RESEARCH ARTICLE

A new mouse model of Canavan leukodystrophy displays hearing impairment due to central nervous system dysmyelination

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ABSTRACT

Canavan disease is a leukodystrophy caused by mutations in the ASPA gene. This gene encodes the enzyme that converts N-acetylaspartate into acetate and aspartic acid. In Canavan disease, spongiform encephalopathy of the brain causes progressive mental retardation, motor deficit and death. We have isolated a mouse with a novel ethylnitrosourea-induced mutation in Aspa. This mutant, named deaf14, carries a c.516T>A mutation that is predicted to cause a p.Y172X protein truncation. No full-length ASPA protein is produced in deaf14 brain and there is extensive spongy degeneration. Interestingly, we found that deaf14 mice have an attenuated startle in response to loud noise. The first auditory brainstem response peak has normal latency and amplitude but peaks II, III, IV and V have increased latency and decreased amplitude in deaf14 mice. Our work reveals a hitherto unappreciated pathology in a mouse model of Canavan disease, implying that auditory brainstem response testing could be used in diagnosis and to monitor the progression of this disease.

KEY WORDS: Canavan disease, Aspa, Aspartoacylase, Leukodystrophy, ENU mutagenesis, Myelin

INTRODUCTION

Canavan disease is a leukodystrophy (disorder of the brain white matter) (Canavan, 1931). Affected babies seem normal at birth but at about 3 months of age start to display hypotonia, macrocephaly, mental retardation, blindness, seizures and spasticity (Matalon et al., 1995). Patients usually die at about 18 months of age (Toriello et al., 2004). Inheritance is autosomal recessive and disease incidence is very low except for in Ashkenazi Jews, where 1 in 57-65 individuals carry a mutant allele (Feigenbaum et al., 2004; Strom et al., 2004). In one pedigree, seven of 26 G3 mice displayed a low ASR phenotype, a meiotic mapping cross was set up. A founder mouse was crossed to a C57BL6+/+ mouse and the offspring intercrossed. The resulting N 1F1 offspring were screened for low acoustic startle response (ASR). The G1 part of this screen has been described previously (Carpinelli et al., 2013). Control BALB/c mice consistently displayed a maximum startle amplitude above 200 mV (data not shown). Therefore, the criterion used to identify mice of interest was maximum startle amplitude below 200 mV. 25% of G3 mice in each pedigree were expected to display recessive phenotypes for mutations segregating in that pedigree. In one pedigree, seven of 26 G3 mice displayed a low ASR (supplementary material Fig. S1). Breeding tests confirmed that this Aspa mutant mouse, named deaf14, is deaf because auditory signals do not transmit normally through its central nervous system (CNS). Our work reveals a hitherto unappreciated pathology in a mouse model of Canavan disease, suggesting that auditory brainstem response (ABR) testing could be used in the diagnosis of this disease.

RESULTS

**deaf14 mice have a nonsense mutation in Aspa**

We undertook an ENU mutagenesis screen for hearing loss, in which we screened 697 third-generation (G3) mice in 40 pedigrees for low acoustic startle response (ASR). The G1 part of this screen has been described previously (Carpinelli et al., 2013). Control BALB/c mice consistently displayed a maximum startle amplitude above 200 mV (data not shown). Therefore, the criterion used to identify mice of interest was maximum startle amplitude below 200 mV. 25% of G3 mice in each pedigree were expected to display recessive phenotypes for mutations segregating in that pedigree. In one pedigree, seven of 26 G3 mice displayed a low ASR (supplementary material Fig. S1). Breeding tests confirmed that this phenotype was inherited in an autosomal-recessive fashion and the mutant strain was named deaf14.

