Title: Structure of long-range direct and indirect spinocerebellar pathways as well as local spinal circuits

mediating proprioception.

Abbreviated Title: Long-range and local proprioceptive circuits.

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Abstract

Proprioception, the sense of limb and body position, generates a map of the body that is essential for proper motor control, yet we know little about precisely how neurons in proprioceptive pathways are wired. Defining the anatomy of secondary neurons in the spinal cord that integrate and relay proprioceptive and potentially cutaneous information from the periphery to the cerebellum is fundamental to understanding how proprioceptive circuits function. Here, we use genetic tools in both male and female mice to define the unique anatomical trajectories of long-range direct and indirect spinocerebellar pathways as well as local intersegmental spinal circuits. We find that Clarke's column (CC) neurons, a major contributor to the direct spinocerebellar pathway, has mossy fiber terminals that diversify extensively in the cerebellar cortex with axons terminating bilaterally, but with no significant axon collaterals within the spinal cord, medulla, or cerebellar nuclei. By contrast, we find that two of the indirect pathways, the spino-lateral reticular nucleus (spino-LRt) and spino-olivary pathways, are in part, derived from cervical *Atoh1*-lineage neurons, while thoracolumbar *Atoh1*-lineage neurons project mostly locally within the spinal cord. Notably, while cervical and thoracolumbar *Atoh1*-lineage neurons connect locally with motor neurons, no CC to motor neuron connections were detected. Silencing of caudal *Atoh1*-lineage neurons results in a subtle motor impairment consistent with a defect in local proprioceptive circuitry. Altogether, we define anatomical differences between long-range direct, indirect, and local proprioceptive subcircuits that likely mediate different components of proprioceptive-motor behaviors.

Significance Statement

We define the anatomy of long-range direct and indirect spinocerebellar pathways as well as local spinal proprioceptive circuits. We observe that mossy fiber axon terminals of Clarke's column (CC) neurons diversify proprioceptive information across granule cells in multiple lobules on both ipsilateral and contralateral sides sending no significant collaterals within the spinal cord, medulla, or cerebellar nuclei. Strikingly, we find that cervical spinal cord *Atoh1*-lineage neurons form mainly the indirect spino-lateral reticular nucleus and spino-olivary tracts and thoracolumbar *Atoh1*-lineage neurons project locally within the spinal cord while only a few *Atoh1*-lineage neurons form a direct spinocerebellar tract.

Altogether, we define the development, anatomical projections, and some behavioral consequences of

silencing spinal proprioceptive pathways.

Introduction

Proprioception, the sense of limb and body position, is critical for generating an online state body

map (Sherrington, 1906; Tuthill and Azim, 2018). When proprioception is lost, gross trajectories are

maintained, but coordinated limb movement is impaired (Gordon et al., 1995; Abelew et al., 2000;

Windhorst, 2007; Akay et al., 2014). Muscle and tendon information detected by proprioceptive sensory

neurons are integrated by secondary neurons in the spinal cord and relayed to the cerebellum through

both direct and indirect spinocerebellar pathways (Oscarsson, 1965; Bosco and Poppele, 2001; Jiang et

al., 2015). In this study, we sought to define the precise anatomy of the proprioceptive system through

the spinal cord using genetic tools in mice.

The direct spinocerebellar pathway consists of ipsilaterally-projecting dorsal and contralaterally-

projecting ventral spinocerebellar tracts (DSCT and VSCT), deriving from several anatomically and

molecularly distinct groups of soma in diverse laminae throughout the spinal cord where they are thought

to convey ongoing locomotor activity (Matsushita and Hosoya, 1979; Sengul et al., 2015). A major

contributor to the DSCT comes from Clarke's column (CC) neurons, whose soma reside in the medial

aspect of the thoracic to upper lumbar spinal cord (Oscarsson, 1965; Baek et al., 2019). While SCT axons

terminate as mossy fiber (MF) terminals on granule cells (GCs) in the cerebellum (Arsenio Nunes and

Sotelo, 1985; Reeber et al., 2011), the extent to which CC neurons send axon collaterals to areas within

the spinal cord, medulla, or cerebellar nuclei (CN) is unclear (Ekerot and Oscarsson, 1976; Matsushita

and Gao, 1997; Mogensen et al., 2017; Luo et al., 2018). Such axon collaterals would be important for

integration with other ascending or descending pathways (Sillitoe et al., 2012; Beitzel et al., 2017).

Compared to the direct spinocerebellar pathways, less is known about the anatomy of the indirect

spino-LRt and spino-olivary (Helweg's tract) pathways. Spino-LRt neurons project ipsilaterally and

contralaterally to the LRt in the medulla where they are involved in posture, reaching, and grasping

(Alstermark and Ekerot, 2013; Jiang et al., 2015). Spino-olivary neurons reside in lamina V-VII of the

spinal cord and project contralaterally to the inferior olive (IO) in the medulla (Oscarsson and Sjolund,

1977a, b; Berkley and Worden, 1978; Swenson and Castro, 1983b, a). Neurons in the IO are thought to

be involved in the timing of motor commands, motor learning, and error correction (Sillitoe et al., 2012;

White and Sillitoe, 2017).

Developmentally, the basic helix-loop-helix (bHLH) transcription factor-expressing progenitor

domains *Atoh1* (atonal homolog 1) and the dorsal *Neurog1* (neurogenin 1) domains are reported to

differentiate into neurons of the direct spinocerebellar pathway (Bermingham et al., 2001; Gowan et al.,

2001; Sakai et al., 2012). The soma of *Atoh1*-lineage neurons reside medially, laterally, and ventrally to

CC neurons suggesting that CC neurons do not develop from *Atoh1*-lineage neurons, but from an

alternate progenitor domain (Yuengert et al., 2015). Based on the location of *Atoh1*-lineage neurons, we

previously hypothesized that they make other direct spinocerebellar neurons such as the lamina V-SCTs

or dorsal horn-SCTs (Matsushita and Hosoya, 1979; Edgley and Gallimore, 1988).

In this study, we sought to provide clarity to the development and anatomy of the proprioceptive

system using genetic labeling strategies, whole tissue clearing and imaging, and tracing tools of CC and

spinal cord *Atoh1*-lineage neurons. We find that CC neurons develop from a *Neurog1*, not *Atoh1*,

progenitor population. We also find that as a population, CC axons do not collateralize considerably to

any structures within the spinal cord, medulla, or CN, although they do collateralize extensively within the

cerebellar cortex with some axons crossing the midline within the cerebellum. Furthermore, we find that

cervical *Atoh1*-lineage neurons make the indirect spino-LRt and spino-olivary tracts rather than the direct

lamina V-SCTs or dorsal horn SCTs as originally hypothesized and that thoracolumbar *Atoh1*-lineage

neurons project mainly locally within the spinal cord. Altogether, we provide novel insights into the

development, anatomy, and function of spinal cord proprioceptive pathways.

Materials & Methods

Mouse strains

The following mouse strains were used: *Gdnf$^{IRES2-CreERT2}$* (Cebrian et al., 2014)(abbreviated

Gdnf^{CreER}, JAX #024948), *Neurog1BAC-Cre* (Quinones et al., 2010)(JAX #012859), *Atoh1$^{P2A-FLPo}$*

(Ogujiofor et al., 2021), *Atoh1^{Cre}* knock-in (Yang et al., 2010), *R26^{LSL-LacZ}* (Soriano, 1999)(JAX #003474),

R26^{LSL-tdTom} (Ai14)(JAX #007914)(Madisen et al., 2010), *R26^{LSL-FSF-tdTom}* (Ai65)(JAX #032864)(Madisen et

al., 2015), *Cdx2::FLPo* (Bourane et al., 2015), *R26^{LSL-FSF-TeTx}* (Kim et al., 2009). All mice were outbred and

thus, are mixed strains (including C57Bl/6J, C57Bl/6N, and ICR). *Atoh1^{Cre/+}* knock-in mice crossed to

Cdx2::FLPo and dual recombinase tdTomato reporter Ai65 mice were screened for "dysregulated"

expression as previously reported (Yuengert et al., 2015). Tamoxifen (Sigma) was injected at P7 and/or

P8 for the *Gdnf^{CreER}* line at 0.1 mg/g mouse using 10 mg/mL Tamoxifen dissolved in sunflower oil (Sigma)

with 10% ethanol. All animal experiments were approved by the Institutional Animal Care and Use

Committee at UT Southwestern.

Tissue processing

Mice are age P0 on the day of birth. Mice older than P10 were anesthetized with Avertin (2,2,2-

Tribromoethanol) (0.025-0.030 mL of 0.04 M Avertin in 2-methyl-2-butanol and distilled water/g mouse)

and transcardially perfused, first with 0.012% w/v Heparin/PBS and then 4% PFA/PBS. A dorsal or ventral

laminectomy exposed the spinal cord to the fixative. Spinal cords were fixed for 2 hrs and the brains

overnight at 4°C. Tissue was washed in PBS for at least one day and cryoprotected in 30% sucrose

dissolved in deionized water. Tissue was marked with 1% Alcian Blue in 3% acetic acid on one side to

keep orientation and were embedded in OCT (Tissue-Tek Optimal Cutting Temperature compound).

Tissue was sectioned using a Leica CM1950 Cryostat.

Immunohistochemistry (IHC) and confocal imaging

Cryosections (20-40 μm) were blocked with PBS/1-3% normal goat or donkey serum (Jackson

labs)/0.3% Triton X-100 (Sigma) for up to 1 hr at room temperature (RT) and incubated overnight with

primary antibody at 4°C. After washing 3 times with PBS, the appropriate secondary antibody (Alexa 488,

567, and/or 647, Invitrogen) was incubated for an hour at RT. Sections were rinsed 3 times in PBS,

mounted with Aqua-Poly/Mount (Polysciences Inc.), and coverslipped (Fisher). The following primary

antibodies and dilutions were used: 1:500 rabbit anti-dsRed (Clontech), 1:500 mouse anti-NEUN

(Millipore Sigma), 1:500 chicken anti-GFP (Aves), 1:5000 guinea pig anti-VGLUT1 (Millipore Sigma),

1:1000 guinea pig anti-VGLUT2 (Millipore Sigma), 1:100 goat anti-CHAT (Millipore Sigma), 1:200 rabbit

anti-PSD-95 (Invitrogen), 1:1000 rabbit anti-PV27 (Swant). Sections were referenced to the Mouse Brain

Atlas (Paxinos and Franklin, 2007) and Christopher Reeves Spinal Cord Atlas (Watson et al., 2009).

Fluorescent images were taken on a Zeiss LSM710 or LSM880 confocal microscope with an

optical slice of 0.5-10 μm depending on the objective used (10x air, 20x air, 40x oil, or 63x oil). Images

were pseudocolored using a magenta/yellow/blue, magenta/green/blue, or magenta/yellow/cyan color

scheme using Adobe Photoshop 2021 (Adobe) or Fiji (Schindelin et al., 2012). Images for quantitation of

soma size were processed in Fiji. Images were thresholded and the soma manually outlined to obtain

the soma area.

In situ hybridization (ISH)

ISH was performed as per standard protocols. Detailed protocol is available upon request. Briefly,

spinal cord sections (30 μm) were dried at 50°C for 15 min. then fixed in 4% paraformaldehyde (PFA) in

DEPC-PBS for 20 min. at RT. The sections were washed in DEPC-PBS for 5 min. at RT before and after

the incubation in RIPA buffer (150 mM NaCl, 1% NP-40, 0.5% Na deoxycholate, 0.1% SDS, 1 mM EDTA,

50 mM Tris pH 8.0) for 60 min. Next, the sections were postfixed in 4% PFA in DEPC-PBS for 15 min at

RT. The sections were then washed in DEPC-water followed by acetylation (500 μL of acetic anhydride

in 200 mL of 0.1 M RNase-free triethanolamine-HCl at pH 8.0), washed in DEPC-PBS for 5 min., and

prehybridized for 2 h at 60-62°C. Sections were incubated overnight at 60-62°C with 1–2 ng/μL of fresh

probe (*Gdnf* or *Vglut1*). A series of low and high stringency washes in 2x and 0.2x SSC as well as

treatment with RNaseA and RNase T1 were performed. The sections were blocked in 10% inactivated

sheep serum for 1 h followed by overnight incubation with 1:1000 anti-digoxygenin (DIG) antibody

(Roche). The sections were washed in PBT and incubated with NBT/BCIP (Roche) staining solution.

