Normal Midbrain Dopaminergic Neuron Development and Function in miR-133b Mutant Mice

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Midbrain dopaminergic (mDA) neurons control movement and emotion, and their degeneration leads to motor and cognitive defects in Parkinson’s disease (PD). miR-133b is a conserved microRNA that is thought to regulate mDA neuron differentiation by targeting Pitx3, a transcription factor required for appropriate development of mDA substantia nigra neurons. Moreover, miR-133b has been found to be depleted in the midbrain of PD patients. However, the function of miR-133b in the intact midbrain has not been determined. Here we show that miR-133b null mice have normal numbers of mDA neurons during development and aging. Dopamine levels are unchanged in the striatum, while expression of dopaminergic genes, including Pitx3, is also unaffected. Finally, motor coordination and both spontaneous and psychostimulant-induced locomotion are unaltered in miR-133b null mice, suggesting that miR-133b does not play a significant role in mDA neuron development and maintenance in vivo.

Introduction

Midbrain dopaminergic (mDA) neurons of the substantia nigra pars compacta (SNpc) and ventral tegmental area (VTA) are critical for the regulation of motor function and emotion-related behaviors. mDA neurons are affected in several debilitating neurological disorders including Parkinson’s disease (PD), which results from selective loss of SNpc DA neurons (Moore et al., 2005). While much progress has been made (Smidt and Burbach, 2007; Andressoo and Saarma, 2008; Cookson and Bandmann, 2010), the molecular mechanisms underlying the development and maintenance of mDA neurons and their loss in PD have not been fully elucidated.

Recently, microRNAs (miRNAs) have been implicated in mDA neuron differentiation and PD (Harraz et al., 2011). miRNAs are small, noncoding RNAs with diverse roles in nervous system development, function, and disease (Cao et al., 2006; Im and Kenny, 2012). miRNAs regulate gene expression by binding to the 3′-UTR of mRNA targets, decreasing mRNA stability and protein translation (Bushati and Cohen, 2007). Deletion of the miRNA processing enzyme Dicer in postmitotic mDA neurons in mice causes extensive cell death, suggesting that miRNAs are critical for maintaining the mDA neuron population (Kim et al., 2007). One miRNA, miR-133b, was found to be enriched in the midbrain and specifically depleted in PD patients (Kim et al., 2007). In a mouse embryonic stem (ES) cell culture system, miR-133b negatively regulated ES cell differentiation into dopamine (DA) neurons. miR-133b has been proposed to mediate these effects by targeting Pitx3, a transcription factor required for differentiation of SNpc DA neurons; Pitx3 mutant mice lack SNpc DA neurons and display severe motor defects (van den Munckhof et al., 2003). miR-133b is a promising candidate in regulating mDA neuron differentiation and degeneration, but its role in vivo has not been determined.

Here we show that the mDA system develops normally in miR-133b null mice. mDA neuron morphology, number, and gene expression are unaltered early in development and in adult and aged miR-133b mutant mice. Whole-tissue levels of DA, norepinephrine (NE), and 5-hydroxytryptamine (5-HT) monoamine neurotransmitters in knock-out (KO) striatum are unchanged, while baseline and amphetamine-induced extracellular DA release are also unaffected. Furthermore, motor and anxiety-like behaviors in miR-133b null mice are equivalent to those of wild-type controls. From these data we conclude that miR-133b is not critical for mDA neuron development or function in vivo. In situ hybridization for mature miR-133b using locked nucleic acid (LNA) probes revealed modest expression in the SNpc as well as other brain regions, suggesting that miR-133b may have as yet undetermined functions in the mammalian nervous system.
Materials and Methods

**miR-133b knock-out mouse generation**

miR-133b conditional KO mice were generated by homologous recombination of a targeting construct containing the floxed miR-133b stem loop in R1129/SvJ mouse ES cells using standard procedures (Nagy et al., 1993; Heyer et al., 2011). A targeting vector containing a loxP-flanked miR-133b stem loop and a FRT-flanked pGK-neo cassette was used to replace the endogenous miR-133b stem loop in ES cells. The floxed stem loop sequence was