Genomic DNA from a female deaf14/deaf14 mouse was subjected to exome enrichment and massively parallel DNA sequencing. 89.3% of the consensus coding sequence (CCDS) exome was sequenced at least fourfold and the average depth of sequencing was 58-fold. 144 single-nucleotide variants (SNVs) were recovered, 11 of which were homozygous. In order to determine which SNV was causative of the deaf14 phenotype, a meiotic mapping cross was set up. A BALB/c deaf14/deaf14 founder mouse was crossed to a C57BL6+/+ mouse and the offspring intercrossed. The resulting N1F1 offspring were...
ABR-tested and sacrificed for liver DNA isolation. DNA samples from 15 affected and 15 unaffected mice were genotyped at 660 single-nucleotide polymorphisms (SNPs) spaced at 5 Mb intervals across the genome. Calculation of log of the odds (LOD) scores revealed that the deaf14 mutation was linked to chromosome 11 (Fig. 1A). This chromosome contained four homoyzous SNVs, one in each of the *Aspa*, *Sez6*, *Thoc4* and *Abca9* genes. *Aspa* and *Sez6* were good candidates for carrying the deaf14 causative mutation because *Aspa*−/− mice (Matalon et al., 2000) and *Sez6*−/− mice (Gunnersen et al., 2007) exhibit nervous-system defects. In order to determine whether *Aspa* carried the causative mutation, we undertook finer-resolution meiotic mapping around its location at 73 Mb. 140 N1F1 mice were genotyped for SNPs between 71 and 79 Mb (Fig. 1B). A region between 71 and 75 Mb was homozygous BALB/c in all affected mice and heterozygous or homozygous C57BL/6 in all unaffected mice. This showed that the deaf14 mutation was in this interval. This excluded the *Sez6*, *Thoc4* and *Abca9* SNVs from being causative of hearing loss in deaf14 mice, because they were outside this chromosomal region. The *Aspa* SNV was confirmed by Sanger DNA sequencing to be a c.516T>A mutation that is predicted to cause a p.Y172X protein truncation (Fig. 1C). Western blotting showed that full-length aspartoacylase was detected in brain of *Aspa*+/− and *Aspa*−/−, but not *Aspa*−/−deaf14, mice at 26 days of age (Fig. 1D). A faint band was visible in all lanes at a slightly higher molecular weight than ASPA and was likely to be non-specific. Truncated protein was not detected, suggesting that *Aspa*−/− is a null allele with respect to protein production. 

**deaf14 mice have little acoustic startle response**

In order to determine the average startle response in deaf14 mice, ASR was measured in mice that had been genotyped for the deaf14 mutation. *Deaf14* mice startled to a lesser degree than wild-type littermates in response to white-noise pulses up to 115 dB sound pressure level (SPL) (Fig. 2A,B). This suggests that auditory signals are not reaching the parts of the brain where behavioral response is generated. Alternatively, motor deficit could cause the failure to startle. A low body weight could potentially lead to a spurious low startle response because of reduced accelerometer readings by the SR-LAB equipment. However, deaf14 male and female mice were not significantly smaller than wild-type littermates (Fig. 2C,D). Thus, the low magnitude of startle response detected in these mice was not caused by low body weight.

**deaf14 mice have an abnormal auditory brainstem response**

ABR testing measures specific responses to auditory stimuli extracted from overall electrical activity in the brain. The ABR was measured in deaf14 mice in order to determine whether their failure to startle was due to deafness. In mice, ABR peak I represents the signal from the auditory nerve, peak II the cochlear nucleus, peak III the superior olivary complex, peak IV the lateral lemniscus and peak V the inferior colliculus (Henry, 1979). *Deaf14* mice had normal ABR thresholds in response to mixed frequency (click) stimuli (Fig. 3A). Thresholds to single-frequency stimuli were normal except for at 16 kHz, where the mean mutant threshold was 8 dB SPL above wild type (Fig. 3B). In our experience, a small elevation in ABR threshold is not sufficient to cause a low ASR. Furthermore, the ASR is elicited by mixed-frequency ‘white’ noise, not a 16 kHz pure tone. The shape of the ABR in deaf14 mice was abnormal (Fig. 3C). Although peak I seemed normal, peaks II-V were reduced in size or absent. This is particularly evident at 50 dB SPL in Fig. 3C. ABR analysis revealed that the latency of peak I was normal in deaf14 mice but peaks II, III, IV and V had longer latency than in wild-type littermates (Fig. 3D). This suggests that transition of the auditory signal through the CNS is abnormal in deaf14 mice. Growth function analysis revealed that peak I increased in amplitude with signal intensity at a normal rate in deaf14 mice (Fig. 3E). This indicates that the auditory nerve, which generates peak I, is able to function in the absence of aspartoacylase.