After the blue precipitate formed, the slides were washed in PBS and coverslipped with Aqua-Poly/Mount

(Polysciences Inc.) mounting media.

The RNAscope Fluorescent Multiplex Assay (Advanced Cell Diagnostics Inc., Hayward, CA) was

performed according to the manufacturer's instructions using a *Vglut1* probe (ACDBio, 416631), *Vglut2*

probe (ACDBio, 319171), or *Gdnf* probe (ACDBio, 421941). All incubation steps were performed in a

HybEZ™ II oven set to 40°C. The slides were then washed with 1x DPBS (Gibco, 14190) and incubated

with a 2:1 1x DPBS:Protease III for 150 sec. Slides were then washed with 1x DPBS three times and

incubated with the probe(s) for 2 hours. The slides were washed two times thoroughly using 1x wash

buffer (ACDBio, 310091) for 2 min, then incubated with Amp 1-Fl for 30 minutes. The same process

(washing then treatment) was repeated for Amp 2-Fl, Amp 3-Fl and Amp 4-Fl for 15, 30 and 15 minutes,

respectively. For antibody staining of β-galactosidase, the sections were transferred to a humidified tray

and blocked for 30-45 minutes in 0.25mL/slide of PBT (PBS with 0.3% Triton) containing 1% goat serum

(Jackson ImmunoResearch). The sections were incubated with chicken anti-β-Galactosidase antibody

(Abcam, 1:500) in PBT with 1% goat serum overnight at 4°C. The slides were then washed three times

in PBS for 10 minutes and incubated at room temperature for 1 hour with goat anti-chicken Alexa Fluor

488 (Life Technologies, 1:500). Slides were washed three times in PBS for 10 minutes and coverslipped

using 2 drops of Aqua-Poly/Mount (Polysciences, Inc.) as the mounting media.

X-gal staining

Slides with spinal cord sections (30 μm) were incubated in staining solution with 5mM $K_3Fe(CN)_6$,

5mM $K_4Fe(CN)_6$ and 1 mg/mL of X-gal (Roche) until precipitate was sufficient to visualize. Sections were

moved to PBS, mounted, and coverslipped.

Viral Injections

Mice aged P7-P8 were anesthetized using isoflurane (Henry Schein) and prepared for injections

into the spinal cord. The back hair was shaved and 70% ethanol and betadine (Avrio Health L.P.) applied.

A midline incision was made on the dorsal surface of the spinal cord. AAV9.hSyn.DIO.eGFP.WPRE.hGH

was injected into the lower thoracic spinal cord through the intervertebral space of P7 or P8 *Gdnf^{Tom}* mice

(100 nL total in 27.6 nL increments at 1-2 min intervals (Nanoject II, Drummond Scientific), 1.07 x 10^{13}

GC/mL, Penn Vector Core). Lenti^{FugE}-Cre was injected into the cervical or lower thoracic to lumbar area

of P7 *Atoh1^{P2A-FLPo};Ai65* mice (total of 50.6 nL in 27.6 nL increments at 1-2 min intervals). Lenti^{FugE}-Cre

was pseudotyped with a fusion glycoprotein enabling efficient retrograde axonal transport (Kato et al.,

2014). To generate Lenti[FugE]-Cre, *Cre* was sub-cloned into the third generation HIV-based lentivirus

vector under the control of a synapsin promoter (FSW-*Cre*). FSW-*Cre* was co-transfected into HEK293

cells with three packing plasmids, pMDLg/pRRE, pRSV-Rev and pCAGGS-FuG-E to generate Lenti[FugE]-

Cre, which was concentrated with ultracentrifugation to 2.0×10^{12} Vg/mL. The incision was closed with

surgical glue (Henry Schein). Carprofen (5 mg/kg) was administered daily 3 days after surgery. Spinal

cords were harvested approximately 3 weeks after injection.

CTB and FG Injections

Gdnf[Tom] mice were injected with 1% (w/v) of CTB-488 (left side) and CTB-647 (right side) (Thermo

Fisher Scientific). Mice were anesthetized with isoflurane and the area above and around the cerebellar

region was prepared for surgery. A midline incision of 0.75 cm and a craniectomy of approximately 1 mm

X 1 mm was performed. Bilateral injections at 4 sites were done at (from Bregma): rostrocaudal -5.7 and

-6.2 mm and at mediolateral ± 0.35 mm. At each site, several injections in 32 nL increments were

performed every 300 μm along the dorsoventral axis at coordinates: -1.8 and -1.5 mm deep for a total of

320 nL of conjugated CTB. Animals were euthanized and tissue harvested 5 days after injection.

Fluorogold (FG) was injected into the vermis of lobules I-V in the cerebella of *Gdnf[Tom]*, *Atoh1[Tom]*,

or *Atoh1[Cre];Cdx2::FLPo;Ai65* mice. Mice (1-2 months old) were injected with 4% (w/v) FG solution in

saline (Fluorochrome). Mice were anesthetized with isoflurane and the area above and around the

cerebellar region was prepared for surgery. A midline incision of ~0.75 cm and a craniectomy of

approximately 1 mm wide by 1.5 mm long was performed. Bilateral injections at six sites were done at

(from Bregma): rostrocaudal -5.6 to -5.5, -5.9, and -6.25 to -6.3 mm and at mediolateral ± 0.2-0.4 mm.

The maximum depth at each rostrocaudal site was -2.0 mm, -2.4 mm, -1.5 mm, respectively. Multiple

injections were done at each site in 32 or 50.6 nL increments every 300 μm along the dorsoventral axis

for a total of 270-720 nL of FG on each side. Animals were euthanized and tissue harvested 7 days after

injection.

For FG injections targeting the LRt and IO, *Atoh1[Tom]* mice (7-9 weeks old) were anesthetized with

isoflurane and the area above and behind the occipital region prepared for surgery. A midline incision of

~1 cm was made. Neck muscles were detached from the occipital bone and retracted laterally to expose

the foramen magnum. A needle with a rostroventral inclination of 47° was used to advance through the

foramen magnum into the brainstem ~3.7 mm from dura. 32.2 nL of 1-2% (w/v) FG solution was injected

4-5 times 25 μm apart while retracting the pipette with an interval of 30 seconds between injections for a

total of 128.8-161 nL of FG. Unilateral injections were done at the following coordinates measured from

the most ventral aspect of the occipital crest: rostrocaudal -0.4 mm, and mediolateral ± 0.75 mm. After

the last injection, the needle was left in place for 3 minutes and then slowly extracted from the brainstem.

Animals were euthanized and tissue was harvested 7 days after injection.

Whole tissue imaging

Mouse hindbrain and spinal cords were processed following the SHIELD protocol (Park et al.,

2018). Tissues were cleared with SmartClear II Pro (LifeCanvas Technologies, Cambridge, MA) for

several days, mounted in a gel of 0.9% agarose in EasyIndex (LifeCanvas Technologies), and then

incubated in EasyIndex for refractive index matching. Tissues were imaged at 3.6X using a SmartSPIM

light sheet microscope (LifeCanvas Technologies). Spinal cords and hindbrains of three mice marking

CC were used for quantitation of the MF/cell body ratio: one $Gdnf^{Tom}$ mouse (female, P23) and two

$Gdnf^{Tom}$;*Cdx::FLPo;Ai65* mice (one male, one female, P28). Mice were imaged with 1.8 μm x 1.8 μm x 2

μm sampling (X, Y, and Z, respectively). The total number of 2 μm image slices for each sample was as

follows: spinal cord (1500, 3300, 2400 slices) and hindbrain (2700, 3000, 3300 slices) for the $Gdnf^{Tom}$,

$Gdnf^{Tom}$;*Cdx::FLPo;Ai65* male, $Gdnf^{Tom}$;Cdx::FLPo;Ai65 female mouse, respectively. One

$Atoh1^{Tom}$;*Cdx::FLPo;Ai65* mouse spinal cord and hindbrain was cleared (male, P30). The hindbrain was

imaged as described above (4800 slices). The spinal cord was imaged with a 15x objective with 0.41 μm

x 0.41 μm x 2 μm sampling (900 slices). All hindbrain and spinal cord samples were cut to less than 2.2

cm to fit in the imaging chamber. Movies were made in arivis Vision4D 2.12.6. Maximum intensity

projections (MIPs) were processed using Fiji (Schindelin et al., 2012).

Behavioral test - Rotarod

Rotarod was performed at 8-13 weeks of age. All testers were blind to genotype. Mice were

acclimated to the testing room for 0.5-1 hr on day of testing. All mice were genotyped for appropriate

alleles using previously published protocols for *Atoh1^{Cre}*, *Cdx::FLPo*, and *R26$^{LSL\text{-}FSF\text{-}TeTx}$* (Kim et al., 2009;

Yang et al., 2010; Bourane et al., 2015). Mice were placed on an accelerating rotarod (IITC Life Science

Series 8, Woodland Hills, CA) from 4 to 40 RPM over 5 min. Four trials were performed each day for two

days with at least a 15 min wait time between trials.

Experimental Design and Statistical Tests

The mossy fiber (MF) to cell body ratio (Fig. 3K) was counted from three cleared spinal cords and

hindbrains. Cells bodies in the spinal cord and MFs in the cerebellar cortex were counted from 100 μm

MIP images of cleared tissue. The ratio calculated is an estimate given that it is impossible to accurately

count all the cell bodies and MF terminals and there are many opportunities for over- or undercounting.

For example, although cell bodies and mossy fibers were counted only when they could be discretely

identified, some MF terminals might appear as two MF terminals, when they in fact come from the same

MF. As an example of undercounting, cell bodies and mossy fibers may overlap in the z axis of the 100

μm MIP and may be counted as one instead of several. Altogether, cell bodies and MFs were counted to

get an estimate rather than an exact count of the MF/cell body ratio.

For the mapping of thoracolumbar CC MF terminals in the cerebellum (Fig. 4H-H''', J-J''', L-L''',

N, P, R), confocal images of 30 μm cryosections were analyzed in Fiji using the ROI Manager to label

individual MF terminals and the SlideSet PlugIn to export the ROIs as a .svg file (Schindelin et al., 2012;

Nanes, 2015). These mapped MF terminals were then overlaid on a traced drawing of the confocal image

in Adobe Illustrator 2021.

All data and graphs were processed in Microsoft Excel 2015 and GraphPad Prism 9. Details of

the number of sections counted and sex of the mice are given in the Results section. Mean ± SEM is

reported throughout the manuscript. Statistical tests used are detailed in the Results and/or Figure

Legends.

Results

Clarke's column is the major direct spinocerebellar pathway in mice.