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5’-AGGCTTGGACAAGTGGTGCTCAAACTCCAAGGACTCAGTCGACGTCACAATCCCTAAAGGGAGTGGCCCCCTGGCTGCTGTTCAAGGGTGAGGTTCCTTGGCTCCCCTTCAAACCAGCTACTGGGAAGTTTGGTCCCCTTCAACCAGCTACGAGGAGTTGGAGAAGAAAATAGCTGCTACAGCCTTGCTTATGAAAAGTAATTGCTGGTTTTGCCATCATAGCCTT
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(mature miR-133b in bold). Correctly targeted ES cells were identified by PCR screening and confirmed by Southern blot of genomic DNA. A correctly targeted clone was injected into C57BL/6J blastocysts, and chimeras mated to C57BL/6J mice. Germline transmission was confirmed by PCR genotyping of tail DNA. miR-133b Neo-fl offspring were mated to FLPe deleter mice (The Jackson Laboratory) (Farley et al., 2000) to remove the neomycin resistance cassette, and miR-133b fl/+ offspring were confirmed by PCR genotyping. miR-133bΔ mice were crossed with a

Figure 1. Generation of a miR-133b knock-out mouse. **A**, Schematic of miR-133b stem-loop targeting strategy. The box containing miR-133b represents the miR-133b stem-loop region. FLP, Mouse expressing germline FLP; Cre, mouse expressing germline Cre. Arrows show locations of PCR primers for genotyping. **B**, Sequence of the miR-133b precursor region flanked by loxP and Neo cassette. Mature miR-133b sequence is in large letters. **C**, Southern blot analysis following EcoRI digestion of WT and correctly targeted ES cell genomic DNA. The 5’ probe binding site is indicated in A. **D**, PCR genotyping of miR-133b floxed, wild-type, heterozygous, and knock-out mice. **E**, RT-PCR demonstrates loss of miR-133b stem-loop expression in brain and muscle of miR-133b KO mice. **F**, Sequencing chromatogram of WT allele genotyping PCR product. miR-133b is underlined in black. **G**, Sequencing chromatogram of KO allele genotyping PCR product. The miR-133b precursor has been deleted following Cre/loxP-mediated recombination. **H**, Quantitative pre-miR-133b RNA expression in whole brain and tibialis muscle of 3-month-old WT and KO mice. Expression was normalized to Gapdh and results were scaled to an average WT value of 1 (muscle); n = 3 WT and 3 KO mice. Average C values were 28.80 (WT brain), 35.27 (KO brain), 23.46 (WT muscle), and 34.70 (KO muscle). Error bars indicate SEM.

**miR-133bΔ**
Cre deleter strain (The Jackson Laboratory) (Tallquist and Soriano, 2000) to create a miR-133-null allele, confirmed by PCR genotyping. miR-133b heterozygous mice were backcrossed to C57Bl/6 for at least 8 generations, and all data were from wild-type (WT) and KO mice bred from miR-133b heterozygotes. Genotyping primers for detecting the floxed, WT, and null alleles were as follows: 133b-F, CAAAGCTCTGT-GAGAGGTAGTCAAGG; and 133b-R, CTCCAGTCTTCCATCATCTTG (where F is forward and R is reverse). WT and KO bands were sequenced using the 133b-F and 133b-R primers to confirm deletion and correct orientation following loxP-mediated excision. Mice were housed 2–5 per cage in an Association for Assessment and Accreditation of Laboratory Animal Care-approved vivarium on a 12 h light–dark cycle. All experiments were carried out according to approved protocols from the Duke University and The Scripps Research Institute Florida Institutional Animal Care and Use Committees.