**deaf14 brain displays spongy encephalopathy**

The cochlea was examined in order to determine whether abnormalities in this structure were responsible for the abnormal ABR in deaf14 mice. The deaf14 cochlea proved indistinguishable from wild type, with three rows of outer hair cells and one row of inner hair cells visible in the middle turn (Fig. 4A,B). The neurons and Schwann cells making up the auditory nerve had normal morphology (Fig. 4C,D) and density (Fig. 4E). Next, the brain was examined for pathological abnormalities that could give rise to an abnormal ABR. The deaf14 brain was grossly abnormal, with widely distributed spongiform encephalopathy and extensive vacuolation (Fig. 5). The affected areas from rostral to caudal were layer V of the frontal and anterior parietal cerebral cortex, the dorsolateral aspects of the caudate-putamen, the lateral septal nuclei, the thalamus, the pyramidal cell layer of CA1, CA2 and CA3 regions of the hippocampus, but not the granule cell layer of the dentate gyrus, the mammillary and supramammillary nuclei, anterior pretectal nuclei, suprageniculate thalamic nuclei, medial geniculate nuclei, intermediate layers of the superior colliculi, periaqueductal nuclei, inferior colliculi, ventral cochlear nuclei,
vestibular nuclei, parabrachial nuclei, dorsal tegmental nuclei, and cerebellar white matter. The cerebellar Purkinje cell layer was affected in some areas.

deaf14 mice have impaired motor co-ordination

deaf14 mice are viable to at least 350 days of age and by the age of 280 days developed a Parkinson’s disease-like tremor that was not
present in age-matched wild-type mice (data not shown). In order to determine whether younger mice also had behavioral abnormalities, in particular motor impairment that could lead to a low ASR, behavioral testing was carried out at 9-10 weeks of age. deaf14 mice had a shorter latency to fall off a rotating rod than wild-type mice (Fig. 6A), indicating impaired motor coordination. In the open-field test, deaf14 mice made more moves but covered less distance than wild-type mice (Fig. 6B). This suggested that deaf14 mice have an ataxic gait. deaf14 mice displayed normal behavior in the Y-maze (Fig. 6C), which measures learning, and in the light-dark test (Fig. 6D), which measures anxiety. These results showed that impaired motor coordination in deaf14 mice could be the cause of their low ASR.

DISCUSSION
The first peak of the ABR had normal latency in deaf14 mice and auditory neurons appeared normal on histological examination of the cochlea. However, latencies of peaks II, III, IV and V were increased in deaf14 mice and the brain had extensive spongiform encephalopathy. This indicates that the auditory signal is able to propagate along the auditory nerve but does not propagate normally through the CNS. In shiverer mice, in which dysmyelination is confined to the CNS, the latency of ABR peak I is not significantly increased (Kanzaki et al., 1985), whereas, in quaking viable and trembler mice, with peripheral nervous system (PNS) dysmyelination, ABR peak I latency is increased (Shah and Salamy, 1980; Zhou et al., 1995). The deaf14 ABR phenotype is similar to that of shiverer, supporting the conclusion that the CNS is the site of the defect causing deafness in these mice.

One rat and three mouse models of Canavan disease have been previously described (Kitada et al., 2000; Matalon et al., 2000; Mersmann et al., 2011; Traka et al., 2008) (Table 1). All carry null alleles of Aspa. Aspadeaf14 is also likely to be a null allele, because (1) the single-nucleotide substitution causes a conversion of codon 172 to a stop codon, (2) no truncated protein was detected in p26 brain and (3) the Aspadeaf14/deaf14 mutant phenotype is similar to that of Aspa null mutant mice (Mersmann et al., 2011). The Human Gene Mutation Database (www.hgmd.org) lists 77 mutations in ASPA (Stenson et al., 2014). The Aspadeaf14 mutation lies in the region encoding Y172, which is orthologous to Y173 in human ASPA. A truncating mutation in codon 184 has been observed in a patient with Canavan disease (Zeng et al., 2002), providing further evidence that a nonsense mutation in this region of the gene disrupts function. The phenotype of deaf14 mice is similar to that of the Aspa<sup>tm1Mata</sup> (Traka et al., 2008) and Aspa<sup>lacZ</sup> (Mersmann et al., 2011) mutants but less severe than the Aspa<sup>tm1Mata</sup> (knockout) strain, which displays ataxia and runting of greater severity (Matalon et al., 2000). This could be due the Aspa<sup>tm1Mata</sup> mutation being on a 129S5/SvEvBrd genetic background and the Aspadeaf14 mutation being on a BALB/c background. Alternatively, the difference could be due to the neo insertion in the knockout allele, which might affect expression of neighboring genes.

deaf14 mice were viable to at least 350 days of age and by the age of 280 days developed a Parkinson’s disease-like tremor that was not present in age-matched wild-type mice (data not shown). This indicated that the disease is progressive in mice, as it is in humans. It is of interest that aspartoacylase activity is required for survival past childhood in humans but not in mice. Given the progressive
pathogenesis of the phenotype, the survival of mice to adulthood might be due to the shorter infancy, adolescence and overall lifespan of mice as compared to humans.