To assess the spinocerebellar system in mice, we identified genetic tools that reproducibly label spinal cord neurons and evaluated their contribution to the spinocerebellar system using a combination of retrograde and anterograde tracing. Previously, we found that the *Atoh1*-expressing progenitor population that makes dorsal interneuron 1 (dI1) neurons, although implicated in making spinocerebellar neurons developmentally (Bermingham et al., 2001; Gowan et al., 2001; Sakai et al., 2012), rarely made CC neurons, which are the major source of the DSCT (Fig. 1A, note the absence of TOM+ cells in the CC area of *Atoh1*-lineage traced neurons, *Atoh1^Cre^;R26^LSL-tdTom^* (Ai14), abbreviated *Atoh1^Tom^*)(Madisen et al., 2010; Yang et al., 2010; Yuengert et al., 2015). Therefore, we sought to identify the progenitor population that gives rise to CC neurons. Evidence from spinal cord development suggested that the neighboring *Neurog1*-expressing progenitor population that makes dI2 neurons also project to the cerebellum (Avraham et al., 2009; Sakai et al., 2012). Because there are no uniquely specific molecular markers for the dI2 population, we traced the lineage of the entire *Neurog1* population, which includes dI2 neurons and ventral domains, using a transgenic *Neurog1BAC-Cre* strain crossed to a *R26^LSL-LacZ^* reporter mouse (Fig. 1A)(Soriano, 1999; Quinones et al., 2010). Large CC cells residing in the medial thoracic spinal cord colocalize with vesicular glutamate transporter 1 (*Vglut1*) mRNA, a marker for CC (Fig. 1A, B)(Llewellyn-Smith et al., 2007; Malet et al., 2013; Yuengert et al., 2015). Therefore, CC neurons come from a *Neurog1*-lineage (dI2 or ventral lineages), but not the *Atoh1*-lineage.

Next, we further characterized molecular tools that label CC neurons. As previously described, CC neurons are marked by glial derived nerve growth factor (*Gdnf*) and *Vglut1* mRNA (Fig. 1B)(Llewellyn-Smith et al., 2007; Hantman and Jessell, 2010; Malet et al., 2013). We found that *Gdnf* is transiently expressed from E18.5-P10 (data not shown) and that *Gdnf* and *Vglut1* mRNA completely overlap at P10 (Fig. 1C, arrowheads). Furthermore, CC neurons that are retrogradely labeled with Fluorogold (FG) injected into the anterior zone (AZ, lobules I-V) of the cerebellum, colocalized with *Vglut1* mRNA (Fig. 1D, arrowheads). A subset of CC neurons is labeled using a *Gdnf^IRES2-CreERT2/+^* mouse line crossed to a CRE-dependent tdTomato reporter (Ai14) (abbreviated *Gdnf^Tom^* from here on)(Fig. 1D, arrows)(Hantman

and Jessell, 2010; Cebrian et al., 2014). Lastly, we found that CC neurons also express vesicular

glutamate transporter 2 (*Vglut2*)(Fig. 1E, arrowheads). We used the *Gdnf^{IRES2-CreERT2/+}* mouse line

(abbreviated *Gdnf^{CreER}* from here on) for the remainder of the study due to its specific labeling of CC

neurons.

To understand the relationship of the direct spinocerebellar system to our two CRE mouse lines

(*Gdnf^{CreER}* and *Atoh1^{Cre}*), we used both anterograde (Fig. 1F-I) and retrograde (Fig. 1J-P) tracing

strategies to and from the cerebellum. To identify ascending projections from the spinal cord, we used

an intersectional strategy to restrict labeling of neurons to regions caudal of cervical 4

(C4)(*Cdx2::FLPo*)(Bourane et al., 2015). As expected, we found that CC neurons (*Gdnf^{CreER}; Cdx2::FLPo;*

Ai65) terminate as mossy fibers (MF) in the AZ of the cerebellum and express VGLUT1+ (VG1) and

VGLUT2+ (VG2) presynaptic markers (Fig. 1F-F'''). However, labeling of caudal *Atoh1*-lineage neurons

(*Atoh1^{Cre}; Cdx2::FLPo; Ai65*) had very few MF terminals in the AZ, although they were VG1- and VG2+,

consistent with a non-Clarke's spinocerebellar population and a previous report that spinocerebellar

neurons are mainly VG2+ with some VG1+ MF terminals (Gebre et al., 2012; Yuengert et al., 2015)(Fig.

1G-G'''; Quantitated in Fig. 1H, in the AZ, 2447 ± 624 *Gdnf^{CreER}; Cdx2::FLPo; Ai65* (n=3, 2 females (F):1

male (M)) vs. 690 ± 213 *Atoh1^{Cre}; Cdx2::FLPo; Ai65* (n=3, 1F:2M), t-test p=0.056, 3 comparable

sections/n; MF terminals in lobules VIII/IXa are similar, 262 ± 75 *Gdnf^{CreER}; Cdx2::FLPo; Ai65* vs. 182 ±

21 *Atoh1^{Cre}; Cdx2::FLPo; Ai65,* 1 comparable section/n; ages P27-67). The difference in MF terminals is

striking given that *Atoh1*-lineage neurons have many more soma per section throughout the rostral-

caudal axis compared to CC neurons (Fig. 1I, *Gdnf^{CreER}; Cdx2::FLPo; Ai65* (n=3, 2F:1M, 4 sections

counted per region per n), *Atoh1^{Cre}; Cdx2::FLPo; Ai65* (n=2, 1F:1M, 3-4 sections counted per region per

n)), suggesting there are many more MF terminals per CC soma in the spinal cord compared to caudal

Atoh1-lineage neurons.

Consistent with our anterograde tracing findings, we found that retrograde labeling of

spinocerebellar neurons colocalized with CC neurons, but few *Atoh1*-lineage neurons (Fig. 1J-P). FG

was injected into the cerebella of *Gdnf^{Tom}* or *Atoh1^{Tom}* mouse strains targeting the AZ where

spinocerebellar neurons are known to project (Fig. 1 J, K, N)(Arsenio Nunes and Sotelo, 1985; Bosco and Poppele, 2001; Reeber et al., 2011). Overall, FG retrograde tracing from all injections were similar with 261 ± 39 total FG+ cells in injections of *Gdnf^{Tom}* (n=3, 1F:2M, ages P38-40, counts from 5 sections per spinal cord region per n) and 228 ± 32 total FG+ cells in injections of *Atoh1^{Tom}* (n=4, 3F:1M, ages P39-40, counts from 5 sections per spinal cord region per n)(Fig. 1L, O shows total FG cells in each spinal cord region). Overall, CC is the most abundantly labeled spinocerebellar projection making up 43-47% of all retrogradely-labeled FG neurons in the spinal cord (Fig. 1M, P). The next most abundant areas of spinocerebellar neurons along the rostral-caudal axis are those in the central cervical (CeCv) nucleus (Cummings and Petras, 1977; Wiksten, 1987; Popova et al., 1995) and cells dorsal or ventral of the central canal in the thoracolumbar areas (Fig. 1K', N', top and lower panels; L-M, O-P), which correspond to LV-SCT, LVII-SCT, LVIII-SCT, and spinal border cells (Baek et al., 2019). Notably, spinocerebellar neurons in the CeCv and thoracolumbar areas (excluding CC) are rarely colabeled with *Gdnf^{Tom}* or *Atoh1^{Tom}* neurons (Fig. 1L-M, O-P) indicating that genetic labels for these spinocerebellar neurons and their developmental origins have yet to be determined. *Gdnf^{Tom}* makes up 12 ± 2% of the FG+ CC neurons out of all FG+ neurons in the spinal cord and therefore labels ~ 29 ± 1% of CC neurons. The remaining approximately 70% of unlabeled CC neurons in the *Gdnf^{Tom}* line could be due to the restricted time point at which tamoxifen was injected (P7-P8), incomplete CRE recombination, or represent a unique subset of CC neurons. *Atoh1^{Tom}* makes up 3 ± 1% of the FG+ CC neurons out of all FG+ neurons in the spinal cord and therefore labels ~ 6 ± 1% of CC neurons, consistent with our previous findings that *Atoh1*-lineage neurons make up very few CC neurons (Yuengert et al., 2015). Significantly, only 4 ± 1% of all spinocerebellar (FG+) neurons projecting to the AZ in the entire spinal cord are *Atoh1*-lineage neurons (FG+TOM+). Altogether, our data suggest that CC makes up a majority of spinocerebellar neurons projecting directly to the AZ, while *Atoh1*-lineage neurons make up very few direct spinocerebellar neurons. Using our genetic tools, we then proceeded to determine the precise anatomy of both CC and *Atoh1*-lineage projections.

Anatomical trajectories of CC neurons.

We used the *Gdnf^Tom* line to meticulously trace axonal trajectories of CC neurons to the

cerebellum and found that the axons cross within the cerebellum and terminate almost exclusively as

MFs on granule cells. We found that CC MF terminals in the cerebellum terminate in the vermis of lobules

II-V, VIII, IXa, and the copula pyramidis (Cop) (Fig. 2A-C), consistent with the termination locations of

spinocerebellar neurons from previous pan-anterograde tracing studies (Arsenio Nunes and Sotelo,

1985; Bosco and Poppele, 2001; Apps and Hawkes, 2009; Reeber et al., 2011). In addition, the three

parasagittal stripes in lobule III on both sides of the midline closely matched those found in anterograde

tracing studies from the thoracic and lumbar spinal cord (Fig. 2A, B)(Ji and Hawkes, 1994; Reeber et al.,

2011). However, while CC axons are known to travel rostrally ipsilaterally in the lateral funiculus of the

spinal cord (Oscarsson, 1965 and see Movie 1), we found that several axons appeared to cross the

midline within the cerebellum (Fig. 2D, E), suggesting that CC axons terminate both ipsilaterally and

contralaterally in the cerebellar cortex, which has been seen in single-cell reconstructions (Luo et al.,

2018). To test whether CC axons from a given CC cell terminates on both sides of the cerebellum, we

injected two different Cholera Toxin subunit B (CTB)-conjugated fluorophores (CTB-488 and CTB-647)

into the left and right sides of the cerebellum (Fig. 2F, G). We found retrogradely labeled cells in CC of

the spinal cord that took up both tracers (Fig. 2H, arrows and arrowheads), some of which were colabeled

with *Gdnf^Tom* (Fig. 2H, arrows). Approximately 30% of the terminals from CC neurons that innervate the

injection area are from the contralateral side (% ipsi and contra CTB-488/total CTB-488: 74 ± 4% and 26

± 4%, respectively; % ipsi and contra CTB-647/total CTB-647: 70 ± 5% and 30 ± 5%, respectively, n=3,

2F:1M, 8 sections/n, age P65-95). This could mean that only 30% of CC neurons cross or that all of them

cross, but only some CC neurons have enough terminations on the contralateral side to allow for sufficient

CTB uptake. Therefore, CC neurons project ipsilaterally within the spinal cord, but send collaterals to

both ipsilateral and contralateral sides within the cerebellum.

Strikingly, we found that CC axons do not make significant axon collaterals within the spinal cord,

medulla, or to the cerebellar nuclei, a feature typical of other MF tracts, but has been ambiguous for the

spinocerebellar system (Fig. 3A-H')(Matsushita and Ikeda, 1970; Matsushita and Gao, 1997; Mogensen

et al., 2017). In three separate samples, we found no axon terminations in the Medial (Med),

(Int), or Lateral (Lat) cerebellar nuclei (CN). Areas near the cerebellar nuclei that had TOM+ signal came

from axons of passage and not synaptic terminations (TOM+ axons are VG1- or VG2- (Fig. 3A', A'', D',

D'')). Furthermore, we find no seeming axon collaterals within the spinal cord (Movie 1), nor do we find

significant synaptic terminations in the LRt or nucleus X, as was reported previously for some CC neurons

(Fig. 3G-H')(Luo et al., 2018). Some synaptic terminals can be seen in the LRt (Fig. 3G', arrow), but the

axons mainly appear to be coursing by the LRt. In summary, our genetic studies of CC neurons show

that these glutamatergic neurons terminate bilaterally in the cerebellar vermis, but do not make significant

axon collaterals to the spinal cord, medulla, or cerebellar nuclei.

Diversification of proprioceptive information through CC neurons.