**Antibodies**

Mouse monoclonal anti-tyrosine hydroxylase (TH) antibody (1:10,000, Immunostar) and rabbit anti-Pitx3 antibody (1:400, a gift from Dr. Marten Smidt, University Medical Center Utrecht, Utrecht, The Netherlands) were used for immunostaining and Western blot. Cy3-conjugated anti-rabbit antibodies (1:400, Jackson ImmuNoResearch) and Alexa Fluor 488-conjugated anti-mouse antibody (1:400, Invitrogen) were used for immunostaining. Mouse anti-GAD1 (1:1000, Millipore), goat anti-ChAT (1:1000, Millipore), anti–β-tubulin (1:5000, Sigma), anti–β-actin (1:5000, Sigma), anti–GAPDH (1:2000,Santa Cruz Biotechnology), and HRP-conjugated goat anti-mouse and anti-rabbit (1:5000, Jackson ImmuNoResearch) antibodies were used for Western blot. Western blots of midbrain protein samples were performed using infra-red dye-conjugated secondary antibodies (1:10000, Li-Cor) and a Li-Cor Odyssey infrared imager.

**Tyrosine hydroxylase immunohistochemistry**

Two-month-old male WT and miR-133b KO mice were deeply anesthetized with isoflurane (Butler Animal Health Supply) and transcardially perfused with physiological Ringer’s solution followed by fixative (4% paraformaldehyde in PBS). Whole brain was fixed overnight, equilibrated in 30% sucrose, and embedded in O.C.T. (Sakura). Thirty micrometer frozen coronal serial sections were collected using a cryostat (Leica CM1850). Heat-mediated antigen retrieval was performed by autoclaving in 1.8 M citric acid and 8.2 M sodium citrate. TH immunohistochemistry was performed as previously described (Johnson et al., 2010). Montage images were acquired using an Axioslager microscope fitted with a motorized stage controlled by the MosaicX functionality within AxioVision 5.1 software (Carl Zeiss MicroImaging).

**Unbiased stereology and cell counting**

Unbiased stereological estimation of the total number of TH immunoreactive (TH-IR) cell bodies in the SNpc and VTA was performed using the optical fractionator method, as described previously (Johnson et al., 2010). Every second section was collected through the midbrain and every fourth section was analyzed for cell counting, totaling 10 sections per animal. Cells at least 10 μm in diameter stained for TH were classified as TH-IR. Embryonic day (E)18.5 embryos were fixed in 4% PFA, 0.1% Triton X-100 in PBS overnight at 4°C. Sections were incubated with Cy3 anti-rabbit and Alexa Fluor 488 anti-mouse antibodies and mounted with Fluoro-Gel (Electron Microscopy Sciences). Montage images were acquired of every second section throughout the rostral section of the SNpc, totaling five images per animal. All SNpc TH-IR, and Pitx3-IR cells were counted in each image using the counter tool in Photoshop (Adobe). All analyses were performed blind to genotype.

**Western blotting**

Three-month-old male and postnatal day (P)0 WT and KO mice were killed and whole brain or ventral midbrain dissected and flash frozen in liquid nitrogen. Tissue was homogenized in RIPA buffer (Sigma) supplemented with protease inhibitors (Complete, Roche). Twenty micrograms of lysate were run on 10–12% SDS-polyacrylamide gels, and Western blotting was carried out according to standard procedures. Bands of whole brain Western blots were visualized using ECL Plus (GE Healthcare Life Sciences) and a LAS-3000 Intelligent Dark Box (Fujifilm). Bands of midbrain Western blots were visualized using a Li-Cor Odyssey infrared imager. Bands were quantified by densitometry analysis using ImageJ software and normalized to β-actin (for TH and GAD1), β-tubulin (for Pitx3) or GAPDH (midbrain samples).

**RNA extraction and real-time PCR**

Three-month-old male and P0 WT and KO mice were sacrificed and whole brain was flash frozen in liquid nitrogen. Total RNA was extracted using TRizol reagent (Invitrogen) and treated with Turbo DNase (Ambion). One microgram of RNA was used for reverse transcription with oligo-dT and random primers and AffinityScript enzyme (Stratagene). cDNA was used for quantitative PCR (Power SYBR Green, ABI 7300 real-time PCR machine, Applied Biosystems). The following intron-spanning primers were used: Gapdh-F, CAGGCCTTCCGTGGTCTC; Gapdh-R, TGATGTCATCATACCTGGCAAGT; TF-F, CTCTCCACCG-GTTGACTGGTTCAC; TF-R, GGCTGGTAGGTTGATCTTGGTAG; DAT-F, GTATGGTGGTGTTGAGCATT; DAT-R, CTTTCACGCGGTAGGCGCATAG; GAD1-F, CAACCGATGTGTTGCAAGCCATC; GAD1-R, GGCTAGAGGATTAAAGCCAGCCTG; ChAT-F, CCTGTTTGCCAAGCCATGAC; ChAT-R, CTGCCATGAACATCTCAGGTTG;
Nissl areas were integrated and interpolated from known standards using Agi-