Deafness has been observed in individuals with Canavan disease (Toriello et al., 2004), but the only reference to this in the primary literature is of two Canavan disease siblings who were found to have an absent organ of Corti upon autopsy (Ishiyama et al., 2003). Because these individuals were from the same family, this abnormality might have been due to another deafness mutation segregating in this family.

deaf14 is the first animal model of Canavan disease to demonstrate deafness and ABR abnormalities. Furthermore, it is the first to indicate that humans with Canavan disease might have an abnormal ABR. If this is the case, then ABR testing might be useful for diagnosis and to monitor the progression of disease, particularly in children with a mild presentation (Yalcinkaya et al., 2005). In a similar manner, increased latency and decreased amplitude of ABR peaks have been used as criteria in the diagnosis of multiple sclerosis (Peyvandi et al., 2010; Sand et al., 2013). ABR testing is already used in universal newborn hearing screening (Mason and Herrmann, 1998) and is a rapid, inexpensive and non-invasive test. Given that other symptoms of Canavan disease are not detected until 3 months of age, inclusion of abnormal ABR in the diagnostic criteria for Canavan disease could aid in the early diagnosis of affected individuals, particularly those with the mild form.

MATERIALS AND METHODS

Mice
Mice were maintained at the Murdoch Childrens Research Institute (MCRI). Animals were group-housed in IVCD blue line micro-isolator cages (Tecniplast, Buguggiate, VA, Italy) on a 14-hour light/10-hour dark cycle. Animals were fed Barastoc mouse breeder cubes (Ridley AgriProducts, Melbourne, VIC, Australia) and water ad libitum. Mice underwent behavioral testing at the Melbourne Brain Centre (University of Melbourne, Parkville, VIC, Australia). All experiments involving animals were approved by the MCRI animal ethics committee (application number A726) and conformed to the Australian Code of Practice for the Care and Use of Animals for Scientific Purposes, 8th edition, 2013.

Mutagenesis screen
Male BALB/c mice were intraperitoneally injected with 75 mg/kg body weight ethynitrosourea (ENU, Sigma-Aldrich, Castle Hill, NSW, Australia) weekly for 3 weeks as described (Bode, 1984). Treated males were rested for 12 weeks before mating with untreated BALB/c females to produce G1 progeny. G1 mice from different fathers were intercrossed to produce G2 mice, which were brother-sister mated to produce G3 progeny. Under this breeding scheme, 25% of G3 mice in each pedigree will display a phenotype resulting from a recessive mutation inherited from their G1 grandparent. G3 mice were screened for deafness using ASR testing. The deaf14 founder mouse was crossed to BALB/c for five generations to remove other ENU-induced mutations. +/-deaf14 mice were then intercrossed to generate N5F1 mice for phenotypic analysis.

Acoustic startle response
ASR was measured using an SR-LAB system (San Diego Instruments, San Diego, CA). Each mouse was restrained in a Perspex chamber and acclimatized to background white noise of 70 dB SPL for 1 minute. Fifty-six trials were presented in pseudorandom order and separated by intervals of 3-8 seconds. Trials included background noise alone and 40 ms white-noise pulses of 85, 90, 95, 100 and 115 dB SPL. The average ASR for each stimulus was plotted against sound intensity using Prism 6 for Mac OS X software (GraphPad Software Inc., La Jolla, CA).
Auditory brainstem response

Mice were anesthetized by intraperitoneal injection of 100 mg/kg body weight ketamine and 20 mg/kg body weight xylazine, and their eyes were moistened with Lacri-Lube. Body temperature was maintained with a 37°C heat pad inside a custom-made faraday chamber. The faraday chamber was placed inside a sound attenuation cabinet, the Habitest isolation cubicle model H10-24A (Coulbourn Instruments, Whitehall, PA). A magnetic speaker (Tucker Davis Technologies, Alachua, FL) was placed 10 cm from the left pinna and computer-generated clicks and pure-tone stimuli of 4, 8, 16 and 32 kHz were presented with maximum intensities of 100 dB SPL. ABRs were recorded differentially using subdermal needle electrodes (S06666-0, Rochester Electro-Medical, Inc., Lutz, FL). These were positioned at the vertex of the skull (+ve) and on the left cheek (–ve) with a ground on the hind left leg. ABRs were averaged over 512 repetitions of the stimulus. The amplitude and latency of ABR peaks I-V were determined using BioSig software (Tucker Davis Technologies). The ABR threshold was defined as the lowest intensity stimulus that reproducibly elicited an ABR.