To obtain a three-dimensional view of CC trajectories, we chemically cleared the spinal cords and

hindbrains of *Gdnf^Tom* and *Gdnf^CreER;Cdx2::FLPo*; *Ai65* mice (Movies 1-2). Because *Gdnf* is also

expressed in smooth and skeletal muscle (Trupp et al., 1995; Suzuki et al., 1998; Rodrigues et al., 2011),

they are prominently labeled with TOM in these samples. In the spinal cord (Movie 1), the CC soma can

be seen straddling the midline, while their axons extend to the lateral funiculus (LF) where they make a

90° turn heading rostrally to the cerebellum. Axons in the inferior cerebellar peduncle are seen traveling

directly to the cerebellum (Movie 2).

A feature that was readily apparent from the cleared specimens was the sheer number of MF

terminals in the cerebellum indicating an immense diversification of proprioceptive information coming

from CC axons (Fig. 3I-K). We counted the number of MF terminals per CC soma in the cerebella and

spinal cords of the three cleared samples. From these counts, we estimate that there are 71.9 ± 6.1 MF

terminals in the entire cerebellum for each CC soma (Fig. 3K, orange bar). The MFs terminate largely in

vermis I-III (34.6 ± 3.0 MF/soma ratio), IV/V (24.7 ± 2.1), VIII (4.6 ± 0.7), IXa (0.6 ± 0.2), and the copula

(7.2 ± 1.3)(n=3, 2F:1M, ages P23-28), consistent with the distribution seen in cryosections (Fig. 2A-C).

The large ratio of MFs to CC soma suggests that CC information is widely distributed within the

cerebellum. Furthermore, the proprioceptive information coming into CC neurons require surprisingly few

CC neurons to relay that information to the cerebellum. We counted a range of 486-816 CC neurons in

the three spinal cords, which represents around 29% or less of all CC neurons labeled in the *Gdnf^Tom* and

Gdnf^CreER;Cdx2::FLPo; *Ai65* mouse models for an estimated 1,620 to 2,720 CC neurons in the mouse

spinal cord. This suggests that most of the mouse proprioceptive direct spinocerebellar system comes

from roughly a couple thousand neurons.

Next, we wanted to test whether CC neurons from a restricted area of the spinal cord terminate

in clustered or diverse locations in the cerebellum. If a given CC neuron sends MFs terminals to one

discrete localized area of the cerebellum, this would suggest that proprioceptive information exists as a

traditional homunculus in the cerebellum. However, if a given CC neuron sends MF terminals to multiple

areas of the cerebellar cortex, this would provide an anatomical substrate for the fractured somatotopic

map that has been detected electrophysiologically (Shambes et al., 1978), where body parts are

represented in discontinuous patches across the cerebellum (Manni and Petrosini, 2004; Apps and

Hawkes, 2009). To label CC neurons specifically in the thoracolumbar area, we injected AAV9-Syn-DIO-

EGFP into *Gdnf^Tom* mice (Fig. 4A). Our injections labeled CC neurons on both sides of the spinal cord

(Fig. 4B, B', arrows) and largely the lower thoracolumbar spinal cord (Fig. 4G, I, K, M, O, Q)(counts for

GFP⁺ infection in the spinal cord are from 15-16 sections per spinal cord region). We found that

thoracolumbar CC neurons targeted multiple lobules (II-V, VIII)(GFP⁺ (green) and GFP⁺TOM⁺ (yellow),

Fig. 4H-H''', J-J''', L-L''', N, P, R, coronal and sagittal sections, n=3 each, 1F:2M for coronal sections,

2F:1M for sagittal sections). Although there were discrete areas that did not contain GFP⁺ cells

(arrowheads, Fig. 4H-H''', J-J''', L-L'''), GFP⁺ cells were found over multiple lobules indicating that CC

axonal projections from the thoracolumbar spinal cord terminate throughout the cerebellar cortex,

consistent with a discontinuous somatotopic map. Examples of GFP⁺ (green, arrowheads) and

GFP⁺TOM⁺ (white, arrows) MF terminals in lobules III and VIII in both coronal and sagittal sections are

shown (Fig. 4S, T). In addition to terminating across several lobules, we found multiple examples of single

axons terminating at regular intervals (50-80 μm) within a GC layer, which has been reported anecdotally

in the literature (Reeber et al., 2011; Houck and Person, 2015; Gilmer and Person, 2017; Luo et al.,

2018), indicating that a single CC neuron synapses on several GCs (Fig. 4C-F). Interestingly, an

individual GC is approximately 40-50 μm from dendrite to dendrite (Gray, 1961; Eccles et al., 1967; Jakab

and Hamori, 1988; Huang et al., 2013). Therefore, individual MF axons from a single CC neuron likely

do not synapse on the same GC suggesting that GCs are multimodal encoders at the single cell level

(Marr, 1969; Albus, 1971). Overall, we find that CC neurons arborize extensively within the cerebellar

cortex, reaching targets over multiple lobules, rather than in clustered locations.

Atoh1-lineage neurons make the spino-LRt and spino-olivary tracts.

Given that *Atoh1*-lineage neurons made few direct spinocerebellar neurons, we sought to identify

where in the hindbrain *Atoh1*-lineage axons project. We pursued an intersectional genetic strategy to

restrict somatic labeling to caudal *Atoh1*-lineage neurons (*Atoh1[Cre]; Cdx2::FLPo; Ai65*)(Fig. 5A). Most

prominently, we found dense projections of caudal *Atoh1*-lineage neurons in the lateral reticular nucleus

(LRt) and inferior olive (IO) (Fig. 5E-H"). To identify whether caudal *Atoh1*-lineage axons synapse on

localized areas of the LRt and IO, we injected FG into the cerebellar AZ (Fig. 5A-B), which retrogradely

labeled LRt MF and IO CF cell bodies. We found that caudal *Atoh1*-lineage axons target almost the

entirety of the LRt and restricted areas of the IO (dorsal fold of the dorsal accessory olive (dfDAO), dorsal

accessory olive (DAO), subnucleus a of the caudal medial accessory olive (cMAO[a]), subnucleus b of

cMAO (cMAO[b])(Fig. 5E'-H'). Consistent with our findings, anterograde tracing in rats reports that the

spino-olivary tract terminates in the DAO, cMAO[a], and cMAO[b] (Swenson and Castro, 1983a; Matsushita

et al., 1992; Oldenbeuving et al., 1999). Caudal *Atoh1*-lineage axons colocalize with the presynaptic

marker VG2 and are in close apposition to FG labeled neurons in the LRt and IO indicative of synaptic

connections (arrows, Fig. 5I-J, Movies 5 and 6). Axon terminations in the LRt and IO were verified in four

caudal *Atoh1*-lineage mice. Moreover, TOM[+] terminals in a cleared brain of *Atoh1[Cre]; Cdx2::FLPo; Ai65*

mice are quite dense in the LRt and IO (Movie 4). Altogether, we find that spinal cord *Atoh1*-lineage

neurons make the spino-LRt and spino-olivary tracts.

In the caudal *Atoh1*-lineage mice, a few places of expression are worth noting. First, the sensory

neurons misexpress tdTomato and their axons can be seen terminating in the dorsal horn of the cleared

spinal cord (Movie 3). *Atoh1* is not known to be expressed in sensory neurons and we do not see sensory

neurons labeled in *Atoh1^P2A-FLPo* mice, whose expression overlaps quite well with the *Atoh1^Cre* knockin

mouse for spinal cord interneurons (data not shown and Ogujiofor et al., 2021). Therefore, the sensory

neuron labeling is due to misexpression of the CRE recombinase in sensory neurons. As a result, axons

from sensory neurons going to the gracile, cuneate, and external cuneate nuclei can be seen in the

cleared brain of *Atoh1^Cre; Cdx2::FLPo; Ai65* mice (Movie 4). Second, we find sparse ectopic labeling of

Atoh1-lineage spinal vestibular (SpVe) soma in the hindbrain (Fig. 5C)(Rose et al., 2009). SpVe neurons

send descending projections to the spinal cord (Liang et al., 2015), therefore, we do not expect that this

sparse ectopic labeling interferes with our analysis of ascending projections from caudal spinal cord

Atoh1-lineage neurons. Lastly, we detect some TOM⁺ axons in the lateral parabrachial nucleus (LPB) in

Atoh1^Cre; Cdx2::FLPo; Ai65 mice (TOM⁺VG2⁺, Fig. 5D-D'). Further studies are needed to determine

exactly from where in the spinal cord these LPB projections originate and if they are truly *Atoh1*-lineage

neurons or ectopic expression.

Spino-LRt and spino-olivary axonal projections originate from cervical Atoh1-lineage neurons.

We pursued both retrograde and anterograde tracing strategies to determine which caudal *Atoh1*-

lineage neurons contribute to the spino-LRt and spino-olivary tracts. In four different FG injections

targeting the LRt and IO in *Atoh1^Tom* mice, we found that the retrogradely labeled *Atoh1*-lineage cells

resided mainly in the cervical to upper thoracic areas (Fig. 6A-G, light purple (left side) and light blue

(right side) FG⁺TOM⁺ cells quantitated in B, C, E, F; n=4, 3F:1M, 5 sections counted per spinal cord

region, 7-9 weeks old). *Atoh1*-lineage neurons have previously been described as clustering into lateral

and medial populations, which are thought to make up ipsilaterally- and contralaterally-projecting

populations, respectively (Bermingham et al., 2001; Wilson et al., 2008; Yuengert et al., 2015).

Retrogradely labeled neurons from the LRt and IO colocalized with both the lateral (Fig. 6D', G') and

medial (Fig. 6G'') *Atoh1*-lineage neurons. Because of the spread of the FG to both the LRt and IO, the

precise ipsilateral or contralateral projections from either tract was not clear, but *Atoh1*-lineage neurons

both ipsilateral (Fig. 6G') and contralateral (Fig. 6G'') to the injection site were retrogradely labeled. Given

the large number of neurons retrogradely labeled from the LRt and IO that are not *Atoh1*-lineage suggests

that there are many other progenitor domains and cell types that contribute to these tracts (Alstermark

and Ekerot, 2013; Azim et al., 2014; Pivetta et al., 2014; Jiang et al., 2015; Choi et al., 2020).

To identify the axonal projection targets of cervical *Atoh1*-lineage neurons, we pursued an

intersectional strategy injecting Lenti[FugE-Cre] into the cervical area of *Atoh1[P2A-FLPo]* mice crossed to an

intersectional tdTomato reporter (*Ai65*) (Fig. 6H). In one mouse, the infected neurons were restricted to

the right spinal cord (Fig. 6I-J) and in another mouse, the infected cells were on both the left and right

sides (Fig. 6 L, M)(n=2 male mice, 8-15 sections counted per spinal cord region, P30). In the mouse with

the injection restricted to the right side, prominent axons were seen in the right LRt and the TOM[+]

terminations express VG2 (Fig. 6K-K'), suggesting that minimally, the spino-LRt *Atoh1*-lineage neurons

are ipsilaterally-projecting. In the other mouse that had TOM^{+} cells on both sides of the spinal cord, likely

due to the virus being taken up by contralaterally-projecting *Atoh1*-lineage neurons, we found axonal

terminations in the right LRt and right cMAOb that were VG2^{+} and closely apposed to the postsynaptic

density protein (PSD-95^{+}), suggesting that these are functional excitatory synapses (Fig. 6N-O'',

TOM[+]VG2^{+}, white arrowheads; PSD95^{+}, grey arrowheads).

We next examined the local inputs and outputs of cervical *Atoh1*-lineage neurons. We had

previously shown that thoracolumbar *Atoh1*-lineage neurons receive proprioceptive input (Yuengert et

al., 2015). Here, we found that both medial and lateral *Atoh1*-lineage neurons in the cervical area (TOM[+])

have processes closely apposed to VG1^{+} and Parvalbumin (PV[+]) synapses indicative of proprioceptive

afferents (Fig. 6Q-Q'). Similar to our previous results for the thoracolumbar *Atoh1*-lineage neurons

(Yuengert et al., 2015), we were able to visualize axo-somatic synapses for the medial population (Fig.