homovanillic acid were 3.5, 4.3, and 7.2 min, respectively. Analyte peak

teristic retention times of dihydroxyphenylacetic acid, dopamine, and

the following primers:

brain cDNA was also used for standard PCR am-

GCTTTGCTAAAGCTGGTAAAATGG. Whole

miR-133b

GACAAGTGGTGCTCAA; and

miR-133a1

GCTAGGTATTTGC; and

miR-133b

as follows:

was delivered at a flow rate of 0.6 ml/min. Following column separation,

1100 liquid chromatography apparatus and run on an MD-150 HPLC

microliters of each sample was automatically injected using an Agilent

Dopamine contents from dialysates were quantified by HPLC-ECD. Ten

Liquid chromatography and electrochemical detection

Dopamine contents from dialysates were quantified by HPLC-ECD. Ten

microliters of each sample was automatically injected using an Agilent 1100 liquid chromatography apparatus and run on an MD-150 HPLC column (3 x 150 mm, 3 μm particle size). MD-TM mobile phase (ESA) was delivered at a flow rate of 0.6 ml/min. Following column separation, monoamines were detected using an ESA 5021A guard cell, an ESA 5011A analytical cell, and an ESA Coulouchem III detector (E_{OC} = +350 mV, E_{I} = -150 mV, E_{S} = +220 mV; filter time constant, 5 s). Character-

teristic retention times of dihydroxyphenylacetic acid, dopamine, and

homovanillic acid were 3.5, 4.3, and 7.2 min, respectively. Analyte peak

areas were integrated and interpolated from known standards using Agi-

lent ChemStation software and GraphPad software. All procedures were

performed blind to genotype.

Behavioral analyses

Open field. The open field test was performed as described previously
(Peça et al., 2011). Briefly, 3- to 4-month-old WT and KO mice were
placed in automated 16 x 16 inch chambers (AccuScan Instruments) for
60 min. Total distance traveled (centimeters) and time spent in the center
were detected in 5 min bins. Two weeks later, the same mice were placed
in 8 x 8 inch chambers, and distance traveled was similarly detected for
60 min. Three milligrams per kilogram of amphetamine was immediately
administered by i.p. injection, the mice were returned to their chambers,
and locomotor activity was recorded for a further 120 min.

Zero maze. Five-month-old WT and KO mice were placed in the closed
arm of an elevated zero maze indirectly illuminated at 100 lux, and their
behavior was videotaped over 5 min (Peça et al., 2011). The time spent in
the closed and open arms was scored blind to genotype using The Ob-

server software (Noldus).

Dark–light emergence. The dark–light emergence task was carried out
as described previously (Peça et al., 2011). Three- to four-month-old WT
and KO mice were tested in an automated dual chamber apparatus (Med
Associates) containing a gate between a “light” (1000 lux) and “dark”
chamber. The mice were placed in the dark chamber and the gate lifted,
allowing the mice to freely move between both chambers. The duration
in the light and dark chambers was recorded over 5 min.

Marble burying. Marble burying behavior of 5-month-old male WT
and KO mice was assessed (Deacon, 2006). Twenty-four 2 cm diameter
marbles were evenly spaced on the surface in an 8.5 inch x 16 inch
chamber filled 5 inches deep with aspen shavings. A mouse was placed in

