The generation of knock-in mice expressing fluorescently tagged galanin receptors 1 and 2

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Abstract

The neuropeptide galanin has diverse roles in the central and peripheral nervous systems, by activating the G protein-coupled receptors Gal1, Gal2 and the less studied Gal3. There is a wealth of data on expression of Gal1,3 at the mRNA level, but not at the protein level due to the lack of specificity of currently available antibodies. Here we report the generation of knock-in mice expressing Gal1 or Gal2 receptors fluorescently tagged at the C-terminus with, respectively, mCherry or hrGFP (humanized Renilla green fluorescent protein). In dorsal root ganglia (DRG) neurons expressing the highest levels of Gal1-mCherry, localization to the somatic cell membrane was detected by live-cell fluorescence and immunohistochemistry, and that fluorescence decreased upon addition of galanin. In spinal cord, abundant Gal1-mCherry immunoreactive processes were detected in the superficial layers of the dorsal horn, and highly expressing intrinsic neurons of the lamina III/IV border showed both somatic cell membrane localization and outward transport of receptor from the cell body, detected as puncta within cell processes. In brain, high levels of Gal1-mCherry immunofluorescence were detected within thalamus, hypothalamus and amygdala, with a high density of nerve endings in the external zone of the median eminence, and regions with lesser immunoreactivity included the dorsal raphe nucleus. Gal2-hrGFP mRNA was detected in DRG, but live-cell fluorescence was at the limits of detection, drawing attention to both the much lower mRNA expression than to Gal1 in mice and the previously unrecognized potential for translational control by upstream open reading frames (uORFs).

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1. Introduction

Galanin is a 29–30 amino acid neuropeptide that is dramatically induced after peripheral or central nervous system injury, and plays physiological roles in nociception, memory and cognition, anxiety-related behaviours, feeding, reproduction, neurite outgrowth and as a neuronal trophic factor (Cortes et al., 1990; Lang et al., 2015; Villar et al., 1989; Webling et al., 2012). The N-terminal 15 residues of galanin are strictly conserved between species and the N-terminal end is essential for biological activity (Lang et al., 2015; Webling et al., 2012), binding to the three galanin receptor subtypes Gal1, Gal2 and Gal3 (GalR1–3 gene products), which are each class A rhodopsin-like G protein-coupled receptors (GPCRs) that differ in sites of expression, functional coupling and signalling activities (Webling et al., 2012). The phenotypes of mice deficient in each of the galanin receptors have recently been reviewed (Brunner et al., 2014; Lang et al., 2015; Webling et al., 2012). Gal1,3 are also bound by galanin-like peptide (GalLP), but not by the GalP alternatively spliced product alarin (Webling et al., 2012), and recently the neuropeptide spexin/NPQ (neuropeptide Q) was also reported to bind to Gal2 and Gal1, but not to Gal1 (Kim et al., 2014).

In adult rat the expression of Gal1 mRNA is largely restricted to brain, spinal cord and dorsal root ganglia (DRG), whereas Gal2 mRNA is also detected in several peripheral tissues such as large intestine and uterus. In contrast, Gal3 mRNA has a more restricted distribution within brain.

Abbreviations: AOTF, acousto-optic tunable filter; BAC, bacterial artificial chromosome; CDS, coding sequence; CMV, cytomegalovirus; DOR, δ-opioid receptor; DR, dorsal raphe nucleus; DRG, dorsal root ganglia; EGFP, enhanced green fluorescent protein; ER, endoplasmic reticulum; ES cell, embryonic stem cell; FRT sites, FLP recombination target sites; GALP, galanin-like peptide; Gapdh, glyceraldehyde 3-phosphate dehydrogenase; GFP, green fluorescent protein; GPCRs, G protein-coupled receptors; hrGFP, humanized Renilla green fluorescent protein; ISH, in situ hybridization; ISN, lateral spinal nucleus; ME, median eminence; NPY, neuropeptide Y; nt, nucleotides; RNA-seq, next generation RNA sequencing; RT-PCR, reverse transcription polymerase chain reaction; TSA, tyramide signal amplification; UTR, untranslated region; uORFs, upstream open reading frames.

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is rare in spinal cord and rare or not present in DRG, and expression in peripheral tissues is controversial (Burazin et al., 2000; Howard et al., 1997; O'Donnell et al., 1999; Shi et al., 2006; Waters and Krause, 2000; Webling et al., 2012). By in situ hybridization (ISH), Gal1 mRNA is more highly expressed than Gal2 overall in brain (Burazin et al., 2000) and by far the highest levels of Gal2 detected in the nervous system are in the DRG (O'Donnell et al., 1999).

In adult mouse brain the distribution of Gal3 mRNA by ISH is largely similar to rat (Hohmann et al., 2003), whereas the absence of specific [125I]-galanin binding sites in any region of adult Gal1-deficient brain (Jungnickel and Gundlach, 2005) suggests a species-specific, greatly reduced expression of Gal3 mRNA. However, it is still detectable by the more sensitive RT-PCR method in both mouse whole brain (Hobson et al., 2006; Jacoby et al., 2002) and subregions including the amygdala, hippocampus and hypothalamus (Brunner et al., 2014; Hawes et al., 2005; He et al., 2005; Shi et al., 2006; Zhao et al., 2013), as well as in spinal cord (Jacoby et al., 2002), DRG, trigeminal and nodose sensory ganglia (Hobson et al., 2006; Page et al., 2007) and several peripheral tissues (Barreto et al., 2011; Hobson et al., 2006; Jacoby et al., 2002; Kim and Park, 2010; Pang et al., 1998). Less work has been reported on Gal4 mRNA expression, but by RT-PCR it is detected in mouse whole brain and some subregions (Brunner et al., 2014; Hawes et al., 2005; Zhao et al., 2013), nodose ganglion (Page et al., 2007) and several peripheral tissues (Barreto et al., 2011; Brunner et al., 2014; Kim and Park, 2010), but is at the limits of detection in both spinal cord and DRG (Hobson et al., 2006; Jacoby et al., 2002).

Current antibodies against Gal1 or Gal3 are non-selective under standard immunodetection conditions, with identical immunoreactivity patterns in wild-type and receptor knockout mice (Hawes and Picciotto, 2005; Lang et al., 2015; Lu and Bartfai, 2009; F.E.H., P.V. and Picciotto, 2005; unpublished). To delineate the expression of Gal1 and Gal2 at patterns in wild-type and receptor knockout mice (Hawes and Picciotto, 2005; Lang et al., 2015; Lu and Bartfai, 2009; F.E.H., P.V. and Picciotto, 2005; unpublished). To delineate the expression of Gal1 and Gal2 at

2. Materials and methods

2.1. DNA sequence analysis

Planning for knock-in gene characterizations used mouse reference genome Build 37.1, vector hrGFP-FRTneoFRT (see below, Section 2.2) and mCherry cDNA (AY678264) sequences. The RepeatMasker 3.2.9 programme (Smit, Hubley and Green, 1996–2010, http://www.repeatmasker.org) was used to select regions of the GalR1 or GalR2 genes for retrieval target sites or Southern probes that avoided repetitive DNA elements, and homology arm targets that minimized the presence of repetitive DNA elements. Ribosome profiling data (Ingolia et al., 2011) was accessed using the GWIPS-viz. browser (http://gwips.ucc.ie; Michel et al., 2014). The ribosome density peaks for the uORF6 and GalR2 initiation codons were at, respectively. Chr11 nucleotides (nt) 116,281,254–286 and 116,281,474–509 of the GRCh38/mm10 genome assembly (GWIPS-viz. ribo-seq coverage plot; Ingolia et al., 2011; Michel et al., 2014).

