Myocardin-related transcription factors regulate the Cdk5/Pctaire1 kinase cascade to control neurite outgrowth, neuronal migration and brain development

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SUMMARY
Numerous motile cell functions depend on signaling from the cytoskeleton to the nucleus. Myocardin-related transcription factors (MRTFs) translocate to the nucleus in response to actin polymerization and cooperate with serum response factor (Srf) to regulate the expression of genes encoding actin and other components of the cytoskeleton. Here, we show that MRTF-A (Mkl1) and MRTF-B (Mkl2) redundantly control neuronal migration and neurite outgrowth during mouse brain development. Conditional deletion of the genes encoding these Srf coactivators disrupts the formation of multiple brain structures, reflecting a failure in neuronal actin polymerization and cytoskeletal assembly. These abnormalities were accompanied by dysregulation of the actin-severing protein gelsolin and Pctaire1 (Cdk16) kinase, which cooperates with Cdk5 to initiate a kinase cascade that governs cytoskeletal rearrangements essential for neuron migration and neurite outgrowth. Thus, the MRTF/Srf partnership interlinks two key signaling pathways that control actin treadmilling and neuronal maturation, thereby fulfilling a regulatory loop that couples cytoskeletal dynamics to nuclear gene transcription during brain development.

KEY WORDS: Neurite outgrowth, Neuronal migration, MRTF, Pctaire1 (Cdk16), Actin dynamics, Mouse

INTRODUCTION
Precisely controlled neuronal migration and neuronal connectivity establish normal brain architecture and maintain neurological and cognitive functions (Ayala et al., 2007; Lin et al., 2009). Aberrant neuronal migration or connectivity causes multiple neurodevelopmental and neurodegenerative disorders, including mental retardation, schizophrenia and Alzheimer’s disease. Although these disorders differ in their onsets and pathologies, they share common etiologies, including the absence of functional neurons in discrete regions of the brain, decreased neurite arborization and weak synapse connections. Elucidating the molecular pathways that control neuronal survival, migration and connectivity represents an important step towards the identification of novel therapeutic targets to enhance neuronal function in these neurodevelopmental and neurodegenerative disorders, including mental retardation, schizophrenia and Alzheimer’s disease.

Brain disorders (Benitez-King et al., 2004; Lin et al., 2009; Spalice et al., 2008; Posern et al., 2004; Vartiainen et al., 2007). Members of the myocardin family of transcription factors modulate cytoskeletal dynamics by sensing actin polymerization and conferring transcriptional activity to serum response factor (Srf) (Olson and Nordheim, 2010). The myocardin family includes myocardin and the myocardin-related transcription factors (MRTFs) -A and -B (also known as Mkl1 and Mkl2 – Mouse Genome Informatics). Unlike myocardin, which is expressed specifically in cardiac and smooth muscle (Oh et al., 2005; Wang et al., 2001; Wang et al., 2002), the expression of MRTF-A and MRTF-B is enriched in the forebrain, particularly in the hippocampus and cerebral cortex (Alberti et al., 2005; Shiotani et al., 2005). Studies in fibroblasts and muscle cells show that MRTFs bind monomeric G-actin in the cytoplasm and translocate into the nucleus in response to signals promoting actin polymerization to form powerful transcriptional complexes with Srf (Guettler et al., 2008; Kuwahara et al., 2005; Periasamy et al., 2003; Pipes et al., 2006; Postern et al., 2004; Variaiinen et al., 2007). Mouse embryos homozygous for an Srf-null mutation fail to generate mesoderm and die at gastrulation (Arsenian et al., 1998); however, tissue-specific deletion of Srf has revealed multiple roles for this transcription factor in brain, muscle, heart and liver.

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Incorporation of the 5 cells. Isolated ES cell clones were analyzed for homologous recombination. The plasmid containing the 5 gene was linearized with SacI and 3' end labeled with [α-32P]dATP using Klenow fill-in method and purified using a G25 DNA purification column (Roche). The 20 μl binding reaction contained 1 μg poly(dI-dC) (Sigma), 100,000 cpm of probe, and increasing amounts (50-500 ng) of purified GST-Srf. After incubation at room temperature for 15 minutes, the reactions were separated on a 5% PAGE gel in 0.5×TBE.