Figure 3. Normal midbrain DA neuron morphology and number in miR-133b KO mice. A, B, TH immunohistochemistry and
Nissl staining of midbrain (A) and dorsal striatum (B) of 2-month-old WT and KO littermates. C, TH and Pitx3 immunofluorescence
in E18.5 SNpc of WT and KO mice. D, Unbiased stereological counts of TH-IR cells in SNpc and VTA of 2-month-old male mice; n =
4 WT and 5 KO mice. E, Unbiased stereological counts of TH-IR cells in SNpc of 12-month-old mice; n = 7 WT and 5 KO mice. 
F, Cell
count of TH-IR, Pitx3-IR, and TH + Pitx3 coexpressing cells in SNpc of E18.5 WT and KO mice. *p < 0.05, Student’s t-test; n = 3 WT
and 3 KO embryos. Scale bars: 0.5 mm in A, 1 mm in B, and 100 μm in C. Error bars indicate SEM.
miRNA fluorescence in situ hybridization

Fluorescence in situ hybridization for miR-133b was performed on 16 μm sagittal sections of 3-month-old WT and KO mouse brains according to a previously described method using 1-ethyl-3-(3-dimethylaminopropyl)carbodiimide fixative to prevent loss of miRNAs (Pena et al., 2009). LNA oligonucleotides (Exiqon) were labeled with digoxigenin using a 3’-end labeling kit (Roche). In situ hybridization was carried out with a miR-133b antisense probe, a miR-124 antisense probe as a positive control, and a scrambled miR-133b probe as a negative control. Images were acquired with an Olympus BX51 microscope and the Virtual Tissue module of Stereo Investigator software.

Statistical analyses

All data were analyzed using Prism software (GraphPad Software). Stereological cell counts, miRNA and protein expression data, zero maze data, dark–light emergence test data, and rotarod data were analyzed by an unpaired two-tailed t test. Tissue monoamine levels were analyzed by one-way ANOVA, and microdialysis and open field data were analyzed by repeated-measures ANOVA followed by Bonferroni post hoc test. Data are presented as mean ± SEM.

Results

Generation of miR-133b mutant mice

miR-133b is embedded in an intergenic noncoding gene, 7H4, located on chromosome 1 (Velleca et al., 1994). loxP sites were placed around the miR-133b stem loop precursor region, and a FRT-flanked PGK-Neo cassette was inserted 3’ to the floxed stem loop (Fig. 1A, B). The targeting vector was introduced into ES cells, and homologous recombination at the miR-133b locus was detected by Southern blot (Fig. 1C). Correctly targeted ES cells were used to generate chimeric mice, and germline transmission of the targeted allele was confirmed by PCR screening. The Neo cassette was excised by mating miR-133b<sup>lox-Neo<sup>+</sup></sup> mice with a FLPe deleter strain, and subsequent miR-133b<sup>lox</sup>/* mice were mated with a Cre deleter strain to remove the miR-133b stem loop. Floxet, WT, heterozygous, and KO mouse genotypes were detected by PCR of tail DNA (Fig. 1D), and WT and KO PCR products were sequenced to detect deletion of miR-133b and presence of a single loxP site in the KO (Fig. 1F, G). Loss of miR-133b was confirmed by RT-PCR and quantitative RT-PCR for the miR-133b stem loop region (Fig. 1E, H). Heterozygous mice were backcrossed at least eight generations to C57BL/6 mice and maintained on a C57BL/6 background. miR-133b KO mice were viable, fertile, and born at a Mendelian ratio. The KO mice appeared viable, fertile, and born at a Mendelian ratio. The KO mice appeared

Detection of miR-133b in brain by fluorescence in situ hybridization

miR-133b has previously been found to be enriched in midbrain; however, its precise expression pattern has not been determined. We performed fluorescence in situ hybridization (FISH) for miR-133b in adult brain using LNA modified, digoxigenin (DIG)-labeled antisense and scrambled probes (Fig. 2). miR-133b signal could be observed in many different brain regions, particularly cortex, hippocampus, and cerebellum (Fig. 2A, B), as well as regions neighboring the midbrain such as hypothalamic and pontine nuclei (Fig. 2A, D). Lack of signal from a miR-133b scrambled probe suggested that these regions were not stained due to nonspecific binding (Fig. 2C). Consistent with previous reports of biochemical enrichment in midbrain, we did detect moderate miR-133b expression in the SNpc region of ventral midbrain (Fig. 2E, F). However, some signal from the miR-133b antisense probe could still be detected in miR-133b KO brain, including the SNpc (Fig. 2G, H). The orthologs of miR-133b, miR-133a1, and miR-133a2 only differ by one base from miR-133b and, although not found to be enriched, have also been biochemically detected in brain and midbrain. Thus, signal from the miR-133b antisense probe in various regions of miR-133b KO brain was quantified in by densitometry and normalized to GAPDH. Results were scaled to the average value of the WT samples (WT average, 1; n = 5 WT and 6 KO mice). Error bars indicate SEM.