2.2. Generation of GalR1-mCherry-[neo−] and GalR2-hrGFP-[neo−] knock-in mice

Mouse genomic clones including either GalR1 or GalR2 genes from the bMQ mouse strain 12957 (129Sv) bacterial artificial chromosome (BAC) library (inserts 89–178 kb; Source: BioScience; Adams et al., 2005) were electroporated into strain EL250 Escherichia coli (Lee et al., 2001). This allowed temperature-inducible, lambda Red-mediated, homologous recombination into the BAC (Copeland et al., 2001; Lee et al., 2001) of PCR products from either vector hrGFP-FRTneoFRT (Balthasar et al., 2004; Parton et al., 2007) or hrGFP derived from Stratagene-Agilent vector phrGFP-1, Zeng et al., 2003; Fig. 2A, middle panel) flanked by GalR2 homologous sequence or vector mCherry-FRTneoFRT (hrGFP exchanged for mCherry; Shaner et al., 2004) flanked by GalR1 homologous sequence. Within the latter PCR product an Asel restriction site was introduced immediately downstream of the 3′ FRT site (Fig. 1A, middle panel), for use in Southern blot digests, and the mCherry/hrGFP heterologous 3′-untranslated region (UTR) has identity to nt 705–1193 of vector pCMV-Script (AF028239) which includes the SV40 early region poly(A) site (Connelly and Manley, 1988; J0 2 4 0 0 , nt 2828–2547). Correct insertion into the BAC was validated by DNA sequencing of cloned PCR products of each junction. All DNA sequencing was by Source BioScience, Oxford.

Retrieval from the recombined BAC clones by gap repair (Copeland et al., 2001; Lee et al., 2001) into PCR-amplified vector pcR-Blunt (Invitrogen) was mediated by either GalR1 target sequences with adjacent introduced rare Swal restriction sites, or GalR2 target sequences with adjacent introduced BstZ17I restriction sites. Recombined plasmid DNAs were transformed into STBL3 E. coli (Invitrogen) and the final targeting constructs were excised with either Swal (GalR1-mCherry-FRTneoFRT; 11.3 kb, with GalR1 homology arms of 4.2 and 3.9 kb) or BstZ17I (GalR2-hrGFP-FRTneoFRT; 8.1 kb, with GalR2 homology arms of 2.3 and 2.7 kb).

Targeting construct inserts were electroporated into embryonic stem (ES) cell line E14.1a (strain 129P2/OlaHsd; Downing and Battey, 1987) and the SV40-neo cassette selected with 250 μg/ml G418 by Geneta (Dept. of Biochemistry, University of Leicester). G418-resistant ES cell clones were screened for correct targeting by PCR (data not shown) and real-time quantitative genomic PCR, and expanded clones were screened by Southern blot analysis (Supplementary Materials and Methods). Selected clones were karyotyped to confirm euploidy, and three ES cell clones of each knock-in gene were injected into 3.5 day old blastocysts from C57BL/6J mice to produce chimeric mice (Geneta). These were crossed to strain 129P2/OlaHsd mice and germline transmission was assessed by PCR genotyping (see below).

2.3. Animals

Mice were housed in a temperature- and humidity-controlled colony on a 14:10 h light–dark cycle, and fed standard chow and water ad libitum. Procedures were carried out in accordance with the U.K. Animals (Scientific Procedures) Act, 1986 and associated guidelines. Ear-punch biopsies were used for PCR genotyping, animals were killed by cervical dislocation to obtain DRG for RT-PCR analysis (Section 2.6), or primary DRG cultures (Section 2.7). Three mice had peripheral transection of the right sciatic nerve prior to perfusion seven days later to obtain ipsilateral (axotomized) lumbar L4 and L5 DRG (Holmes et al., 2008) for immunohistochemistry (Section 2.9).
2.4. PCR genotyping to distinguish knock-in from endogenous receptor alleles

Mouse PCR genotyping for GalR1 used the three primers 5′-AGCGCTTCCACCTGACCCCGCCTTT-3′, 5′-CAGAAACTACTTCTCACCTAGGAGAC-3′ and 5′-TCGAACTCTGGCCGTCAGCCA-3′, which amplified an endogenous GalR1 product of 547 bp and a GalR1-mCherry knock-in product of 348 bp. PCR genotyping for GalR2 used primers 5′-CAGAGGAGACGTCGGCCGGCTATGGCAGAGAGC-3′ and 5′-CTGGCTGCGCAAGAGGATGTCG-3′, which amplified an endogenous GalR2 product of 543 bp and a GalR2-hrGFP knock-in product of 308 bp. PCRs with FastStart Taq DNA polymerase (Roche) and HPLC-purified primers (MWG Eurofins) used cycling conditions of 94 °C for 7 min, 40 cycles of [94 °C, 30 s; 63 °C, 45 s; 72 °C, 45 s], and a final 72 °C incubation for 10 min.

2.5. Deletion of the FRT-flanked SV40-neo cassette from knock-in mice

Homozygous strain C57Bl/6j ACTB:FLPe transgenic mice (Buchholz et al., 1998; Rodriguez et al., 2000) from the Bristol University colony (provided by Dr. Alastair Poole and N.B.) were PCR genotyped using primers 5′-CATAATCTGATACCTTACCTAAGTAAGCAAACTAGCTC-3′ and 5′-CATGCTCTGATCTCCAGGACGTC-3′ under standard cycling conditions (Section 2.4), which amplified the expected 362 bp sequenced product.

Heterozygous GalR1-mCherry-[neo+] knock-in mice were crossed to ACTB:FLPe transgenic mice, and offspring both heterozygous for GalR1-mCherry and genetically mosaic for deletion of the SV40-neo cassette (Δneo) by PCR genotyping (i.e. both Δneo and neo−) were then crossed to strain 129P2/OlaHsd. Offspring were PCR genotyped in separate reactions for GalR1-mCherry heterozygosity (Section 2.4), presence of neo and presence of Δneo. Primers for presence of neo were 5′-CGATACGGTTATCCGGCTACCTA-3′ and 5′-CTCCCTCCTGTGTCCAGTACTC-3′ (630 bp product), and for presence of Δneo were 5′-CTGCTGTCTAATACACGCGATCT-3′ (UTR-F; heterogeneous 3′-UTR sequence) and 5′-CGAGAACCTTACATGGAGATC-3′. PCR genotyping for GalR1-mCherry-[neo−] α-flanked SV40-neo cassette from knock-in mice were deposited at the MRC Frozen Embryo and Sperm Archive and are available from https://www.infrarfrontier.eu/(GalR1-mCherry, EMMA stock ID EM:08192; GalR2-hrGFP, EMMA stock ID EM:08193).

