of age. It is known that the early-onset hearing loss of DBA/2J mice is caused by affects in the ahl (Cdh23ahl) and ahl8 (Fscn2ahl8) alleles of the cadherin 23 and fascin 2 genes, respectively. Although the strong contributions of the Fscn2ahl8 allele were detected in hearing loss at 8- and 16- kHz stimuli with LOD scores of 5.02 at 8 kHz and 8.84 at 16 kHz, hearing loss effects were also demonstrated for three new quantitative trait loci (QTLs) for the intervals of 50.3–54.5, 64.6–119.9, and 119.9–137.0 Mb, respectively, on chromosome 5, with significant LOD scores of 2.80–3.91 for specific high-frequency hearing loss at 16 kHz by quantitative trait loci linkage mapping using a (DBA/2J × C57BL/6J) F1 × DBA/2J backcross mice. Moreover, we showed that the contribution of Fscn2ahl8 to early-onset hearing loss with 32-kHz stimuli is extremely low and raised the possibility of effects from the Cdh23ahl allele and another dominant quantitative trait locus (loci) for hearing loss at this ultrasonic frequency. Therefore, our results suggested that frequency-specific QTLs control early-onset hearing loss in DBA/2J mice.

Key Word :
ahl locus, chromosome 5, DBA/2J, early-onset hearing loss, quantitative trait loci (QTL)

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