6Q, VG1^{+}PV[+], white arrowhead), but we were unable to identify axo-somatic synapses on the lateral

population. We could only find VG1^{+}PV[+] afferents passing near TOM[+] processes in the vicinity of the

lateral soma (Fig. 6Q', VG1^{+}PV[+], white arrowhead; TOM[+], grey arrowhead). Lastly, we found that the

axons of sparsely labeled cervical *Atoh1*-lineage neurons made synapses on motor neurons (MNs)(Fig.

6R-R'). Altogether, we found that cervical *Atoh1*-lineage neurons can receive proprioceptive input and do

indeed project to the LRt and IO as well as locally to MNs in the cervical spinal cord.

Thoracolumbar Atoh1-lineage neurons project locally.

We next examined whether sparsely labeled thoracolumbar *Atoh1*-lineage neurons send axonal

projections to the medulla or cerebellum. Using the same intersectional injection strategy except with the

Lenti[FugE-Cre] targeted to the right thoracolumbar spinal cord (light blue), we again found several cell bodies

on the contralateral side labeled (Fig. 7B, 786 ± 20 cells, right side vs. 598 ± 223 cells, left side; n=4,

3F:1M, total number of cells infected was estimated from counts of 20% of each spinal cord region),

which is likely due to the virus being taken up by axons of passage projecting contralaterally (Fig. 7C,

axons labeled in the right ventral funiculus (Rt VF)(light blue arrowhead)). Most of the cell bodies labeled

were in the thoracolumbar area (Fig. 7D)(cell bodies counted from 13-30 sections per spinal cord region).

Strikingly, we found that axons in the right ventral and lateral funiculi (VF, LF) decreased both rostrally

and caudally, suggesting that most of these axons are local projections (Fig. 7E)(axons counted from the

right and left LF and VF from one section/spinal cord region) and that few thoracolumbar *Atoh1*-lineage

neurons project to the LRt, IO, and cerebellar cortex.

Interestingly, the neurons labeled on the left side of the spinal cord, contralateral to the injected

side, were located more dorsolaterally than expected for the medial *Atoh1*-lineage population that is

known to project contralaterally (Fig. 7C, purple arrows)(Bermingham et al., 2001; Wilson et al., 2008;

Yuengert et al., 2015). This observation prompted us to characterize the distribution and cell soma size

of infected *Atoh1*-lineage neurons (Fig. 7F-H'). In the spinal cord areas of peak infection (T11-13, L1-3,

and L4-6), we found that medial, lateral, and the ill-described ventral *Atoh1*-lineage populations on both

sides of the spinal cord were labeled (Fig. 7F-H, n=4, 3-6 sections/n). Quantitation of the soma area

found no size differences between the lateral, medial, and ventral population on either side (one-way

ANOVA of clusters that had n > 5 cells). We believe that the cells infected on the left side are labeled

through their contralaterally-projecting axons that take up the virus on the right side. This suggests that

at least a subset of lateral *Atoh1*-lineage cells can also project contralaterally. Indeed, imaging of some

of the neurons on the left side shows processes projecting both ventromedially and dorsolaterally (inset

in Fig. 7F, arrows), suggesting that these neurons could project both ipsilaterally and contralaterally.

While it is possible that cells labeled on the left side are due to diffusion of the virus across the midline,

we would have expected the lateral *Atoh1*-lineage neurons in this scenario to project ipsilaterally and

therefore, there should be almost equal numbers of axons in the left and right LF given that the number

of soma on each side is similar. However, the number of axons in the left LF are low compared to the

right LF (Fig. 7E). Therefore, we surmise that the neurons infected on the left side are contralaterally-

projecting lateral *Atoh1*-lineage cells, a subset of which could also project ipsilaterally.

Because of the dense ventral projections in our sparsely labeled *Atoh1*-lineage neurons (Fig. 7C,

T11-13 and L1-3), we asked whether thoracolumbar *Atoh1*-lineage neurons also synapse on motor

neurons. Similar to the cervical *Atoh1*-lineage neurons, we found in all four injections a high density of

TOM+VG2+ puncta (arrowheads, Fig. 7I-I') near and some very closely apposed to CHAT+ motor neurons

(arrowhead, Fig. 7I"). Some of these TOM+VG2+ puncta might be axo-dendritic synapses (Fig. 7I',

arrowheads), while only a few axo-somatic contacts are detected (Fig. 7I"). Thus, we find that

thoracolumbar *Atoh1*-lineage neurons primarily project locally, where they synapse onto motor neurons,

with few neurons projecting to higher brain regions.

Expression of a silencing allele in caudal Atoh1-lineage neurons leads to a subtle motor defect.

To understand how caudal *Atoh1*-lineage neurons affect motor behavior, we expressed GFP-

tetanus toxin light chain fusion protein (TeTx), which should inhibit vesicle neurotransmission (Kim et al.,

2009), in these neurons using an intersectional genetic strategy (*Atoh1^Cre^;Cdx2::FLPo;R26^LSL-FSF-*

*^TeTx^*)(Fig. 8A). In caudal *Atoh1*-lineage neurons heterozygous for the TeTx allele, we found a subtle motor

phenotype. We only analyzed mice heterozygous for the TeTx allele because the *Atoh1* gene is close to

the *ROSA* locus on chromosome 6 and thus, homologous recombination occurs too infrequently to get

homozygosity at the *ROSA* locus along with the *Atoh1^Cre^* allele. Caudal *Atoh1*-lineage neurons

expressing the TeTx allele fell off the rotarod sooner compared to controls (Fig. 8B, p=0.0255 for a main

effect due to genotype).

The way that the *R26^{LSL-FSF-TeTx}* mouse was designed, CRE recombinase expression allows for

mCherry expression while CRE and FLPo recombinase allows for expression of the GFP-TeTx fusion

protein (Kim et al., 2009). We performed immunofluorescence and immunohistochemistry with three

different GFP antibodies, but were unable to verify expression of the GFP-TeTx fusion protein. Instead,

we were able to verify that mCherry was expressed in the upper cervical areas of the spinal cord where

Atoh1^{Cre} is expressed, but not Cdx2*::FLPo* (Fig. 8C-C'). Correspondingly, in the lumbar area of the spinal

cord where both *Atoh1^{Cre}* and *Cdx2::FLPo* are expressed, the mCherry is no longer expressed indicating

that the FLPo recombinase had recombined out the mCherry. All twenty-two heterozygous mice

expressing TeTx were confirmed to lack mCherry expression in the lumbar compared to cervical spinal

cord.

Discussion

In this study, we define the anatomy of proprioceptive spinal pathways and find surprising features

of these ascending projections (summarized in Fig. 9). We find that CC neurons avoid significant

collateralization within the spinal cord, medulla, and CN, although they do collateralize extensively within

the cerebellar cortex with some axons crossing the midline. We also discover that cervical *Atoh1*-lineage

neurons make up the indirect spino-LRt and spino-olivary pathways while thoracolumbar *Atoh1*-lineage

neurons project mostly locally within the spinal cord. In contrast to CC neurons, cervical and

thoracolumbar *Atoh1*-lineage neurons make direct connections to MNs and these local connections likely

underlie the subtle motor defect seen when a silencing gene is expressed in these neurons. Altogether,

we find that the proprioceptive circuits within the spinal cord consist of long-range direct (CC) as well as

indirect and locally-projecting (cervical and thoracolumbar *Atoh1*-lineage) neurons that likely mediate

different aspects of proprioception.

Diversification of proprioceptive information through CC neurons

We find many unique anatomical features of CC neurons that lend insight into how proprioceptive

information through CC neurons is relayed. First, we find that a couple thousand CC neurons make up

43-47% of the direct DSCT and VSCT pathways from the AZ relaying hindlimb proprioceptive information.

Second, our work clarifies that CC neurons synapse primarily on GCs and do not collateralize significantly

within the spinal cord, medulla, or CN, which has been a matter of debate in the literature (Ekerot and

Oscarsson, 1976; Szabo et al., 1990; Jiang et al., 2015; Luo et al., 2018). The fact that CC neurons do

not collateralize to other parts of the brainstem or CN, as is seen for other MF terminal sources (Sillitoe

et al., 2012; Beitzel et al., 2017), suggests that they are not involved in the integration of inputs with other

ascending or descending proprioceptive-motor pathways except at the GC level. Lastly, we do find,

though, that within the cerebellar cortex, CC neurons extensively diversify their MF terminals between

lobules, within a lobule, and even crossing the cerebellum to the contralateral side. Our estimate of

approximately 72 MF terminals for 1 CC soma at a population level is similar to the reported 99

terminals/neuron for CC neurons from single axon reconstructions (Luo et al., 2018). Part of the reason

for this expansion of proprioceptive information could be for parallel processing across many domains of

the cerebellar cortex.

Atoh1-lineage spino-LRt and spino-olivary neurons

We initially hypothesized that *Atoh1*-lineage neurons made lamina V-SCT or dhSCT neurons

based on their anatomical location and developmental studies that reported *Atoh1*-lineage axons go to

the cerebellum (Matsushita and Hosoya, 1979; Bermingham et al., 2001; Sakai et al., 2012; Yuengert et

al., 2015). Instead, we found that cervical *Atoh1*-lineage neurons make mainly the indirect spino-LRt and

spino-olivary pathways. Thus, the cerebellar axonal projections seen during development either extend

to the cerebellum and retract during development or die. However, it is possible that *Atoh1*-lineage

neurons make a subset of direct spinocerebellar neurons that project to the posterior zone (PZ – lobules

VIII/IXa), which was not assessed in our study. Cervical *Atoh1*-lineage neurons could contribute to any

of three possible spino-LRt populations that function in posture (bilateral ventral reflex tract), reaching

(propriospinal), or grasping (ipsilateral forelimb tract)(Alstermark and Ekerot, 2013; Jiang et al., 2015).

We found that cervical *Atoh1*-lineage neurons appear to target the LRt ipsilaterally and as a population

can synapse on MNs as well, therefore, it seems likely that *Atoh1*-lineage neurons are at least

propriospinal spino-LRt neurons. For the spino-olivary pathway, we found cervical *Atoh1*-lineage neurons

targeted areas of the IO (dfDAO, DAO, cMAO[a], cMAO[b]) consistent with previously described tracing

studies and that retrograde tracing from the IO colocalizes with *Atoh1*-lineage neurons in laminae V-VIII

(Swenson and Castro, 1983a, b; Matsushita et al., 1992; Oldenbeuving et al., 1999; Flavell et al., 2014).

Overall, though, there are numerous other spino-LRt and spino-olivary neurons in the spinal cord

suggesting that there are additional sources that are not from the *Atoh1*-lineage (Azim et al., 2014; Pivetta

et al., 2014; Choi et al., 2020).

Local projections of Atoh1-lineage neurons

We find some interesting features of locally-projecting *Atoh1*-lineage neurons and compare and

contrast our findings with those of a previous study using an *Atoh1*-enhancer driving CRE recombinase

electroporated into mouse embryos (Kaneyama and Shirasaki, 2018). First, we find that thoracolumbar

Atoh1-lineage neurons project mostly locally, consistent with the findings by Kaneyama and Shiraskai,

who found that crossing dI1 axons are intersegmental with only a few traveling far from the soma. Second,

we found that *Atoh1*-lineage neurons in both the cervical and thoracolumbar areas of the mature spinal

cord make local circuit connections with MNs as previously described during embryogenesis and thus,

are a source of pre-motor neurons (Goetz et al., 2015). Kaneyama and Shiraskai found that dI1

commissural axons made synapses on axial MNs, while we found that *Atoh1*-lineage neurons as a

population can target the lateral motor column as well. Lastly, similar to our findings, Kaneyama and

Shiraskai also found that some dI1 commissural axons come from a fairly dorsolateral population, rather

than a medial population, and that these neurons in the lateral population appear to project both

contralaterally and ipsilaterally.