2.6. Real-time quantitative RT-PCR

Lumbar DRG from individual, age-matched 7–8 week old wild-type, GalR1-mCherry or GalR2-hrGFP mice (each n = 5; 1 male, 4 females) were frozen on dry ice and stored at −80 °C, prior to total RNA isolation and reactions containing reverse transcriptase (RT+) or without enzyme (RT− control) (Kerr et al., 2004). Real-time quantitative RT-PCR (reverse transcription polymerase chain reaction) assays and primer and probe sets (Applied Biosystems) for Galα1, Galα2, galanin and endogenous control glyceraldehyde 3-phosphate dehydrogenase (Gapdh) were as reported (Hobson et al., 2006), except for the corrected Galα2 probe sequence 5′-TTCCTCCTATCGAAGCCGGACGAGC-3′ (mGalR2-G6TAQ) used then and herein. Relative mRNA expression levels were derived by the comparative threshold cycle (Ct) method (2−ΔΔCt) normalized to Gapdh (Hobson et al., 2006), with results presented as mean of log transformed data plus SEM. Sample identities were confirmed by standard RT-PCR for Galα1-mCherry and Galα2-hrGFP receptor-fluorescent tag products (data not shown).

2.7. DRG culture and live-cell imaging

DRG cultures from 8 week old mice (Hobson et al., 2013) were generated from individual animals, and neurons were replated onto

Fig. 1. Gene-targeting of GalR1 and genotype analysis. (A) Schematic diagram of endogenous GalR1 (top panel), knock-in GalR1-mCherry-[neo+] (middle panel) and knock-in GalR1-mCherry-[Δneo] (bottom panel) alleles. Indicated relative locations are GalR1 exon 3 with coding sequence (CDS; black filled box) and endogenous 3′-UTR (UTR; NM_000802, not full-length), and restriction sites Ase I (A), BsrGI (Bs) and BamHI (B). The knock-in GalR1-mCherry-[neo+] DNA (middle panel) includes the following elements: the targeting construct (grey horizontal thickened line); the 3′ end of the GalR1 CDS joined in-frame by a 21 nucleotide linker, encoding the flexible linker RDPVPAT (Gibbs et al., 2003; Lobbestael et al., 2010), to mCherry CDS (dashed boxed; mCherry protein sequence AAV52164); a heterologous 3′-UTR including the SV40 early region poly(A) site (grey filled box); downstream FRT sites (right arrowheads) flanking a SV40-neo cassette selection marker with a HSV (herpes simplex virus) thymidine kinase (TK) poly(A) site; an introduced Ase I restriction site (A) immediately downstream of the 3′ FRT site; and the endogenous 3′-UTR (UTR) (see Materials and methods section). Locations of external 5′ and 3′ probes, neo, probe, and hybridizing DNA fragments are also shown (see Supplementary Fig. 1A for more detailed image of [neo−] allele). Note that in the GalR1-mCherry-[Δneo] knock-in allele (bottom panel) the SV40-neo cassette flanked by FRT sites has been removed by FLPe. (B) Southern blot analysis validates correct insertion of the targeting construct. Wild-type (W) and GalR1-mCherry-[Δneo] knock-in line 33 (K) mouse tail DNA were digested and hybridized with: BsrGI and Asel 5′-probe (left panel; W: 7821 bp, K: 6158 bp); Asel and GalR1 3′-external probe (middle panel; W: 12924 bp, K: 5386 bp); and BamHI and neo probe, which only hybridized to positive-control heterozygous GalR1-mCherry-[neo+] ES cell clone 33 (right panel; lane N: 3030 bp). The relative distance travelled by DNA ladder fragments (1 kb Plus, Life Technologies) is indicated in kb on the left of each panel.
The polyclonal anti-hrGFP antibody (Salaka et al., 2009; Zhang et al., 2013; Stratagene-Agilent 240,142) was used as above diluted at 1:500 or 1:5000 on DRG (+ axotomy) and brain, and at 1:500–1:30,000 on spinal cord (+ axotomy), each with wild-type control tissue. 

Gal1-mCherry immunofluorescence was detected by excitation with a 488 nm argon laser and emission detected at 492–538 nm on a Leica TCS SP5-II confocal system attached to a Leica DMi6000 inverted microscope with dry 20× or oil 40× objective lenses. Confocal images were detected as z stacks of x–y images taken at 1 μm (DRG/brain) or 2 μm (cord, unless stated in Fig. 6N and O) intervals with 4× line accumulation, and selected images extracted using Velocity software (Perkin Elmer). Photomicrographs of Gal1-mCherry immunofluorescence in brain at lower magnifications (2.5×××5×) used IM50 Image Manager software (Leica; Holmes et al., 2008) with gain set at 1 (Fig. 7), as constrained by high immunoreactivity in thalamic nuclei, and regions with lesser immunoreactivity used gain set at 2 (Supplementary Fig. 6). Images were adjusted using linear brightness/contrast functions of Adobe Photoshop software. Identification of mouse lumbar spinal cord laminae followed Zelhofeer et al. (2012) and brain regions followed Franklin and Paxinos (1997).

Quantification of Gal1-mCherry-immunoreactive neuron profiles in 16 μm sections of lumbar L4 and L5 DRG from control unaxotomized animals (n = 3) and axotomized animals seven days after axotomy (n = 3, ipsilateral; Section 2.3) was as reported, with counting of 6–10 sections and at least 800 profiles per DRG (Holmes et al., 2008).

2.10. Statistical analysis

Statistical significance of real-time quantitative RT-PCR results (Section 2.6) and changes in somatic cell membrane fluorescence after galanin addition (Section 2.8) were judged by two-tailed Student’s t-test, with P values <0.05 considered significant. P values of <0.05 and <0.01 are indicated by one and two asterisks, respectively.

2.11. Nomenclature

With respect to nomenclature, the genes GalR1 and GalR2 (official symbols, Mouse Genome Informatics Database) encode the gene products Gal1 and Gal2 (http://www.guidetopharmacology.org/GRAC/FamilyDisplayForward?familyId=27), and for convenience transcripts are designated here as Gal1 and Gal2 mRNAs.

3. Results

3.1. Generation of GalR1-mCherry and GalR2-hrGFP knock-in mouse lines

The coding sequences of the fluorescent tags mCherry or hrGFP were cloned in-frame onto the 3′ ends of genomic GalR1 or GalR2 coding sequences by lambda Red-mediated recombineering, and a smaller subcloned fragment of each was electroporated into embryonic stem (ES) cells (see Materials and methods section; Figs. 1A and 2A, middle panels). Screening of ES cell clones by real-time quantitative genomic PCR resulted in 6/97 GalR1-mCherry clones and 10/40 GalR2-hrGFP clones with one correctly targeted, knock-in allele and one endogenous allele of the receptor gene. Correct targeting of selected ES cell clones was confirmed further by Southern blot analysis using 5′ and 3′ probes external to the targeting construct sequence, and internal neo probe (Supplementary Figs. 1 and 2). Three heterozygous knock-in ES cell clones of GalR1-mCherry or GalR2-hrGFP were injected into blastocysts to generate chimeras, from which germline transmission of the knock-in allele was confirmed by PCR genotyping for all three GalR1-mCherry lines (33, 63 and 97) and one GalR2-hrGFP line (32). Expression of knock-in receptor and neo mRNAs in adult DRG was demonstrated by RT-PCR (Supplementary Figs. 3 and 4).