Figure 4. Unaltered dopaminergic gene expression in miR-133b KO mice. A, B, TH, DAT, GAD1, ChAT, Pitx3, and miR-133a1 mRNA expression in brain of whole brain of 3-month-old male (A) and P0 (B) WT and miR-133b KO mice. Gene expression is normalized to Gapdh and results are scaled to the average value of the WT samples (WT average, 1; n = 4 WT and 4 KO mice). C, TH, GAD1, and Pitx3 protein expression in whole brain of 3-month-old male (quantified in D) and P0 (quantified in E) WT and miR-133b KO mice. Western blot bands were quantified by densitometry and normalized to β-actin (for TH and GAD1) or β-tubulin (for Pitx3). Results were scaled to the average value of the WT samples (WT average, 1; n = 5 WT and 6 KO mice). Error bars indicate SEM.

Figure 4. Unaltered dopaminergic gene expression in miR-133b KO mice. A, B, TH, DAT, GAD1, ChAT, Pitx3, and miR-133a1 mRNA expression in whole brain of 3-month-old male (A) and P0 (B) WT and miR-133b KO mice. Gene expression is normalized to Gapdh and results are scaled to the average value of the WT samples (WT average, 1; n = 4 WT and 4 KO mice). C, TH, GAD1, and Pitx3 protein expression in whole brain of 3-month-old male (quantified in D) and P0 (quantified in E) WT and miR-133b KO mice. Western blot bands were quantified by densitometry and normalized to GAPDH. Results were scaled to the average value of the WT samples (WT average, 1; n = 5 WT and 6 KO mice). Error bars indicate SEM.
brain is likely due to binding to the remaining miR-133 family members.

Detection of miR-133b expression in SNpc by FISH, together with previous findings that miR-133b is enriched in midbrain and expressed in ES cell-derived DA neurons in vitro, warranted further investigation into its function in the midbrain dopaminergic system in vivo.

The midbrain is morphologically unchanged in miR-133b mutant mice

miR-133b has been shown to negatively regulate dopaminergic neuron differentiation in cultured mouse ES cells (Kim et al., 2007); therefore, miR-133b KO mice might be expected to have altered numbers of mDA neurons. The general morphology of the midbrain and striatum of 2-month-old male KO mice was indistinguishable from those of WT mice (Fig. 3A, B), while morphology and unbiased stereological counts of TH-IR cells in VTA and SNpc were also unchanged (Fig. 3A, D). miR-133b is selectively depleted in the midbrain of PD patients; if loss of miR-133b contributes to PD pathogenesis, deletion of miR-133b could lead to decreased numbers of DA neurons in aged mice. We found no difference in midbrain TH-IR cell number in 12-month-old WT and KO animals (Fig. 3C, F), suggesting that loss of miR-133b does not cause degeneration of mDA neurons. To determine whether KO mice have abnormal DA neuron development that is corrected postnatally, TH-IR cells were counted in E18.5 WT and KO SNpc. No difference was observed in number or morphology of TH-IR cells (Fig. 3C, F), consistent with normal development of DA neurons. A small increase in the number of Pitx3-IR cells was observed in the KO (Fig. 3F), suggesting that miR-133b may target Pitx3 in vivo. However, the number of cells immunoreactive for both TH and Pitx3 was equivalent in WT and KO (Fig. 3F), suggesting that the increased number of Pitx3-expressing cells in KOs does not have a major influence on mDA cell fate.