Histology and Immunohistochemistry
Control and bdKO mice were anesthetized and transcardially perfused with PBS, followed by 4% paraformaldehyde (PFA) prior to brain dissection. Brains were then postfixed in 4% PFA for 2 days, embedded in paraffin and sectioned. Sections were stained with Hematoxylin and Eosin, Nissl stain, or phallolidin stain using standard procedures. TUNEL assay and Golgi staining were performed according to manufacturers’ instructions (Roche and BD Neurosciences, respectively). Immunohistochemistry was performed using monoclonal anti-BrdU (Roche), monoclonal anti-MAP2 (Sigma), anti-Ptau1 (Santa Cruz Biotechnology), anti-phospho-Cdk5 (Santa Cruz Biotechnology), anti-phospho-Pak (Cell Signaling), anti-phospho-LIMK (Abcam), anti-phospho-cofilin (Sigma), anti-β-tubulin J1 (Tubb3) (Abcam) and anti-Gfap (Sigma) antibodies was performed using standard protocols.

BrdU labeling
Timed matings were set up between Mrtfa+/–;Mrtfb+/– female and Mrtfa+/–;Mrtfb+/–,GFAP-Cre male mice. Pregnant females were intraperitoneally injected with BrdU (Roche; 100 μg/g body weight) at embryonic day (E) 15.5. The pups were genotyped and sacrificed at P7. Mrtfa+/–;Mrtfb+/–,GFAP-Cre and Mrtfb+/–;Mrtfb+/– control brains were sectioned for Hematoxylin and Eosin staining and for BrdU labeling.

Neurite outgrowth assay
Mrtfa−/−,Mrtfb+/– and Mrtfa+/−,Mrtfb−/– mouse pups (P0–P3) were used for hippocampal and cortical cultures as described (Ahlemeyer and Baumgart-Vogt, 2005). The cultures were plated on poly-D-lysine/laminin-coated coverslips (BD Biosciences) and infected with either Ad5CMVCre-eGFP or Ad5CMVeGFP adenovirus constructs (University of Iowa Gene Transfer Vector Core). After 2 weeks, the cells were fixed with 4% PFA, permeabilized and blocked with 3% bovine serum albumin in PBST buffer (PBS containing 0.1% Tween 20). The cells were then incubated with anti-MAP2 primary antibody (1:500 in PBST) for 45 minutes followed by three washes in PBST and incubation with Texas-Red-conjugated secondary antibody. After three washes in PBST, coverslips were mounted on glass slides using VectaShield mounting medium with DAPI (Vector Laboratories) and visualized with a confocal microscope.

RT-PCR analysis
Total RNA was purified from tissues using TRIzol reagent according to the manufacturer’s instructions (Invitrogen). For RT-PCR, total RNA was used as a template for reverse transcription (RT) using random hexamer primers. Quantitative real-time PCR (qPCR) was performed using TaqMan probes (ABI).

Western blots
Cortical brain tissues were homogenized in lysis buffer (50 mM Tris pH 7.4, 150 mM NaCl, 1% Triton X-100, 1 mM EDTA) supplemented with protease inhibitors (Complete Mini, EDTA-free, Roche) and phosphatase inhibitors (Sigma). The lysates were then centrifuged at 14,000 g for 15 minutes and supernatants were recovered. Equal amounts of protein extracts were resolved by SDS-PAGE on a 12% acrylamide gel and analyzed by western blot using primary antibodies for phospho-cofilin (Sigma), total cofilin (Sigma), total Cdk5 (Santa Cruz), total cofilin J1 (Tubb3) (Abcam) and anti-Gfap (Sigma) antibodies.

Gel mobility shift assays
GST-Srf and control GST proteins were purified from Erichesica coli cultures using standard protocols. Wild-type and mutant DNA probes were labeled with [α-35P]dCTP using a Klenow fill-in method and purified using a G25 DNA purification column (Roche). The 20 μl binding reaction contained 1 μg poly(dI-dC) (Sigma), 100,000 cpm of probe, and increasing amounts (50-500 ng) of purified GST-Srf. After incubation at room temperature for 15 minutes, the reactions were separated on a 5% PAGE gel in 0.5×TBE.