Gene expression can be perturbed by the presence of a nearby neo gene under the control of a strong promoter (Ema et al., 2006; Maguire et al., 2007; ..., 2011).
et al., 2014; Revell et al., 2005), so the downstream SV40-neo cassette selection marker flanked by FRT (FLP recombination target) sites (Figs. 1A and 2A, middle panels) was excised in vivo by crossing with ACTB:FLPe transgenic mice in which FLPe recombinase is under the direction of the human 5′-actin promoter (Buchholz et al., 1998; Rodriguez et al., 2000). Animals heterozygous for GalR1-mCherry, negative for neo, and positive for deletion of the SV40-neo cassette (Δneo) by PCR genotyping were inbred to produce homozygous GalR1-mCherry-Δneo knock-in mice (lines 33 and 97), and the corresponding strategy was used to produce homozygous GalR2-hrGFP-Δneo knock-in mice (see Materials and methods section). DNA sequencing of Δneo PCR genotyping products confirmed that FLPe had precisely excised the SV40-neo cassette resulting in a product with a single remaining recombined FRT site (Figs. 1A and 2A, bottom panels), while Southern blot analysis confirmed both the expected different restriction fragment sizes of knock-in compared to endogenous alleles and the absence of neo-hybridizing sequences in GalR1-mCherry lines 33 (Fig. 1B) and 97 (data not shown), and in the GalR2-hrGFP knock-in (Fig. 2B).

3.2. mRNA expression in DRG from knock-in mice

Expression and correct splicing of transcripts from the knock-in genes was assessed by RT-PCR of adult DRG, the GalR1 and GalR2 genes having respectively three and two exons (Pang et al., 1998; Wang et al., 1997). GalR1-mCherry line 33 expressed the expected spliced product of GalR1 exons 1–3 fused to mCherry coding sequence (637 bp), mCherry to the heterologous 3′-UTR (431 bp), and did not express neo (Supplementary Fig. 3). Similar results were obtained for GalR1-mCherry line 97 (data not shown) which was therefore discontinued. The GalR2-hrGFP knock-in expressed the spliced product of coding sequences from GalR2 exons 1–2 (426 bp), both GalR2 fused to hrGFP (533 bp) and hrGFP to the heterologous 3′-UTR (483 bp), and did not express neo (Supplementary Fig. 4). The identities of knock-in RT-PCR products were confirmed by DNA sequencing, and it is important to note that products that did not span exons were shown to be RT-dependent i.e. derived from mRNA and not genomic DNA contamination (Supplementary Figs. 3 and 4).

Quantitative RT-PCR was used to determine whether expression levels of the knock-in mRNA either differed from wild-type mouse endogenous receptor or led to adaptive regulation of galanin and galanin receptor mRNAs (Hawes et al., 2005; Hohmann et al., 2003). Expression levels in DRG from five individual wild-type, GalR1-mCherry knock-in or GalR2-hrGFP knock-in mice were compared using previously published assays for Gal1, Gal2 and galanin spliced coding sequences (Hobson et al., 2006) that are common to both the wild-type and knock-in animals. We have reported previously that Gal1 mRNA expression in mouse DRG is too low for reliable comparisons (Hobson et al., 2006). Compared to wild-type mice, there were no significant differences in the levels of Gal1 or galanin mRNAs detected in either GalR1-mCherry knock-in (0.856 ± 0.177, P = 0.165 and 0.904 ± 0.072, P = 0.477, respectively) or GalR2-hrGFP knock-in mice (1.261 ± 0.099, P = 0.067 and 1.102 ± 0.195, P = 0.850, respectively). In contrast, levels of Gal2 mRNA varied depending on genotype, with a small but significant increase in GalR1-mCherry knock-ins (1.361 ± 0.076, P = 0.020; *P < 0.05) and a significant decrease in GalR2-hrGFP knock-ins (0.524 ± 0.080, P = 0.004; **P < 0.01).

The quantitative RT-PCR results were also used to compare the relative abundance of different transcripts (Marsh et al., 2012; Pollema-Mays et al., 2013). In wild-type DRG Gal1 and Gal2 mRNAs were amplified to detectable levels (mean threshold cycle, Ct) at respectively 25.37 and 32.58 cycles (each n = 5), the difference of 7.21 cycles was too low for reliable comparisons (Hobson et al., 2006). Compared to wild-type mice, there were no signiﬁcant differences in the levels of Gal1 or galanin mRNAs detected in either GalR1-mCherry knock-in (0.856 ± 0.177, P = 0.165 and 0.904 ± 0.072, P = 0.477, respectively) or GalR2-hrGFP knock-in mice (1.261 ± 0.099, P = 0.067 and 1.102 ± 0.195, P = 0.850, respectively). In contrast, levels of Gal2 mRNA varied depending on genotype, with a small but significant increase in GalR1-mCherry knock-ins (1.361 ± 0.076, P = 0.020; *P < 0.05) and a significant decrease in GalR2-hrGFP knock-ins (0.524 ± 0.080, P = 0.004; **P < 0.01).

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3.3. Live-cell imaging of Gal1-mCherry and Gal2-hrGFP proteins in primary DRG neurons from knock-in mice

In preliminary experiments to detect mCherry or hrGFP fluorescence by confocal microscopy, the PC12 cell line was transiently transfected

Fig. 2. Gene-targeting of GalR2 and genotype analysis. (A) Schematic diagram of endogenous GalR2 (top panel), knock-in GalR2-hrGFP-Δneo+ allele (middle panel) and knock-in GalR2-hrGFP-Δneo (bottom panel) alleles. Indicated relative locations are the two exons of GalR2 (boxed with coding sequences (CDS; black filled boxes)); the downstream terminal exon of ExoC7 (exocyst complex component 7) on the other DNA strand (box with arrowhead); and restriction sites XmnI (X), Bpl (B, grey tone) and BciVI (B). [XmnI sites are shown as used to characterize the Δneo+ allele (Supplementary Fig. 2)]. The knock-in GalR2-hrGFP-Δneo+ DNA (middle panel) includes the targeting construct (grey horizontal thickened line), and the 3′ end of the GalR2 CDS (exon 2) joined to knock-in elements as in Fig. 1A except for exchanging hrGFP (diagonal banded box: hrGFP protein sequence AAK63811) for mCherry. Locations of external 5′ and 3′ probes, neo probe, and hybridizing DNA fragments are also shown (see Supplementary Fig. 2A for more detailed image of Δneo+ allele). Note that in the GalR2-hrGFP-Δneo knock-in allele (bottom panel) the SV40-neo cassette flanked by FRT sites has been removed by FLPe. (B) Southern blot analysis of tail DNA from wild-type (W) and GalR2-hrGFP-Δneo knock-in line 32 (left panel; W: 5366 bp, K: 6664 bp); Bpl and GalR2 3′ external probe (middle panel; W: 5466 bp, K: 6767 bp); and BciVI and neo probe, which only hybridized to positive-control heterozygous GalR2-hrGFP-Δneo+ ES cell clone 32 (right panel; lane N: 1653 bp). DNA ladder as Fig. 1B.
with either human (h) Gal1-mCherry or hGal2-hrGFP cDNAs under the control of the strong CMV (cytomegalovirus) promoter/enhancer (data not shown). Imaging conditions were then established for detecting the much lower fluorescence of each knock-in gene product under the control of the endogenous promoter in primary DRG neurons (Materials and methods section). Cells were detected that expressed a wide range of different levels of Gal1-mCherry fluorescence associated with the somatic cell membrane (Fig. 3A, middle row). However, under these sensitive detection conditions the globular, intracellular autofluorescence from lipofuscin (see Discussion section; Terman and Brunk, 2004) was also readily apparent within the cell bodies of both knock-in and wild-type neurons, which made it impossible to distinguish between specific Gal1-mCherry fluorescence and non-specific lipofuscin autofluorescence within the neuronal cell bodies (Schnell et al., 1999). Growth cones were also examined, as lipofuscin is limited to the neuronal cell body (Gorenstein and Ribak, 1985), but Gal1-mCherry fluorescence was not detected.