Meiotic mapping

A BALB/c<sup>deaf14/deaf14</sup> mouse was crossed to a C57BL/6 +/+ mouse to generate N<sub>1</sub> offspring, which were intercrossed to produce 140 N<sub>1</sub>F<sub>1</sub> mice. All mice were 9- to 10-weeks of age. *P<0.05 versus Aspa<sup>+/+</sup>.
Table 1. Mouse models of Canavan disease

| Name     | Allele | Background | Phenotype | Reference          |
|----------|--------|------------|-----------|--------------------|
| nur7     | Null   | C57BL/6    | Mild      | Traka et al., 2008 |
| lacZ     | Null   | C57BL/6    | Mild      | Mersmann et al., 2011 |
| Tmt1Mata | Null   | 129S5/SvEvBrd | Severe    | Matalon et al., 2000 |
| deaf14   | Null   | BALB/c     | Mild      | This paper         |

offsprings. These mice were ABR-tested at 8 weeks of age and genomic DNA was extracted as described (Laird et al., 1991). Genomic DNA samples of 15 affected and 15 unaffected N1F1 mice were sent to the Australian Genome Research Facility (AGRF, Melbourne, VIC, Australia) where they were genotyped for 660 SNPs spaced at 5-Mb intervals throughout the genome using the iPLEX Gold method (Mendisco et al., 2011), the MassARRAY System (Sequenom, San Diego, CA) and an Autoflex MALDI-TOF mass spectrometer (Bruker, Billerica, MA). Mapmaker software (Lander et al., 1987) was used to calculate LOD scores, with the assumption that the phenotype was recessive. A Manhattan plot was drawn with Prism 6 for Mac OS X software.

Histology

Cochlea

Mice were euthanized by intraperitoneal injection of 400 mg/kg body weight ketamine and 80 mg/kg body weight xylazine. After cessation of breathing, PBS was perfused through each animal via a cannula inserted into the left ventricle for 5 minutes, followed by 10% neutral buffered formalin for 5 minutes. Cochleae were dissected from the temporal bones and post-fixed for 1 hour at room temperature. Cochleae were washed in tris-buffered saline and decalcified in 10% EDTA for 5 days at 4°C with gentle rolling. Cochleae were oriented in 1% agarose in PBS in 10 mm×10 mm×5 mm cryomolds (Sakura Finetek, Torrance, CA) and paraffin-embedded. 2-μm sections were cut parallel to the modiolus using a microtome and stained with hematoxylin and eosin (H&E). Images were captured with a DM1000 compound microscope (Leica Microsystems, North Ryde, Australia) and DFC450 C camera (Leica Microsystems).

Neuron and Schwann cell counting

ImageJ 1.46r software (imagej.nih.gov/ij) was used to determine the area of Rosenthal’s canal and to count cells. Cells with a large pink-stained nucleolus, prominent nucleoli and a white halo were counted as neurons. Cells with a smaller purple-staining nucleolus and without a white halo were counted as Schwann cells.

Behavioral testing

Ten Aspadeaf14/deaf14 mice (six female, four male) and nine BALB/c mice (four female, five male) underwent behavioral testing at the Melbourne Brain Centre (University of Melbourne, Parkville, VIC, Australia). These mice were 9- to 10-weeks old.

Rotarod

Mice were placed on the Rotarod (Ugo Basile, Comerio, Basil, Italy) for four 5-minute trials, with a 1-hour inter-trial interval. During each trial, the Rotarod accelerated from 4 to 40 rpm over 5 minutes. The time taken for the mouse to fall off the Rotarod was measured in seconds.

Open-field locomotor activity

Locomotor behavior was monitored using a TruScan photobeam activity monitoring system (Coulbourn Instruments, Allentown, PA). Animals were placed in the test arena for a 30-minute trial period and activity was detected electronically. The test arena was 40.6 cm wide×40.6 cm high and encased by twin photo-optic arrays (sensor rings). The photo-optic beams were spaced 2.5 cm apart within each array, providing 1.3 cm spatial resolution. Distance travelled and number of moves were calculated using the TruScan software.
Y-maze
Mice were placed in a custom-made Y-maze with three symmetrical 30-cm-long arms. Each of the arms had a distinctive visual cue at the end. The mouse was placed at the end of the home arm, facing away from the center, and was permitted to explore the home and familiar arms (a partition was used to block the novel arm) for 5 minutes. After a 2-hour interval, the mouse was once again placed in the maze, this time with the novel arm accessible. The time spent in each of the three arms was recorded over a 5-minute period.