MATERIALS AND METHODS

Mouse lines
The Mrtfb conditional null allele was generated using homologous recombination in embryonic stem (ES) cells. The pGKNEO-F2L2DTA vector, which contains a neomycin resistance gene flanked by FRT and loxP sites and a diphertheria toxin gene cassette, was used for Mrtfb targeting. The 5' arm, knockout arm and 3' arm of the targeting construct were generated using high-fidelity PCR amplification (Expand High-Fidelity Long Template, Roche) of 129SveV genomic DNA. The targeting vector was linearized with PvuI and electroporated into 129SveV-derived ES cells. Isolated ES cell clones were analyzed for homologous recombination. Incorporation of the 5' and 3' loxP sites was confirmed by Southern blotting using 5' and 3' probes following digestion with XbaI and SacI, respectively. Clones with the targeted Mrtfb allele were injected into 5.5-day C57BL/6 blastocysts, and the resulting chimeras were crossed to C57BL/6 females to achieve germline transmission of the targeted (Mrtfb<sup>neo-loxP</sup>) allele. The Mrtfb<sup><ins>neo-loxP</ins></sup> mice were crossed to FLPe transgenic mice (Zhuo et al., 2001) to obtain the Mrtfb<sup><ins>flp</ins></sup> and Mrtfb<sup><ins>flp</ins></sup><sup>DD</sup> alleles, respectively. Mrtfb<sup>flp/flp</sup>,GFAP-Cre mice were then crossed to Mrtfb<sup>−/−</sup> mice (Li et al., 2006) to generate Mrtfa<sup>−/−</sup>,Mrtfb<sup>ff</sup>,GFAP-Cre (MRTF bdKO) mice. Srf heterozygous mice (Arsenian et al., 1998) were used as controls.

Development (Charvet et al., 2006; Latasa et al., 2007; Miano et al., 2004; Niu et al., 2005; Parlakian et al., 2005). Conditional deletion of Srf in the brain impairs neurite outgrowth, axon guidance and directional neuron migration (Alberti et al., 2005; Knoll et al., 2006). Deletion of Srf in the brain also disrupts the formation of hippocampal neuronal circuitry, resulting in defective memory formation. Srf-null CA1 pyramidal neurons display diminished long-term synaptic potentiation (LTP) and impaired induction of long-term synaptic depression (LTD), indicating that Srf is required for plastic modification of synaptic strength in response to activity in the adult brain (Etkin et al., 2006; Ramanan et al., 2005). However, mice lacking any single member of the myocardin family fail to phenocopy Srf loss-of-function mutations. Mrtfa knockout mice have defects in mammary myoepithelial cell differentiation but appear otherwise normal (Li et al., 2006; Sun et al., 2006), whereas global deletion of Mrtfb causes defects in the patterning of the branchial arch arteries and post-gastrulation embryonic lethality (Li et al., 2005; Oh et al., 2005). These studies suggest either that in vivo Srf activity relies on transcriptional co-factors outside of the myocardin family or that functional redundancy among MRTF members obscures individual gene functions.

Here, we show that a single allele of either Mrtfa or Mrtfb is sufficient to support normal brain development; however, brain-specific deletion of Mrtfb in Mrtfb-null mice causes lethality between postnatal day (P) 16 and 21. Mice lacking both Mrtfa and Mrtfb in the brain show several morphological abnormalities that phenocopy the defects reported for brain-specific deletion of Srf (Alberti et al., 2005; Knoll et al., 2006). The morphological defects in Mrtfa/b mutant mice are accompanied by aberrant neuronal migration, impaired neurite outgrowth and decreased expression and activity of actin and the actin-severing proteins gelsolin and cofilin. We also identify the gene encoding Ptau1 kinase as a novel target of the MRTF/Srf pathway in the brain. Ptau1 links MRTF/Srf signaling to the Cdk5 pathway, a known regulator of neuronal outgrowth. We conclude that MRTF-A and MRTF-B are key molecular sensors in a tightly controlled regulatory feedback loop that links extracellular signaling and cytoskeletal activity with Srf transcriptional regulation to modulate actin dynamics during brain development in vivo.
To explore the potential functions of MRTFs in postnatal development, we generated a conditional null Mrtfb allele by homologous recombination in ES cells (Fig. 1A). Deletion of exon 8 eliminates binding to Srf, thereby allowing analysis of the influence of MRTF on Srf activity in vivo. Correct targeting and homologous recombination in ES cells (Fig. 1A). Deletion of exon 1 to 7. Portions of the Mrtfb transcript 3’ of exon 7 could not be detected in homozygous mutant embryos (Fig. 1D).

Given the overlapping expression and homology between MRTF-A and MRTF-B (Pipes et al., 2006; Shiota et al., 2006), we speculated that MRTF-A could compensate for MRTF-B function in the brains of Mrtfb-null mice. To test this, we crossed our Mrtfb

Luciferase assays
The Pctaire1-luciferase construct contained the 500 bp region of Pctaire1 containing the Srf binding site. Cos cells were plated in 24-well plates (5 x 10^5 cells per well) and transfected with 150 ng of the Pctaire1-luciferase construct together with 50 ng of the expression plasmids encoding myocardin and 10, 50 and 100 ng of the Srf expression plasmid using 1.4 μl of FuGENE 6 Reagent (Roche Molecular Biochemicals). Transfection efficiency was normalized by cotransfection of 10 ng pCMV-lacZ. Forty-eight hours post-transfection, the cells were harvested in 150 μl of Passive Lysate Buffer (Promega) and 20 μl of cell lysate was used for luciferase or β-galactosidase assays.