Gal2-hrGFP fluorescence was expected to be more difficult to detect than Gal1-mCherry, due to the much lower mRNA expression (see above, Section 3.2). Gal2-hrGFP fluorescence at the somatic cell membrane was near the limits of detection, but was detectable in 3 of 150 DRG neurons analysed (Fig. 3B).

A previous study in transfected CHO cells demonstrated a decrease in fluorescently-tagged Gal1 receptor at the cell membrane following incubation with 100 nM–2 μM galanin (Wirz et al., 2005). To study the effect of galanin on Gal1-mCherry localization in primary DRG neurons, cells with comparatively high somatic cell membrane fluorescence were selected and imaged at 37 °C in a recently available medium.

Fig. 3. Detection of Gal1-mCherry and Gal2-hrGFP fluorescence by live-cell imaging. (A) Primary DRG neurons from GalR1-mCherry knock-in (cells 1–5) or wild-type (wt) mice are shown in brightfield images (top row); corresponding original fluorescent images, each acquired during the same imaging session with identical confocal settings (middle row); and corresponding adjusted images to emphasize somatic cell membrane fluorescence (see Materials and methods section), with cells 4, 5 and wt images treated identically (bottom row). Note that knock-in and wild-type cells have intracellular autofluorescence within the neuronal cell body due to lipofuscin, but only knock-in cells have somatic cell membrane fluorescence. (B) Primary DRG neurons from GalR2-hrGFP knock-in (cells 1–3) or wild-type (wt1–3) mice are shown in brightfield images (top row); corresponding adjusted confocal fluorescent images (second row); corresponding brighter images to emphasize somatic cell membrane fluorescence (third row); and magnified fluorescent images from knock-in cells 1–3 at each of the two relative brightness levels (areas boxed in second and third rows), with arrows indicating the position of somatic cell membrane (bottom row). Knock-in and wild-type cells from the same imaging sessions are shown (1/wt1, 2/wt2 or 3/wt3). Note that expression of Gal2-hrGFP fluorescence at the somatic cell membrane is at the limits of detection, and that both knock-in and wild-type cells have intracellular autofluorescence within the cell body due to lipofuscin. For (A) and (B), each fluorescent image is a single optical section from a z stack, and the scale bar is 5 μm.
with reduced background fluorescence (Materials and methods section). In control Gal1-mCherry neurons there was no significant decrease in somatic cell membrane fluorescence on re-imaging at 20 min, i.e. no apparent photo-bleaching, whereas the somatic cell membrane fluorescence significantly decreased by 35% in neurons re-imaged 20 min after the addition of 1 μM galanin (65.17 ± 5.18%; \( P = 0.0067 \); Fig. 4), demonstrating agonist-induced internalization.

3.4. Immunohistochemical detection of Gal1-mCherry protein in DRG, spinal cord and brain of adult knock-in mice

In order to detect Gal1-mCherry protein expression with higher sensitivity, we used a previously characterized antibody to mCherry (Erbs et al., 2015; Voigt et al., 2012) that specifically detected the protein expressed from CMV-driven hGal1-mCherry cDNA in transiently transfected PC12 cells (data not shown). Gal1-mCherry immunofluorescence in adult lumbar DRG was detected as comparatively high expression in a restricted subset of neurons (Fig. 5A–C, I), with localization to the somatic cell membrane and a punctate distribution within the cytoplasm (Fig. 5E–H, J), whereas in neurons with lesser immunofluorescence localization to the cell surface was often not detected (Fig. 5K–L). In wild-type DRG specific immunofluorescence was not apparent (Fig. 5D). Previously we reported quantitative RT-PCR results showing that Gal1 mRNA decreased by 37% in wild-type mouse DRG seven days after sciatic nerve transection (axotomy; Hobson et al., 2006), whereas here by cell counts of Gal1-mCherry immunoreactive neuronal profiles no apparent difference was detected between 10.9 ± 1.9% in control lumbar L4 and L5 DRG and 9.5 ± 1.1% in ipsilateral L4 and L5 DRG seven days after axotomy (each \( n = 3, \) ± SEM).

Within adult lumbar spinal cord, high levels of Gal1-mCherry immunofluorescence were detected in the superficial layers of the dorsal horn in lamina I–II processes, with lesser levels in the lateral spinal nucleus (LSN) and around the central canal in lamina X (Fig. 6A–C). Little immunofluorescence was detected in the ventral horn (Fig. 6D), and specific immunofluorescence was not detected in wild-type cord (Supplementary Fig. 5). Occasional intrinsic cell bodies were detected in lamina I/II, the lamina III/IV border and lamina X (boxed, Fig. 6E, G and H; Supplementary Fig. 5), the most highly expressing cells showing somatic cell membrane localization and puncta within the cell bodies (Fig. 6I–M). Outward transport of Gal1-mCherry from the cell body was detected as puncta within cell processes of multipolar neurons within the lamina III/IV border area (Fig. 6, with further sections in Supplementary Fig. 5–J). In addition, we show a neuron within the medial part of lamina IV (Zeilhofer et al., 2012) extending a process laterally ~75 μm to end in a terminal containing multiple Gal1-mCherry immunofluorescent puncta, as opposed to another Gal1-mCherry expressing neuron (Fig. 6N–P).

In wild-type brain no specific immunofluorescence was detected, whereas in similar sections of knock-in brain high levels of Gal1-mCherry immunoreactivity were detected within thalamus, hypothalamus and amygdala (Fig. 7A and B). Examples of the most immunoreactive brain regions are shown at higher magnification (5 ×), including the intermediate and ventral parts of the lateral septal nucleus (Fig. 7C and D); a number of thalamic nuclei including the paraventricular thalamic nucleus (Fig. 7E and F); the dorsomedial and ventromedial hypothalamic nuclei and median eminence (Fig. 7G); medial amygdala nuclei (Fig. 7H); and the locus coeruleus (Fig. 7I). Confocal images at higher magnification show localization of Gal1-mCherry to the somatic cell membrane of neurons within the lateral septal nucleus (Fig. 7J), high levels of expression in nerve endings within the external zone of the median eminence (Fig. 7K and L) and numerous nerve fibres in the locus coeruleus area (Fig. 7M).