Light-dark test
The light-dark test was conducted using the TruScan locomotor system. A black Perspex insert (650 lux) was used to create a test field in which half the arena was dark and half was light. Each mouse was placed into the dark side of the chamber and permitted to move freely for 10 minutes. TruScan software was used to calculate the amount of time spent in the light versus the dark zones of the test arena.

Western blotting
Mice were sacrificed by cervical dislocation and brains were snap frozen in liquid nitrogen. Each brain was dissolved in 5 ml lysis buffer containing 150 mM NaCl, 1% NP-40, 50 mM Tris pH 8.0 and protease inhibitors (88665, Pierce Biotechnology Inc., Rockford, IL) using a mortar and pestle on ice. Samples were agitated for 2 hours at 4°C then centrifuged at 13,400 g for 20 minutes. The concentration of protein in collected supernatant was determined using the QuickStart Bradford protein assay according to the manufacturer’s instructions (Bio-Rad Laboratories, Hercules, CA). 50 μg lysate was mixed with 2× reducing buffer (100 mM Tris pH 6.8, 4% SDS, 0.2 mg/ml bromophenol blue, 20% glycerol, 200 mM DTT) and denatured at 95°C for 5 minutes. Samples were electrophoresed on a 10% Bis-Tris gel (Life Technologies Australia Pty Ltd, Mulgrave, VIC, Australia) in 1× MOPS buffer (Life Technologies) then blotted onto Amersham Hybond-P PVDF membrane (GE Healthcare Australia Pty Ltd, Rydalmere, NSW, Australia) at 100 V for 1 hour in transfer buffer (200 mM glycine, 25 mM tris, 20% methanol). Blots were blocked in 5% skim milk powder in PBS for 1 hour then incubated with primary antibody in PBS 0.1% tween for 2 hours. Anti-ASPA antibody (ab154503, Abcam, Cambridge, UK) was used at 1:5000 and anti-actin antibody (ab95347, Abcam) was used at 1:500. Blots were washed for 5-10 minutes in PBS 0.1% tween then incubated in anti-rabbit IgG HRP (Cayman Chemical, Ann Arbor, MI) at 1:10,000 in PBS 0.1% tween for 1 hour. Blots were washed for 5-10 minutes in PBS 0.1% tween then incubated with Amersham ECL western blotting detection reagents (GE Healthcare) for 1 minute. Light emission was detected using an ImageQuant LAS 4000 (GE Healthcare).

Statistics
ASR data was analyzed with one-way ANOVA to determine whether there was a significant difference between Aspa+/+, Aspa+/deaf14 and Aspa+/+deaf14 mice. When a significant difference was found, Aspa+/deaf14 and Aspa+/+deaf14 data were compared to Aspa+/+ data with Dunnett’s multiple comparison test. All other data were analyzed with unpaired t-tests assuming equal variance. All statistical tests were performed using Prism 6 for Mac OS X software.

Acknowledgements
The authors wish to acknowledge Matthew Salzone and Melanie Salzone for technical assistance.

Competing interests
The authors declare no competing financial interests.

Author contributions
M.R.C., B.T.K., A.K.V. and R.A.B. conceived and designed the experiments. All authors performed the experiments. M.R.C. and R.A.B. analyzed the data. M.R.C., A.K.V. and R.A.B. wrote the manuscript.

Funding
The authors acknowledge the financial support of the HEARing CRC, established and supported under the Cooperative Research Centres Program – an Australian Government initiative; the Victorian State Government’s Operational Infrastructure Support Program; Program grant (1016647); project grants, senior research fellowship (A.K.V.), fellowship (B.T.K.) and an Independent Research Institutes Infrastructure Support Scheme Grant (361646) from the Australian National Health and Medical Research Council; a National Collaborative Research Infrastructure Strategy grant to the Australian Phenomics Network; the Garnet Passe and Rodney Williams Memorial Foundation (fellowship to M.R.C.) and the Sylvia and Charles Viertel Foundation (fellowship to B.T.K.).

Supplementary material
Supplementary material available online at http://dmm.biologists.org/lookup/suppl doi:10.1242/dmm.014605/DC1

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