Comparison of motor behaviors mediated by proprioceptive spinal pathways

Loss of proprioceptive input in animal models leads to defects in limb coordination and lack of

adaptation to uneven surfaces (Abelew et al., 2000; Windhorst, 2007; Akay et al., 2014). Differences in

circuitry between CC (long-range) and caudal *Atoh1*-lineage neurons (indirect and local) suggests that

different aspects of proprioceptive-motor behaviors could be mediated by separable microcircuits. We

examined the function of CC and caudal *Atoh1*-lineage neurons by expressing a silencing gene,

tetanus toxin light chain, in these neurons. Motor function and motor learning were unimpaired when we

attempted to silence CC neurons (data not shown), possibly due to sparse expression of our silencing

allele, attenuated activity of the silencing allele, or redundancy or compensation of the proprioceptive-

motor system. In contrast, we found a slight motor defect in the accelerating rotarod when we silenced

caudal *Atoh1*-lineage neurons, consistent with a potential defect in reflexive behavior or postural

adjustments that would occur in local circuits.

To assess the function of cervical *Atoh1*-lineage neurons that contribute to the spino-LRt tract,

we assessed the behavior of the silenced caudal *Atoh1*-lineage mice in a pellet reaching task (Azim et

al., 2014; Becker et al., 2020). We analyzed the reach in five control mice and seven silenced caudal

Atoh1-lineage littermates, but we did not see any significant differences in pellet reach trajectories due

to the low sample size and potentially attenuated function of the TeTx allele (data not shown).

Cervical *Atoh1*-lineage neurons also contribute to the spino-olivary tract. We are not aware of any

studies that have manipulated the activity of spino-olivary neurons. However, mice that had glutamatergic

signaling in IO neurons knocked out had dystonia-like features, such as twisting, stiff limbs, and tremor,

and were unable to perform on the accelerating rotarod test (White and Sillitoe, 2017). We saw no overt

twisting, stiff limbs, or tremor in the genetically silenced caudal *Atoh1*-lineage mice, however, these mice

did have a defect in the accelerating rotarod and similarly, mice that had *Atoh1* knocked out caudal to

the lower medulla were completely unable to perform the rotarod test (Yuengert et al., 2015), suggesting

that the spino-olivary system is important for updating motor outcomes. Altogether, caudal *Atoh1*-lineage

neurons are heterogeneous comprising parts of the spino-LRt and spino-olivary tracts as well as

projecting locally within the spinal cord. Future experiments uncoupling the function of these different

components using more robust ablation or acute silencing strategies will lend further insight into the

function of discrete proprioceptive circuits.

Future directions

Our work and others suggest that the spinocerebellar and spino-LRt systems come from several

developmental progenitor domains and that any given developmental progenitor domain (*Atoh1*, for

example) contributes to several neuronal types (minimally, spino-LRt and spino-olivary tracts, as well as

local spinal neurons). Comparing and contrasting features of neurons with similar anatomical connectivity

but generated from different progenitor domains may lend insights into the varied functions mediated by

seemingly similar anatomical classes. Conversely, separating out different pathways, such as the spino-

LRt and spino-olivary tracts that are generated from a single progenitor domain (*Atoh1*) will be important

for determining the separate functions of these pathways.

We found that direct CC neurons do not send significant axon collaterals to the LRt or IO and

that information to the LRt and IO are in part coming from *Atoh1*-lineage neurons. Therefore, the MF and

CF input coming from the spinal cord into the cerebellar cortex comes from different information streams

and are not simply collateral copies of the direct CC pathway. Future work focused on how the direct and

indirect information streams from the spinal cord either converge or diverge within the cerebellar cortex

and the timing with which this information comes in from the two different information streams will be

particularly interesting.

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     Legends

Figure 1. Clarke's column (CC) is the major direct spinocerebellar pathway in mice. (A) Lineage

tracing of *Neurog1*-expressing progenitors (*Neurog1BAC-Cre* crossed to $R26^{LSL-LacZ}$) in the neural tube

identifies large CC neurons in the thoracic spinal cord (box in X-gal stain). β-Gal expressing cells (green)

colocalize with the CC marker, *Vglut1* mRNA (magenta, arrows). *Atoh1*-lineage neurons ($Atoh1^{Tom}$)

reside lateral and ventral to CC. (B) CC is marked by expression of *Gdnf* and *Vglut1* mRNA. (C) *Gdnf*

and *Vglut1* mRNA colocalize in CC neurons at P10 by RNAscope (arrowheads). (D) CC neurons

retrogradely labeled with fluorogold (FG) colocalize with *Vglut1* mRNA (FG$^+$*Vglut1*$^+$, arrowheads). A

subset of CC neurons are labeled with $Gdnf^{Tom}$ (FG$^+$TOM$^+$*Vglut1*$^+$, arrows). (E) CC neurons marked by

$Gdnf^{Tom}$ express both *Vglut1* and *Vglut2* mRNA (arrowheads). (F-I) Comparison of mossy fiber (MF)

terminals in the cerebellum of CC and caudal *Atoh1*-lineage neurons. Diagram of CC and caudal *Atoh1*-

lineage neurons labeled with tdTomato (TOM)(F, G). MF terminals in the cerebellum of CC neurons are

VGLUT1$^+$ (VG1) and VGLUT2$^+$ (VG2) (F', arrows). MF terminals of caudal *Atoh1*-lineage neurons are

VG2$^+$ (G', arrows), but VG1$^-$ (G', arrowheads). Fewer MF terminals are seen in the cerebellum from

caudal *Atoh1*-lineage neurons (G'') than CC neurons (F''). Representative thoracic sections of CC and

caudal *Atoh1*-lineage neurons (F''', G'''). Quantitation of MF terminals in the vermis of lobules I-V and

VIII/IX (H) and of the number of soma in the spinal cord (I) for CC and caudal *Atoh1*-lineage neurons. (J-

P) Comparison of spinocerebellar neurons retrogradely labeled with FG in mice with CC ($Gdnf^{Tom}$) or

Atoh1-lineage ($Atoh1^{Tom}$) neurons labeled with tdTomato (TOM). Diagram of FG cerebellar injections into

the anterior zone (AZ, lobules I-V) of either $Gdnf^{Tom}$ or $Atoh1^{Tom}$ mice to retrogradely label direct

spinocerebellar projections (J). FG injection in the cerebellum (K, N, green) retrogradely labels central

cervical (CeCv) cells in the cervical spinal cord (K', N', upper panels), CC in the thoracic spinal cord (K',

N', middle panels), and neurons in other areas of the spinal cord (K', N', lower panels). Retrogradely

labeled CC neurons (green) colocalizes with the genetic label for CC ($Gdnf^{Tom}$)(K', middle panel,

FG$^+$TOM$^+$, arrows), but only occasionally colocalizes with *Atoh1*-lineage ($Atoh1^{Tom}$) neurons in CeCv or

CC (N', arrows). Quantitation of the total number of FG$^+$ cells (L, O) and percentage of total FG$^+$ cells (M,

P) in a given region of the spinal cord (light orange or light blue) with the total number or percentage of

FG+TOM+ cells superimposed (dark orange or dark blue) for CC and caudal *Atoh1*-lineage neurons is

shown. Spinal cords were divided into cervical (C), thoracic (T), and lumbar (L) areas. The CeCv and CC

areas are delineated separately with all other cells categorized based on their C, T, or L location and

whether they were dorsal or ventral to the central canal. Spinocerebellar cells dorsal or ventral to the

central canal are generally not labeled by *Gdnf^Tom* or *Atoh1^Tom* (L, M, O, P). Abbrev: P, postnatal. Scale

bars: 1 mm (K, N), 100 μm (A-E, F"-F"', G"-G"', K', N'), 10 μm (F',G'). Results in graphs presented as

mean ± SEM.

Figure 2. CC mossy fibers terminate ipsilaterally and contralaterally in the cerebellar vermis. (A-

C) Coronal sections from *Gdnf^Tom* mice reveal CC mossy fiber (MF) terminals (TOM+) in lobules II-V, VIII,

IXa, and the copula (C, Cop, arrows). Parasagittal stripes (1, 2, 3) in lobule III are apparent. (D-E) Some

CC axons (TOM+) cross the midline (D, arrow, cryosection, and E, arrows, cleared sample, 200 μm

maximum intensity projection (MIP)). (F) Diagram of dual CTB-488 and CTB-647 injections in *Gdnf^Tom*

mice. (G) Coronal section showing the injection site of CTB-488 and CTB-647. (H) CC neurons are co-

labeled with the fluorescent CTB injected on the ipsilateral side as well as the fluorescent CTB injected

on the contralateral side (CTB-488+CTB-647+, arrows and arrowheads,). Some cells also colocalize with

the *Gdnf^Tom* genetic label for CC (TOM+CTB-488+CTB-647+, arrows) and some do not (TOM-CTB-

488+CTB-647+, arrowheads). (I) Quantitation of the percentage of ipsilaterally or contralaterally labeled

CTB+ cells out of all CTB+ cells labeled in the spinal cord with a particular CTB fluorophore (mean ± SEM).

Abbrev: Med, Medial; Int, Interpositus; Lat, Lateral. Scale bars: 1 mm (A, B, C, G), 100 μm (D, E, H).

Figure 3. CC neurons do not collateralize to the medulla or cerebellar nuclei (CN), but arborize

extensively in the cerebellar cortex. (A-D") Almost no CC *Gdnf^Tom* axons enter or are near the CN

(arrowheads, Med, Int, Lat)(A, B, C, and D are successive sections 160 μm apart). Areas of TOM+ signal

near CN do not colocalize with presynaptic markers VG1 (A', D') or VG2 (A", D") indicating these are

axons of passage and not presynaptic terminals. (E) CC axons (TOM+) avoid the CN in another *Gdnf^Tom*

mouse whose cerebellum was cleared (100 μm MIP). (F) CC axons (TOM+) avoid the CN (40 μm

cryosection) in another example *Gdnf^Tom* mouse. Images are from two female (A-E) and one male (F)

mice (n=3). (G-H') Only a few axonal terminations are seen in the LRt (G-G', arrow) and none in nucleus

X (H-H')(verified in n=3 mice, representative sections shown). (I-K) Example images of 100 μm MIP from

a *Gdnf^Tom* cleared cerebellum. CC MF terminals (TOM+) are seen in II-V, VIII, IXa, and Cop. (K)

Quantification of the MF/cell body ratio (n=3 mice, one *Gdnf^Tom* and two *Gdnf^CreER; Cdx2::FLPo; Ai65*

mice). Overall the whole cerebellum (Cb) has an estimated 71.9 MF terminals per CC cell body in the

spinal cord (orange bar, mean ± SEM). Most MF terminals from CC cells terminate in I-III, IV/V, VIII/IXa,

and Cop (light orange bars). Abbrev: Med, Medial; Int, Interpositus; Lat, Lateral. Lateral reticular nucleus,

LRt; X, Nucleus X; icp, inferior cerebellar peduncle; Sp5, spinal trigeminal tract. Scale bars: 1 mm (G, H,

I, I', J), 100 μm (A-F, G', H', J inset), 10 μm (A'-A'', D'-D'').