Midbrain dopaminergic neuron gene expression is unaffected in miR-133b mutant mice

While miR-133b does not appear to regulate the differentiation of DA neurons in vivo, it could act by regulating expression of genes that affect neuron function but not cell number. Therefore, we quantified the expression levels of several genes important for mDA neuron function. TH, DAT, and Pitx3 transcripts were at WT levels in neonatal and adult KO brain, and levels of GAD1 and ChAT, expressed in GABAergic and cholinergic midbrain neurons, respectively, were also unchanged (Fig. 4A, B). Furthermore, expression of the related miRNA, miR-133a1, was unaltered in KO brain. Since many miRNAs act post-transcriptionally, miR-133b deletion could affect protein expression without altering transcript levels. However, no difference in neonatal or adult brain TH, GAD1, or Pitx3 protein levels was observed between WT and KO animals (Fig. 4C–E). To more specifically determine whether dopaminergic, GABAergic or cholinergic neurons had altered protein expression in midbrain, TH, GAD1, ChAT, and Pitx3 levels were quantified in WT and KO ventral midbrain, and no difference was observed (Fig. 4F, G), suggesting that global expression patterns in brain and midbrain are not affected by loss of miR-133b.

Monoamine neurotransmitters are unaffected in miR-133b mutant mice

To evaluate whether the activity of mDA neurons was altered in miR-133b KO mice, whole tissue monoamine neurotransmitter levels were quantified by HPLC-ECD. Levels of DA, NE, 5-HT, and their metabolites were unchanged in dorsal striatum (Fig. 5A), nucleus accumbens (B), frontal cortex (C), thalamus (D), and hypothalamus (E) from 2-month-old male WT and miR-133b KO mice; n = 8 WT and 7 KO mice. F, Neurochemical analysis of baseline and amphetamine-stimulated extracellular DA levels in dorsal striatum of 3-month-old male WT and KO mice. Amphetamine at 100 µg/kg was continuously infused via reverse microdialysis after 40 min (arrow); n = 9 WT and 8 KO mice. Error bars indicate SEM.

Locomotor and anxiety-like behaviors in miR-133b mutants are similar to those of wild-type mice

Movement and motivation-related behaviors are directly linked to mDA neuron function. To determine whether miR-133b KO mice have an underlying defect in the midbrain dopaminergic system, mice underwent a battery of behavioral tests. KO mice exhibited spontaneous locomotor behavior in the open field test that was indistinguishable from that of WT mice (Fig. 6A). The response of KO mice after injection of the psychostimulant am-

Figure 5. Unchanged monoamine neurotransmitter levels in miR-133b KO mice. A – E, Neurochemical analysis of whole-tissue monoamine contents in dorsal striatum (A), nucleus accumbens (B), frontal cortex (C), thalamus (D), and hypothalamus (E) from 2-month-old male WT and miR-133b KO mice; n = 8 WT and 7 KO mice, F, Neurochemical analysis of baseline and amphetamine-stimulated extracellular DA levels in dorsal striatum of 3-month-old male WT and KO mice. Amphetamine at 100 µg/kg was continuously infused via reverse microdialysis after 40 min (arrow); n = 9 WT and 8 KO mice. Error bars indicate SEM.
Figure 6. Motor and anxiety-like behaviors are similar in miR-133b WT and KO mice. A, Spontaneous locomotor activity of 3- to 4-month-old WT and KO mice in the open field test; n = 12 WT and 12 KO mice. B, Amphetamine-induced locomotor activity of 3- to 4-month-old WT and KO mice in the open field test. Three milligrams per kilogram of amphetamine was administered by i.p. injection at 60 min (arrow); n = 9 WT and 11 KO mice. C, miR-133b KO mice spend more time in the center of the open field chamber during the first 30 min of the open field test; *p < 0.05, Student’s t test. n = 12 WT and 12 KO mice. D, Time spent by 3- to 4-month-old WT and KO mice in the open arm of the elevated plus zero maze over 5 min; n = 18 WT and 13 KO mice. E, Number of marbles buried beneath bedding by 5-month-old male WT and KO mice after 30 min; n = 13 WT and 9 KO mice. F, Time spent in the light versus dark chamber by 3- to 4-month-old WT and KO mice in the dark–light emergence test over 5 min; n = 15 WT and 10 KO mice. G, Average latency to fall of 5-month-old male WT and KO mice trained on a rotarod at a fixed speed of 24 rpm for 4 trials per day over 3 days. H, Latency to fall from an accelerating rotarod (4–40 rpm) on the fourth day, averaged over 3 trials; n = 13 WT and 9 KO mice. Error bars indicate SEM.