Examples of brain regions with lesser Gal1-mCherry immunoreactivity (Materials and Methods) are shown in Supplementary Fig. 6. These include the mediocaudal part of the lateral posterior thalamic nucleus; pretectal nucleus; subiculum; medial mammillary nucleus; periaqueductal grey; postero-medial hippocampal amygdala; scattered cells in the ventral most hippocampal pyramidal cell layer; the ventral part of the dorsal raphe nucleus and medial raphe nucleus. The correspondence of the higher magnification images (Fig. 7 and Supplementary Fig. 6) to those at a lower magnification are shown in Supplementary Fig. 7, which also localize Gal1-mCherry immunoreactivity in the anterior hypothalamic area and anterior part of basomedial amygdala (Supplementary Fig. 7).

3.5. Absence of immunohistochemical detection of Gal2-hrGFP protein in adult knock-in mouse tissues

A previously characterized antibody to hrGFP (Sakata et al., 2009; Zhang et al., 2013) specifically detected the protein expressed by CMV-driven hGal2-hrGFP cDNA in transiently transfected PC12 cells (data not shown). However, we could not detect specific Gal2-hrGFP protein expression by immunohistochemistry in adult normal DRG,

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Fig. 4. Live-cell imaging of changes in Gal1-mCherry fluorescence at the somatic cell membrane following the addition of galanin. (A) Primary DRG neuron *1 from GalR1-mCherry knock-in mouse shown (left to right) in brightfield image; corresponding original confocal fluorescent images at time zero and at 20 min after addition of 1 μM galanin (+gal), from which quantifications in (D) were made; and the same fluorescent images adjusted to emphasize cell membrane fluorescence (see Materials and methods section). (B) Corresponding images of primary DRG neuron *2. (C) Magnified fluorescent images of each cell at both timepoints (areas boxed in (A) and (B)), with arrows indicating the position of somatic cell membranes. Each fluorescent image is a single optical section, and the scale bar ((A) and (B)) is 5 μm. (D) Quantification of changes in Gal1-mCherry fluorescence at the somatic cell membrane. Compared to somatic cell membrane fluorescence at time zero, defined as 100%, there was not a significant decrease in somatic cell membrane fluorescence in control neurons re-imaging 20 min later (left; 91.75 ± 3.76%, \( n = 4, \) \( P = 0.1155 \)). In other cells imaged and then re-imaged 20 min after 1 μM galanin addition, there was a significant decrease in somatic cell membrane fluorescence to 65.17 ± 5.18% (right; \( n = 4, \) \( P = 0.0067 \); **, \( P < 0.01 \)). The somatic cell membrane fluorescence at the 20 min timepoint also is significantly decreased in galanin-treated compared to control neurons (\( n = 4, \) \( P = 0.0089 \); **, \( P < 0.01 \)).
spinal cord or brain, or in DRG and spinal cord after sciatic nerve axotomy which markedly induces Gal1 mRNA in rat ventral horn motoneurons (Brumovsky et al., 2006b). Immunofluorescence did not differ from wild-type tissue using a range of primary antibody dilutions (Materials and Methods), and omission of the primary antibody eliminated fluorescence. The inability to detect Gal2-hrGFP is compatible with the low endogenous expression of Gal2/Gal2-hrGFP mRNA (Section 3.2; see Discussion section).

4. Discussion

The goal of this study was to produce knock-in mice expressing fluorescently-tagged Gal1 or Gal2 receptors for live-cell functional imaging and immunohistochemical localization studies. The Gal1-mCherry and Gal2-hrGFP mRNAs were each expressed and correctly spliced in adult DRG from the respective knock-in mice, but the steady-state levels of Gal2-hrGFP mRNA were decreased by ~50% compared to the endogenous Gal2 transcript of wild-type DRG. This may be due to the presence of mRNA stabilization sequence(s) present in the endogenous Gal2 mRNA 3′-UTR that do not occur in the heterologous 3′-UTR of Gal2-hrGFP mRNA (Fig. 2A), such as the stabilization motif CCTnCCTG-′UTR that do not occur in the heterologous 3′-UTR of Gal2-hrGFP mRNA (Section 3.2.6; see Discussion section).

Lipofuscin autofluorescence is known to complicate fluorescent microscopy of brain, spinal cord and DRG (Schnell et al., 1999), for example identifying GFP-GR (glucocorticoid receptor) knock-in expression in brain (Usuku et al., 2005), and will be exaggerated by the very sensitive detection conditions used here (Spitzer et al., 2011; Materials and methods section). Lipofuscin is composed of oxidized protein and lipid degradation residues, that is located within lysosomes but cannot be degraded by lysosomal hydrolases and so accumulates over time within post-mitotic cells such as neurons or cardiac myocytes (Sulzer et al., 2008; Terman and Brunk, 2004). Studies on lipofuscin generally focus on aged animals, but it has been reported in 2 month old rat brain and heart (Ikeda et al., 1985; Nakano et al., 1995; Sulzer et al., 2008), and in 6 week old brain and 1–3 month old spinal cord from mouse (Bandyopadhyay et al., 2014; Constantinides et al., 1986; Usuku et al., 2005). The classical defining characteristic of lipofuscin is broad spectrum autofluorescence (Eldred et al., 1982; Sulzer et al., 2008), as we detected in 500–700 nm emission spectral scans of wild-type DRG neurons (data not shown), which overlaps the commonly used fluorophores such as mCherry and hrGFP with emission peaks of respectively 610 and 506 nm (Shaner et al., 2004; Stratagene-Agilent).

Gal1-mCherry protein was localized within DRG, spinal cord and brain using the higher sensitivity of immunohistochemistry (Figs. 5–7).
Similarly, in the δ-opioid receptor (DOR)-EGFP knock-in mouse fluorescence was often weak and required EGFP-specific antibodies for proper visualization (Erbs et al., 2015), and DOR and Gal1 mRNA are expressed at similar levels in mouse DRG based on next generation RNA sequencing (RNA-Seq; Supplementary Table 1 of Thakur et al., 2014). Cellular localization of a specific GPCR can differ between different regions of the nervous system, for example DOR-EGFP is localized to the somatic cell membrane in DRG but is not readily detected at the cell surface of spinal cord neurons (Ceredig and Massotte, 2014; Erbs et al., 2015; Nathanson, 2008). In highly immunofluorescent Gal1-mCherry neurons, somatic cell membrane localization was detected in DRG (Fig. 5E–H), in spinal cord lamina I/II, lamina III/IV border, medial lamina IV and lamina X (Fig. 6I–K, M and O; Supplementary Fig. 5) and within brain in the lateral septal nucleus and locus coeruleus (Fig. 7J and M). In the live-cell imaging of primary DRG neurons we did not detect Gal1-mCherry fluorescence in growth cones or axons, which could be clearly viewed because lipofuscin autofluorescence is limited to the neuronal cell body (Gorenstein and Ribak, 1985). In contrast, the combination of the immunohistochemistry and the generally restricted expression among intrinsic spinal cord neurons allowed the detection of Gal1-mCherry transport within cell processes as puncta in successive confocal images of neurons within the lamina III/IV border area (Fig. 5J and Supplementary Fig. 5–J) and medial lamina IV (Fig. 6N–P; Zeilhofer et al., 2012).