Figure 4. Thoracolumbar CC MFs send diverse projections to multiple lobules. (A-B') Spinal cord

injections of AAV9-Syn-DIO-EGFP at lower thoracic levels into *Gdnf^Tom* mice labels CC neurons on both

sides of the spinal cord (B', GFP+TOM+ (arrows), GFP+ only (arrowheads)). (C-F) Examples of individual

MF axons and terminals from three mice: a cleared female mouse sample (C, 76 μm maximum intensity

projection (MIP)), one female mouse (D, 40 μm cryosection), and one male mouse (E, F, 40 μm

cryosection). Axons appear to have branching points (black arrowheads) and regularly spaced MF

terminals (white arrowheads)(C-D). MF terminals from an individual axon are spaced 50-80 μm apart (E-

F). (G-L''') Thoracolumbar injections whose MF terminations were analyzed in coronal sections.

Distribution of GFP+ cells in the spinal cord on left (orange) and right (light orange) sides (G, I, K, M, O,

Q). Schematics of coronal cerebellar sections of the spinal cord injections (G, I, K) indicating the location

of CC MF terminations (H-H''', J-J''', L-L''', TOM+, red areas, respectively). Schematics of sagittal

cerebellar sections of the spinal cord injections (M, O, Q) indicating the location of CC MF terminations

(N, P, R, red areas, respectively). The subset of CC MF terminations that are from the lower thoracic-

lumbar region (GFP+, green, and GFP+TOM+, yellow) are spread over multiple lobules (II-V, VIII). Certain

CC MF termination regions do not have thoracolumbar CC neuronal projections (red areas, arrowheads

with an absence of any GFP+ terminations). (S, T) Examples of CC MF terminations (GFP+TOM+, arrows,

and GFP+-only arrowheads) in lobules III and VIII from 13-15 μm maximum intensity projections (MIP).

Scale bars: 100 μm (B, B', C, D, S, T); 10 μm (E, F).

Figure 5. Spinal cord *Atoh1*-lineage neurons make spino-LRt and spino-olivary pathways. (A)

Schematic of FG injections into the AZ of mice to identify LRt and IO neurons in the medulla. Axons of

caudal *Atoh1*-lineage neurons are genetically labeled (*Atoh1Cre; Cdx2::FLPo; Ai65* mice). (B) FG injected

into lobules I-V. (C) Sparse cell bodies in the SpVe are detected in *Atoh1Cre; Cdx2::FLPo; Ai65* mice. (D-

D'') TOM+ terminals seen in the lateral parabrachial (LPB) nucleus (D) are VG2+ (D'', arrows). (E-H'') A

high density of caudal *Atoh1*-lineage axons from the spinal cord are found in the LRt as well as areas of

the IO (dfDAO, DAO, cMAOa, cMAOb). (I-J) Caudal *Atoh1*-lineage axon terminals (TOM+, magenta)

expressing the presynaptic VG2 marker (cyan) are closely apposed to retrogradely labeled FG+ cells in

the LRt (I) and IO (J)(arrows). Axonal terminations in the LRt and IO were verified in n=4 mice.

Representative sections shown in E-H''. Abbrev: ECu, external cuneate nucleus; IO, inferior olive;

cMAOa, subnucleus a of caudal medial accessory olive; cMAOb, subnucleus b of caudal medial accessory

olive; cMAOc, subnucleus c of caudal medial accessory olive; MAO, medial accessory olive; DAO, dorsal

accessory olive; dfDAO, dorsal fold of the DAO; PO, principal olive; IRt, intermediate reticular nucleus;

LRt, lateral reticular nucleus; SpVe, spinal vestibular nucleus. Scale bars: 1 mm (B, D), 100 μm (C, D',

E-H''), 10 μm (D'', I, J).

Figure 6. Cervical spinal cord *Atoh1*-lineage neurons project to the LRt and IO. (A) Schematic of

FG injections into the right LRt and IO of *Atoh1Tom* mice. (B-G) Retrogradely labeled *Atoh1*-lineage

neurons reside mainly in the cervical to upper thoracic levels. Four injections targeting the LRt and IO in

the medulla are shown (B, C, E, F – upper panels). The spinal cords of these four injections have dual

labeled cells (FG+TOM+) mainly in the cervical to upper thoracic regions (light purple - left side, light blue

- right side) with many other FG+ only cells elsewhere in the spinal cord (dark purple – left side, dark blue

- right side). Representative spinal cord sections of the injection in C is shown in D-D' and the injection

in F is shown in G-G''. *Atoh1*-lineage neurons in both the medial (G'') and lateral (D' and G') clusters are

retrogradely labeled with FG (arrowheads). (H) Schematic of dual recombinase anterograde tracing.

Lenti[FugE]-Cre was injected into the right cervical spinal cord of *Atoh1[P2A-FLPo]*; *Ai65* mice. (I-O'') Anterograde

tracing of *Atoh1*-lineage neurons finds axons in the LRt and IO. Injection of the right spinal cord (I) where

mostly neurons on the right side are labeled (J) has axonal projections to the right LRt, which express

the presynaptic marker VG2 (K-K', arrowheads). Injection of the right spinal cord (L) where *Atoh1*-lineage

neurons on both the left and right are labeled (M) has axonal projections to both the right LRt and IO,

specifically the cMAOb (N, O). The *Atoh1*-lineage axonal terminals (TOM+) express the presynaptic

marker VG2 (white arrowheads) and are closely apposed to postsynaptic PSD95+ punta (grey

arrowheads)(N', O', O''). (P) Schematic of inputs and local outputs of cervical *Atoh1*-lineage neurons. (Q-

Q') Synaptic terminals of proprioceptive afferents (VG1+PV+, white arrowheads) are closely apposed to

TOM+ signal near medial and lateral *Atoh1*-lineage neurons. (R-R') Axons of cervical *Atoh1*-lineage

neurons synapse on motor neurons (VG2+TOM+ puncta closely apposed to PSD95+ puncta on CHAT+

motor neurons, white and grey arrowheads). CHAT+ neurons in R-R' were imaged from the area of the

spinal cord indicated in L. Abbrev: nd, not determined. Scale bars: 100 μm (B, C, D-D', E, F, G-G'', I, K,

L, O, Q, Q'), 10 μm (K', N', O'-O'', Q-Q' high magnification, R-R' high magnification).

Figure 7. Thoracolumbar *Atoh1*-lineage neurons project locally within the spinal cord. (A) Diagram

of rostral to caudal sections of the spinal cord (LF (left-dark blue, right-blue); grey matter and VF (left-

purple, right-light blue)). Lenti[FugE]-Cre was injected into *Atoh1[P2A-FLPo]*;*Ai65* mice, such that *Atoh1*-lineage

neurons in the right thoracolumbar spinal cord were labeled. (B) Quantitation of the total estimated

number of infected cells (TOM+) on the left and right sides. The virus appears to be taken up by axons of

passage that project from the contralateral side (see C). (C) Representative sections of the spinal cord

from a Lenti[FugE]-Cre-injected *Atoh1[P2A-FLPo]*;*Ai65* mouse. Cell bodies on the right side of the spinal cord

and axons in the right (Rt) LF (blue arrowhead) are labeled. Axons in the Rt VF (light blue arrowhead)

appear to be axons from cell bodies that are located on the contralateral side of the spinal cord (purple

arrows). Some axons in the left LF (dark blue arrowhead) are also seen. (D) L1-3 is the site of peak

infection (number of TOM+ cell bodies labeled per section) and the number of cell bodies labeled tapers

off both rostrally and caudally further away from the injection site. (E) Very few axons on the right side

(blue (LF) and light blue (VF)) are detected in rostral sections (C6-8) compared to the site of injection L1-

3. (F-H') Distribution of infected cells in T11-13, L1-3, and L4-6 regions of the spinal cord (F, G, H, arrows

indicate injection on right side). Quantitation of the soma area size of infected medial (M), lateral (L), and

ventral (V) *Atoh1*-lineage neurons on the left and right sides of the spinal cord (F', G', H'). Inset in F

shows two cell bodies labeled on the left side contralateral to the injection that have projections extending

dorsolaterally and medioventrally (arrows). (I-I'') Some of the sparsely labeled thoracolumbar *Atoh1*-

lineage neurons have presynaptic terminals near (TOM$^+$VG2$^+$, arrowheads) or closely apposed (F'',

TOM$^+$VG2$^+$, arrowhead) to motor neurons (CHAT$^+$)(detected in n=4 samples, representative image

shown). See Materials and Methods and Results for details of quantitation for B, D, E, F', G', H'. Abbrev:

LF, lateral funiculus; VF, ventral funiculus. Scale bars: 100 μm (C, I), 10 μm (I', I''). Results in graphs

presented as mean ± SEM.

Figure 8. Silencing of caudal *Atoh1*-lineage neurons leads to a subtle motor phenotype. (A)

Schematic of dual recombinase strategy to silence caudal *Atoh1*-lineage neurons. (B) Mice heterozygous

for the TeTx allele in caudal *Atoh1*-lineage neurons are significantly impaired in the rotarod assay (two-

way ANOVA, $F_{(1,448)} = 5.025$, p=0.0255 for genotype, Control: n=36 (20F:16M), Het: n=22 (10F:12M)).

(C-C') Upper cervical areas of the spinal cord in *Atoh1^{Cre};Cdx2::FLPo;TeTx* mice only have *Atoh1^{Cre}*

expressed and thus, are mCherry$^+$ (C). Lumbar areas of the spinal cord that have both *Atoh1^{Cre}* and

Cdx2::FLPo expressed have lost the mCherry signal (C'). In both panels (C-C'), mCherry signal was

amplified using a dsRed antibody. Scale bars: 100 μm (C-C').

Figure 9. Long-range direct and local indirect proprioceptive pathways. (A) *Neurog1*-lineage

neurons of the developing neural tube generate CC neurons that project directly from the spinal cord to

the cerebellum while *Atoh1*-lineage neurons form mostly indirect spinocerebellar and local spinal

projections. (B) Schematic of major anatomical findings. CC neurons (orange) project ipsilaterally mainly

from the thoracic spinal cord directly to the cerebellum. Some CC axons cross the midline (dotted

orange). Cervical *Atoh1*-lineage neurons project mainly to the IO and LRt in the medulla (dark and light

blue). The LRt neurons then project either ipsilaterally or contralaterally to terminate in the cerebellar

cortex as MFs. The neurons in the IO then project contralaterally as well to synapse as climbing fiber

(CF) axons onto Purkinje cells (PCs) in the cerebellar cortex. Thoracolumbar *Atoh1*-lineage neurons

project mostly within the spinal cord (dark blue, horizontal arrows), although a few project to more rostral

regions within the medulla and cerebellum (dotted blue arrows). (C-D) Illustrations of long-range direct

and local indirect spinocerebellar pathways. CC neurons project rostrally in the ipsilateral funiculus where

they branch extensively in the cerebellum, avoiding the medulla and cerebellar nuclei (Med, Int, Lat) to

terminate in vermis I-V, VIII, IXa, and Cop (C). Some CC axons cross the midline within the cerebellum.

Atoh1-lineage neurons are heterogeneous with diverse projections. Cervical *Atoh1*-lineage neurons in

the spinal cord project both ipsilaterally and contralaterally to target mainly the LRt and IO in the hindbrain

(D). While we found that some of the *Atoh1*-lineage spino-LRt axons project ipsilaterally, whether some

spino-LRt projections come from the contralateral side was not determined in this study (question mark

along axons). The spino-IO tract is likely contralateral based on previous literature. *Atoh1*-lineage

neurons in the thoracolumbar area project mostly locally within the spinal cord. A few of the axons from

thoracolumbar *Atoh1*-lineage neurons may project to the medulla or cerebellar cortex (dotted blue).

Presynaptic terminals from *Atoh1*-lineage neurons are found on motor neurons (MN) in both the cervical

and thoracolumbar spinal cord. Abbrev: IRt, intermediate reticular nucleus; LRt, lateral reticular nucleus;

IO, inferior olive.