Discussion

Here we show that mice with a deletion of miR-133b, a miRNA previously proposed to regulate differentiation and survival of mDA neurons (Kim et al., 2007), display no differences in development or maintenance of mDA neurons. We could detect no significant abnormalities in mDA neuron morphology, cell number, gene expression, monoamine levels, or motor and anxiety-like behaviors in these mice. These data suggest that the function of miR-133b in an in vitro model of DA neuron differentiation does not translate to a similar role in the intact animal. There are several explanations for this discrepancy. First, miR-133b expression in the midbrain may not contribute significantly to mDA neuron function. Indeed, miR-133b is part of the miR-133 family of miRNAs that is highly expressed in muscle and has been more extensively characterized in skeletal muscle development (Townley-Tilson et al., 2010). Overexpression of muscle miRNAs in heterologous cells globally inhibits brain-specific gene expression (Lim et al., 2005); introduction of miR-133b in a neuron culture system could be expected to inhibit neuronal differentiation in a broad manner without having a specific role in DA neurons.

Second, while not found to be enriched, expression of the miR-133b paralogs miR-133a1 and miR-133a2 has also been detected in the midbrain (Kim et al., 2007) and could compensate for the loss of miR-133b. miR-133a1 expression was below our detection limits. Therefore, the lack of miR-133b does not appear to feed back to increase expression of its paralogs, although we cannot rule out the possibility of compensation by existing levels of miR-133a in midbrain. miR-133a1 and miR-133a2 double KO mice have recently been reported (Liu et al., 2008). It will now be possible to generate mice with a triple deletion of miR-133a1, miR-133a2, and miR-133b to determine whether the miR-133 family of miRNAs is important for brain development and function.

We have found that miR-133b is expressed in the SNpc region of midbrain, in addition to many other brain regions, including cortex, hippocampus, and cerebellum. Recently, cell type-specific miRNA biochemical purification combined with deep sequencing has shown that miR-133b is expressed in GABAergic neurons of cortex and cerebellum (He et al., 2012). This method will be critical for teasing apart the specific expression patterns of miR-133b, miR-133a1, and miR-133a2 in various neuronal subtypes and brain regions. The specific functions of miR-133b in these cell types may subsequently be explored using the constitutive or conditional miR-133b knock-out mouse lines described here.

There is growing evidence that miRNAs are implicated in neurodegenerative disorders (Hébert and De Strooper, 2009), presenting new possibilities for therapeutic intervention (Seto,
miR-133b depletion in the midbrain of PD patients led to the hypothesis that loss or dysfunction of miR-133b could promote PD progression (Kim et al., 2007). However, we did not detect mDA neuron degeneration or impaired motor function in aged miR-133b KO animals. Moreover, no association has been found between miR-133b genetic variants and PD (de Mena et al., 2010). These results suggest that miR-133b depletion may not be causal in PD neurodegeneration; rather, loss of mDA neurons during disease progression would necessarily lead to a reduction in levels of miR-133b, along with other genes expressed in mDA neurons. However, we cannot exclude the possibility that a decrease in miR-133b may enhance the susceptibility of mDA neurons to neurodegeneration resulting from PD or toxic insults. This could be tested in the future by comparing PD-like disease progression in WT and miR-133b KO mice following MPTP or 6-OHDA treatment. Although miR-133b does not appear to play a causal role in midbrain neurodegeneration, loss of all miRNAs in mDA neurons in vivo does cause profound neuronal cell death (Kim et al., 2007). Therefore, other miRNAs expressed in mDA neurons may act alone or in concert to promote neuronal development and survival. In vivo analyses of these miRNAs may pave the way for novel therapeutic strategies in PD and other disorders of the mDA system.

References