Previously, we detected Gal1 mRNA in mouse DRG by RT-PCR (Hobson et al., 2006), and here detected Gal1-mCherry immunofluorescence in a restricted subset of neurons (Fig. 5A–C, I) corresponding to 10.9% of lumbar L4 and L5 neuronal profiles. Published data on Gal1 mRNA + neuron profiles is not available for mouse DRG, but in adult

Fig. 6. Detection of Gal1-mCherry immunofluorescence in spinal cord. (A) Low-power photomicrograph (10 × objective) and (B–D) confocal images (20 × objective) of adult GalR1-mCherry knock-in lumbar spinal cord showing high levels of immunofluorescence in the superficial dorsal horn laminae I–II, with lesser levels in the lateral spinal nucleus (LSN, labelled ‘T’) and around the central canal (white asterisk) in lamina X (A–C), whereas little immunofluorescence was detected in the ventral horn (D). (E–H) Higher magnified confocal images (40 × objective) of mid superficial dorsal horn (E); lateral superficial dorsal horn and LSN (labelled ‘T’; F); lamina III/IV border (G); and lamina X (H; central canal, white asterisk); with examples of local cell bodies boxed. (I–L, M) Higher magnification confocal images (40 × objective, zoom 6 ×) of local neurons (boxed in row above) show distinct somatic cell membrane localization in highly fluorescent cells of the superficial dorsal horn (J), lamina III/IV border (J) and lamina X (M; location arrowed in N, mainly different plane), whereas in less fluorescent neurons cell surface localization may (K; arrow; insert merged 3 z-sections) or may not be detected (K–L; L, merged 4 z-sections). Note the multiple Gal1-mCherry immunofluorescent puncta within neuronal processes (J, arrows; additional images in Supplementary Fig. 5A–F), and insert of M shows three main neuronal projections (each double arrows; merged 16 z-sections, 1 μm intervals). (N–P) Confocal images of medial spinal cord including a lamina IV neuron sending a process laterally to another Gal1-mCherry expressing neuron (boxed, N; 40 × objective); as shown at higher magnification to show the neuronal process (O; objective 40 ×, zoom 3 ×; merged 8 z-sections, 1 μm intervals), with insert images showing somatic cell membrane localization of each cell (right cell, merged 3 z-sections); and at further magnification Gal1-mCherry puncta are seen in the terminal process of the lamina IV neuron (arrows, P; objective 40 ×, zoom 8 ×; merged 7 z-sections, 1 μm intervals), with insert images of details from successive z-sections of the terminal process. FD is funiculus dorsalis. Each confocal image is a single optical section from a z stack unless indicated, with (B–D) at same brightness intensity, as are (E–H and N). Scale bars: 150 μm for 20 × objective; 70 μm for 40 × objective; 40 μm for 40 × objective with zoom 3 ×; and 15 μm for 40 × objective with either zoom 6 × or 8 ×.
rat DRG the initial figure was 23% whereas in a more sensitive study using labelled riboprobes the figure was 51% (Kerekes et al., 2003; O'Donnell et al., 1999; Xu et al., 1996). Differences between mouse and rat DRG neuron profiles are not uncommon, for example between 7 and 20% for NPY receptor Y1 mRNA+ or between 39 and 8% for P2X5 immunopositive profiles (Shi et al., 1998; Zeng et al., 2013). In addition, immunohistochemical analysis can give lower numbers of positive neurons compared to ISH, as for example with DOR-EGFP immunostaining compared to DOR mRNA ISH in mouse DRG (Scherrer et al., 2009; Wang et al., 2010). The apparent lack of effect of axotomy on Gal1-mCherry immunoreactive neuronal profiles (9.5% versus control 10.9%), in combination with our previous quantitative RT-PCR results showing a 37% decrease in Gal1 mRNA in wild-type DRG (Hobson et al., 2006), may be explained in part by a threshold for immunoreactive detection. If the mRNA decrease occurs mainly in the highly expressing neurons they would still maintain sufficient expression to be counted as Gal1-mCherry immunopositive. Consistent with this, an ISH study of NPY mRNA expression in rat superior cervical ganglion (SCG) after axotomy detected a 40% decrease in average grain density/neuron, but the number of NPY mRNA+ neurons was unchanged (Kroesen et al., 1997).

In DRG the potential sources of galanin to bind to somatic cell membrane Gal1 are either via fenestrated capillaries that allow access into the neuronal extracellular space (Hanani, 2005) or locally produced ligand. Basal expression of galanin mRNA and protein in DRG are low but increase dramatically after axotomy (Villar et al., 1989; Zhang et al., 1998; Zhang and Nimmerjahn, 2002).
et al., 1995a), when it is abundant in the Golgi region and also present stored in large dense-core vesicles within the cell body (Zhang et al., 1995a). Somatic eoxytosis of galanin has yet to be studied, though it has been demonstrated for substance P (SP) and calcitonin gene-related peptide (CGRP) (Liu et al., 2011; Trueba and De-Miguel, 2012) and references therein), and in addition to post-axotomy would also be relevant following galanin induction in several other neuropathic pain models (Lang et al., 2015) and during nerve regeneration following nerve crush injury (Villar et al., 1989).

In mouse spinal cord expression of Gal1 mRNA has previously been detected by northern blot and RT-PCR (Jacoby et al., 2002; Wang et al., 1997), and by ISH was reported as enriched in the dorsal horn (Table 1 of Guo et al., 2012). We detected dense Gal1-mCherry immunofluorescence in the superficial dorsal horn laminae I–II with lesser levels in the lateral spinal nucleus and lamina X, similar to previous rat Gal1 mRNA ISH studies (Brunovsky et al., 2006b; O’Donnell et al., 1999). It will be of interest to determine the expression of other neurochemical markers within intrinsic neurons highly expressing Gal1-mCherry. For example, the potential relationship of the multipolar neurons of the lamina III/IV border (Fig. 6G and J; Supplementary Fig. 5) to the occasional multipolar neurons of similar location that express galanin, NPY receptor Y1-R or somatostatin receptor Sstr2 (Brunovsky et al., 2006a; Melander et al., 1986; Shi et al., 2014), and the relationship of neurons lateral to the central canal and potentially interacting medial lamina IV neurons (Fig. 6M–P) to galanin or Y1R expressing cells (Brunovsky et al., 2006a; Ch’ng et al., 1985; Melander et al., 1986).