Multimedia

Movie 1. *Gdnf^{Tom}* cleared spinal cord. CC cell bodies line the thoracic midline with axons projecting to

the lateral funiculus (LF) and then turning rostrally. The *Gdnf^{Tom}* mouse line also labels smooth muscle

cells lining blood vessels within the spinal cord and along the meninges. TOM⁺ cells along the central

canal are also labeled.

Movie 2. *Gdnf^{CreER}; Cdx2::FLPo; Ai65* cleared hindbrain. CC axons terminate as mossy fibers (MF) in

the vermis of lobules I-V, VIII, IXa, and copula (cop). Axons from the spinal cord project directly to the

cerebellar cortex avoiding the medulla and cerebellar nuclei.

Movie 3. *Atoh1^{Cre}; Cdx2::FLPo; Ai65* **cleared spinal cord.** *Atoh1*-lineage neurons in the spinal cord cluster into medial (M), lateral (L), and ventral (V) populations whose axons travel in the lateral and ventral funiculi (LF and VF). tdTomato is misexpressed in sensory neurons.

Movie 4. *Atoh1^{Cre}; Cdx2::FLPo; Ai65* **cleared brain.** The most prominent axonal projections in *Atoh1^{Cre}; Cdx2::FLPo; Ai65* mice are to the lateral reticular nucleus (LRt) and inferior olive (IO). Although MF projections are seen in cryosections, they are not obvious in the cleared spinal cord. There is diffuse tdTomato fluorescence in the thalamus and cortex. The misexpression of tdTomato in sensory neurons seen in the spinal cord is seen as projections to the cuneate (Cu), gracile (Gr), and external cuneate nucleus (ECu).

Movie 5. **Three-dimensional projection of cells in the LRt of** *Atoh1^{Cre}; Cdx2::FLPo; Ai65* **mice.** Cropped cell in Fig. 5I is taken from this z-stack of 0.5 μm optical slices with 0.25 μm step. Dense terminations are seen in the LRt. FG (yellow), *Atoh1^{Cre}; Cdx2::FLPo; Ai65* axons (TOM+, magenta), VG2 (cyan).

Movie 6. **Three-dimensional projection of cells in the IO of** *Atoh1^{Cre}; Cdx2::FLPo; Ai65* **mice.** Cropped cell in Fig. 5J is taken from this z-stack of 0.5 μm optical slices with 0.25 μm step. Dense terminations are seen in the IO. FG (yellow), *Atoh1^{Cre}; Cdx2::FLPo; Ai65* axons (TOM+, magenta), VG2 (cyan).

Fig. 1

A Embryonic

*Atoh1^Tom^*

CC

T11-13   Adult

Neurog1BAC-Cre; LacZ

βGal Ab

Vglut1 RNAscope

Merge

X-gal

CC

T11-13   P14

B *Gdnf* ISH

CC

P10

Vglut1 ISH

CC

P14

C

Vglut1

Gdnf

Merge

P10

D *Gdnf^Tom^*

FG

Vglut1

TOM

Merge

E *Gdnf^Tom^*

Vglut1

Vglut2

TOM

Merge

Anterograde

F *Gdnf^CreER^; Cdx2::FLPo; Ai65*

F',F''

F'''

F' TOM

VG1

VG2

F'' TOM   III

F''' TOM

T11-13

G *Atoh1^Cre^; Cdx2::FLPo; Ai65*

G',G''

G'''

G' TOM

VG1

VG2

G'' TOM   III

G''' TOM

T11-13

H

■ *Gdnf^CreER^;Cdx2::FLPo*
■ *Atoh1^Cre^;Cdx2::FLPo*

MF terminals

I-V   VIII/IX

I

soma/section

C6-8 T1-4 T5-7 T8-10 T11-13 L1-3 L4-6 S

Retrograde

J

FG inj into AZ

K,N

*Gdnf^Tom^* or *Atoh1^Tom^*

K',N'

K *Gdnf^Tom^*   FG

III

N *Atoh1^Tom^*   FG

III

K' FG TOM   C2-5

CeCv

CC

L1-3

N' FG TOM   C2-5

CeCv

CC

L1-3

L *Gdnf^Tom^*

Total FG cells

▲ Total FG⁺
● FG⁺TOM⁺

CeCv | C1-8 T1-13 L1-3 | C1-8 T1-13 L1-6 | C1-8 T1-13 L1-6
CeCv   CC   Dorsal   Ventral

O *Atoh1^Tom^*

Total FG cells

▲ Total FG⁺
● FG⁺TOM⁺

CeCv   CC   Dorsal   Ventral

M

% of Total FG cells

▲ % Total FG⁺
● % FG⁺TOM⁺

43%

12%

CeCv   CC   Dorsal   Ventral

P

% of Total FG cells

▲ % Total FG⁺
● % FG⁺TOM⁺

47%

3%

CeCv   CC   Dorsal   Ventral

Fig. 2

A B C
VI
V
IV VII
III VIII
II IXa
IXb
X IXc

Gdnf^Tom   TOM

IV/V
III 1 2 3
II

B
IV/V
III 1 2 3   Int
Med   Lat

C
VIII
Cop
IXa
P30

D   Δ40 μm   TOM
P30

E   MIP Δ200 μm   TOM
P23

F   CTB-488 CTB-647
Gdnf^Tom
H

G
IV/V CTB-488
III   TOM
      CTB-647
-6.00 mm   Adult

H
T11-13

I
% ipsi or contra / total
▲ % CTB-488
● % CTB-647
%ipsi %contra %ipsi %contra

Fig. 3

A TOM — A-D F; A',A"; Int; Lat

B Med; Int; Lat

C Med; Int

D D',D"; Med; Int — P30

E MIP Δ100 μm; Int — Cleared

F TOM; Int; Int; Lat — P30

A' VG1 / TOM

A" VG2 / TOM

D' VG1 / TOM

D" VG2 / TOM

I MIP Δ100 μm; G H; III; G'; E — P23 Cleared

I' MIP Δ100 μm — Cleared

J MIP Δ100 μm; Cop; VIII; IXa — Cleared

K MF/cell body ratio

- I-III: 34.6
- IV/V: 24.7
- VI
- VII
- VIII: 4.6
- IXa: 0.6
- IXb
- Sim: 0.1
- CrusI
- CrusII
- PML
- Cop: 7.2
- Whole Cb: 71.9

Vermis

G TOM / NEUN; G'; LRt

G' VG1 / TOM / NEUN

H TOM / NEUN; X; H'; icp; Sp5

H' MIP 9 μm; VG1 / TOM / NEUN

Fig. 4

A Gdnf^Tom

AAV9-Syn-DIO-EGFP

B GFP TOM NEUN

T12-13 — P30

B' GFP NEUN TOM Merge

C TOM Cleared — MIP 76 µm — P23

D TOM — P30

E ~50 µm — P29

F ~80 µm — P29

Coronal — CC TOM⁺ MF terminations ● GFP⁺ ○ GFP⁺TOM⁺

G GFP⁺ cell bodies/sect — L / R — T5-6 T7-8 T9 T10-11 T12-13 L1-2 L3-4

I GFP⁺ cell bodies/sect

K GFP⁺ cell bodies/sect

H -5.68 mm — IV/V, III, II

H' -5.80 mm — IV/V, III

H'' -6.00 mm — IV/V, III

H''' -7.92 mm — VIII, IX, Cop

J, **J'**, **J''**, **J'''**

L, **L'**, **L''**, **L'''**

Sagittal

M GFP⁺ cell bodies/sect — L / R

N VI, VII, IV/V, VIII, III, II, IX, I, X

O GFP⁺ cell bodies/sect

P

Q GFP⁺ cell bodies/sect

R

S Coronal — GFP TOM NEUN — III (MIP 14 µm), VIII (MIP 13 µm)

T Sagittal — III (MIP 13 µm), VIII (MIP 15 µm)

Fig. 5

Fig. 6

A Retrograde — FG inj LRt and/or IO — Atoh1^Tom

B nd nd — Cells/section — L R — FG⁺TOM⁺ / FG⁺ only — C2-5 C6-8 T1-4 T5-7 T8-10 T11-13 L1-3 L4-6

C Cells/section — C2-5 C6-8 T1-4 T5-7 T8-10 T11-13 L1-3 L4-6 S

D FG TOM Merge — D' — T1 — Adult

E Cells/section — C2-5 C6-8 T1-4 T5-7 T8-10 T11-13 L1-3 L4-6 S

F Cells/section — C2-5 C6-8 T1-4 T5-7 T8-10 T11-13 L1-3 L4-6 S

G FG TOM Merge — G' — G'' — C6-8 — Adult

H Anterograde — Lenti^FugE-Cre — Atoh1^P2A-FLPo;Ai65

I TOM — C2-5 — P30

J Cells/section — L R — C2-5 C6-8 T1-4 T5-7 T8-10 T11-13 L-S

K TOM NEUN — K' VG2 NEUN TOM Merge — Rt LRt — MIP 18 μm

L TOM — R,R' — C6-8 — P30

M Cells/section — C2-5 C6-8 T1-4 T5-7 T8-10 T11-13 L-S

N TOM NEUN — N' PSD95 VG2 TOM Merge — Rt LRt — MIP 12 μm

O TOM NEUN — O' VG2 NEUN TOM Merge — O'' PSD95 VG2 TOM Merge — Rt cMAOb — MIP 14 μm

P VG1⁺PV⁺ afferents — Lateral — Medial — MN

Q Atoh1^Tom — Medial — VG1 PV TOM Merge — C6-8

Q' Lateral — VG1 PV TOM Merge — C6-8

R Lenti^FugE-Cre Atoh1^P2A-FLPo;Ai65 — VG2 CHAT TOM Merge — C6-8

R' PSD95 CHAT TOM Merge — C6-8

Fig. 7

A *Atoh1^{P2A-FLPo}; Ai65*

Rostral
C6-8, T1-4, T5-7, T8-10, T11-13, L1-3, L4-6, S
Caudal
LF, VF
Lenti^{FugE}-Cre

B Est. Total# TOM⁺ Cells — Left, Right

C TOM
C6-8, Left LF, Rt LF
T11-13, Rt VF
L1-3, P30

D Cells/section — Left, Right
C6-8, T1-4, T5-7, T8-10, T11-13, L1-3, L4-6, S

E # axons — LF/VF Left, VF/LF Right
C6-8, T1-4, T5-7, T8-10, T11-13, L1-3, L4-6, S

F T11-13 — Lateral (L), Medial (M), Ventral (V)

G L1-3

H L4-6

F' T11-13 — soma area (μm²) — V L M / M L V — Left / Right

G' L1-3 — soma area (μm²) — V L M / M L V — Left / Right

H' L4-6 — soma area (μm²) — V L M / M L V — Left / Right

I TOM CHAT, L1-3

I' VG2 TOM CHAT

I" VG2, CHAT, TOM, Merge

Fig. 8

A

Atoh1^Cre;
Cdx2::FLPo;
TeTx

Upper Cervical
CRE+
mCherry+

Lumbar
CRE+FLPo+
mCherry-

mCherry+

Upper Cervical

B

Rotarod

Time (s)

* [Control (36)
    Het (22)
p = 0.0255 (geno)

1 2 3 4   1 2 3 4
Day 1   Day 2

C'

mCherry-

Lumbar

Fig. 9

A Embryonic neural tube

VZ   Mantle

Atoh1 → *Atoh1*-lineage

Neurog1 → CC

dI1
dI2

dI6
V0
V1
V2
MN

B

Cb

Medulla

IO LRt

SC

CC

Atoh1-lineage

C Direct and long-range

IV/V

III
II

Int Lat
Med

-5.88 mm

VIII

Cop IX

IRt

LRt IO

-7.32 mm

Cervical

Thoracic

D Indirect and local

IV/V

III
II

-5.88 mm

VIII

IX

IRt

LRt IO

-7.32 mm

Cervical

MN

?

Thoraco-
Lumbar

MN