The heterogeneous distribution of Gal1 mRNA in mouse forebrain has been determined by ISH (Hohmann et al., 2003) and was highly similar to [^{125}I]-galanin binding sites, which were not detected in mice deficient for Gal1 (Jungnickel and Gundlach, 2005). The examples of brain regions shown as the most Gal1-mCherry immunoreactive (Fig. 7 and Supplementary Fig. 7) correspond, with three exceptions, to areas expressing Gal1 mRNA which on an intensity scale of + to +++++ (from weak to very dense) were in the range of ++ to +++++ (Hohmann et al., 2003). The ISH study did not extend caudally to the locus coeruleus and posterodorsal tegmental nucleus (Fig. 7I) which are known to bind [^{125}I]-galanin (Jungnickel and Gundlach, 2005), so the apparent discrepancy is in median eminence (ME) between the high level of Gal1-mCherry immunofluorescence (Fig. 7G, K and L) and the absence of Gal1 mRNA expression in both mouse and rat (Fig. 4d of Hohmann et al., 2003; Mitchell et al., 1997). However, Gal1 mRNA is detected in most hypothalamic nuclei that project towards it, and as there is a high density of [^{125}I]-galanin binding sites in the ME of mouse and rat (Jungnickel and Gundlach, 2005), these brain regions shown as the most Gal1-mCherry immunoreactive and terminals (Mitchell et al., 1997). This is now clearly demonstrated by Gal1-mCherry immunofluorescence localized to densely packed nerve endings within the extranuclear zone of the ME (Fig. 7K–L), a blood–brain barrier-free circumventricular organ (Fekete and Lechan, 2014; Mullier et al., 2010) with a very high density of galanin-immunoreactive fibres in both mouse and rat (Melander et al., 1986; Perez et al., 2001).

Brain regions with lesser Gal1-mCherry immunoreactivity (Materials and methods section; Supplementary Fig. 6) correspond to Gal1 mRNA intensities in the range + to ++++ (Hohmann et al., 2003), or in the case of the lateral posterior thalamic nucleus is known to bind [^{125}I]-galanin (Jungnickel and Gundlach, 2005), while the dorsal raphe nucleus (DR) and median raphe nucleus were too caudal to be included in the ISH study. Gal1 mRNA is expressed in adult rat DR (Burazin et al., 2000; O’Donnell et al., 1999), but on the basis of a lack of Gal1-immunoreactivity or detection of Gal1 mRNA by ISH in mouse, a species difference in expression was proposed (Larm et al., 2003). Since then, [^{125}I]-galanin binding sites and weak expression of Gal1 mRNA in the ventral part of mouse DR have been detected (Borotto-Escuela et al., 2010; Jungnickel and Gundlach, 2005). Here we show Gal1-mCherry immunoreactivity in the DR (Supplementary Fig. 6), galanin receptor agonists having implicated mouse DR Gal1 in facilitating limbic seizures (Mazarati et al., 2005).

The difficulty in detecting Gal2-hrGFP fluorescence in the somatic cell membrane of DRG neurons can mainly be ascribed to comparatively low mRNA expression from the endogenous promoter. In wild-type mouse DRG the endogenous Gal2 mRNA was 148-fold less highly expressed than Gal1 (Section 3.2), which is consistent with data used in our previous report (Hobson et al., 2006) in which Gal2 was 136-fold less highly expressed (difference of 7.09 cycles; each n = 5). This wide difference in expression of the two receptors is confirmed by RNA-Seq data of adult mouse DRG in which Gal1 and Gal2 had FPKM (Fragment Per Kilobase of exon per Million fragments mapped) values of 4.865 and 0.020, respectively (Supplementary Table 1 of Thakur et al., 2014). The expression levels of Gal2-hrGFP in DRG, spinal cord and brain may be below the sensitivity for detection by immunohistochemistry, but Gal2 expression appears to be sufficient to affect behaviour. Gal2-deficient mice have anxiogenic-like and depression-like phenotypes (Bailey et al., 2007; Lu et al., 2008), and compounds with a marked preference for binding Gal2 over Gal1 have anticonvulsant and anti-nociceptive activities (Metcalf et al., 2015; Robertson et al., 2010).

Of direct relevance to the very low levels of Gal2-hrGFP, is the observation that Gal2 is likely to be under translational control mediated by upstream open reading frames (uORFs) within the 5′–UTR. This will tend to diminish translation of the main ORF by reducing the number of ribosomes reaching and initiating at the main start codon (Barbosa et al., 2013; Calvo et al., 2009). Unlike the 5′–UTR of mouse and rat Gal1 mRNA sequences that do not contain upstream ATG triplets (NM_008082; NM_012958), those of mouse Gal2 contains six uORFs (here designated uORF1–6) whilst rat Gal2 contains only two uORFs (Fig. 8). These latter two are conserved between mouse and rat (hereafter uORF3 and uORF6) in both relative position and approximate length, potentially encoding 5 and 71/69 amino acids respectively, and the mouse/rat uORF6 terminates only 4 nucleotides upstream of the Gal2 initiation codon. Such proximity has previously been correlated with translational repression of the main coding sequence (Child et al., 1999; Kozak, 1987; but see Calvo et al., 2009), as has uORF length (Calvo et al., 2009; Kozak, 2001), and uORF-mediated repression may or may not depend on the potential uORF-encoded protein sequence (Child et al., 1999; Iacono et al., 2005; Morris and Geballe, 2000) but conservation of the uORF mRNA sequence between species suggests a functional selection (Churbakov et al., 2005; Crowe et al., 2006; Iacono et al., 2005).

Ribosomal profiling (ribo-seq) data based on deep-sequencing of ribosome-protected mRNA fragments is not yet available for mouse neurons (Michel et al., 2014), but is for initiating ribosomes of the mouse ES cell line E14 in which Gal2 has low expression and ribosome density (Ingolia et al., 2011). The predicted initiation site of uORF6 has a ribosomal footprint, with a peak density –1.7-fold higher than at the Gal2 initiation site (Materials and methods section, Section 2.1; Ingolia et al., 2011; Michel et al., 2014), which suggests a functional role for the conserved uORF6. Intriguingly, endoplasmic reticulum (ER)-stress and a number of other stressors that transiently inhibit the translation of most mRNAs can also promote translation initiation of mRNAs with uORFs (Barbosa et al., 2013; Spriggs et al., 2010), and ER-stress is known to occur in vivo following neuronal axon damage, spinal cord injury or brain trauma (Li et al., 2013; Nakka et al., in press; Yasuda et al., 2014). However, attempts to detect Gal2-hrGFP protein in DRG or spinal cord at 3 or 7 days after sciatic nerve peripheral axotomy were unsuccessful (Section 3.5). Further studies could be useful either in DRG after carrageenan-induced inflammation when Gal2 mRNA is induced in rat (Shen et al., 1997) or in the carotid body which has 100-fold more Gal2 than Gal1 mRNA in rat (Hawes and Picciotto, 2005; Porzionato et al., 2010). There is now a clear need for in vitro studies on the mechanism of Gal2 translational control using various stressors (Barbosa et al., 2013; Spriggs et al., 2010) in order to understand both
the conditions and time-courses of Gal2 protein expression, preferably in a neuronal-like cell line.

5. Conclusions

The generation and initial characterization of the Gal1-mCherry knock-in mice will allow more detailed regional tissue distribution studies, co-localization studies, interactome analysis (Bauch et al., 2014) and provide an impetus to understand the function of Gal1 at the somatic cell membrane. Expression of Gal2-hrGFP was at the limits of detection and a possible mechanism involving uORFs is discussed.

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Competing interests

The authors declare that they have no competing financial interests.

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