Chromatin immunoprecipitation (ChIP)
ChIP assays were performed using EZ ChIP (Millipore) following the manufacturer’s instructions. Briefly, human 293T cells were transfected with either control empty vector or with flag-Srf-encoding vector. For each immunoprecipitation, chromatin from 3 x 10^6 cells was cross-linked with 1% formaldehyde and sonicated to produce chromatin fragments between 400 and 1000 bp. Ten percent of the chromatin was used as input control. The other 90% of the chromatin was incubated with anti-flag agarose affinity beads (Sigma). DNA was purified from the ChIP and the control input samples and analyzed by RT-PCR or by qPCR using primers spanning the predicted Srf binding site of the human PCTAIRE1 gene.

Kinase assay
Cdk5 was immunoprecipitated from control or MRTF bdKO cortices using anti-Cdk5 antibody (Santa Cruz Biotechnology), conjugated to glutathione-agarose beads, and washed with PBS. Immunoprecipitated Cdk5 beads were then resuspended in kinase reaction buffer (30 μM ATP and 5 μCi of [γ-32P]ATP, and recombinant histone H1 protein (100 μg). Reactions were allowed to proceed for 30 minutes at room temperature and phosphoproteins were then bound to Whatman filter papers and analyzed in a Beckman coulter counter.

Quantification of phalloidin staining
ImageQuant (Molecular Dynamics) was used to compute the integrated density or pixel density per area. A total of 30 fields of phalloidin-stained sections from three different animals were analyzed (ten fields per animal). The percentage integrated density for MRTF bdKO sections was calculated relative to control sections.

Statistical analysis
Results are expressed as mean ± s.e.m. An unpaired two-tailed Student’s t-test with Welch correction was performed to determine statistical significance between groups. P<0.05 was considered significant.

RESULTS
Conditional deletion of Mrtfa and Mrtfb in the brain
To explore the potential functions of MRTFs in postnatal development, we generated a conditional null Mrtfb allele by homologous recombination in ES cells (Fig. 1A). Deletion of exon 8 eliminates binding to Srf, thereby allowing analysis of the influence of MRTF on Srf activity in vivo. Correct targeting and germline transmission were confirmed by Southern blot and PCR of genomic DNA (Fig. 1B,C). Specific deletion of Mrtfb in the brain was achieved using GFAP-Cre transgenic mice, which express Cre recombinase in radial glial cells as early as E12.5. Radial glial cells give rise to glial cells, to the majority of neurons in the cerebral cortex, hippocampus and cerebellum, and to adult subventricular zone (SVZ) stem cells that produce neurons throughout adult life (Zhuo et al., 2001). Mrtfb^{flox};GEAP-Cre (Mrtfb^{bKO}) mice were phenotypically normal. Significant Mrtfb knockout in the brain was confirmed by RT-PCR analysis of mRNA from the cortical regions of Mrtfb^{bKO} and Mrtfb^{flox} mice using primers detecting exons 7, 9 and 10, which flank the deleted region of the gene. The mutant allele included exons 1 to 7. Portions of the Mrtfb transcript 3’ of exon 7 could not be detected in homozygous mutant embryos (Fig. 1D).

Given the overlapping expression and homology between MRTF-A and MRTF-B (Pipes et al., 2006; Shiota et al., 2006), we speculated that MRTF-A could compensate for MRTF-B function in the brains of Mrtfb-null mice. To test this, we crossed our Mrtfb

Fig. 1. Generation of MRTF brain double-knockout (bdKO) mice. (A) Strategy to generate a conditional Mrtfb allele. The protein, corresponding exonic structure, and targeted alleles are shown. The targeted Mrtfb^{neoloxP} allele was generated by homologous recombination in ES cells. To generate the Mrtfb^{bKO} allele, the neomycin resistance cassette, flanked by FRT sites, was removed by crossing to FLPe transgenic mice. The Mrtfb^{bKO} allele includes twoloxP sites inserted into introns 7 and 8. The Mrtfb^{bKO} allele was generated using Cre-mediated excision, which results in oneloxP site in place of exon 8. (B) Southern blot analysis confirming targeting of ES cells. The corresponding wild-type (8 kb) and targeted bands (4 kb and 6 kb) are indicated for the 5’ and 3’ probes. (C) Genotyping of Mrtfb^{bKO} and Mrtfb^{bKO} mice by genomic PCR. Primer set includes three primers, with two flanking the 5’loxP site and the third downstream of the 3’loxP site. (D) MRTF knockout in MRTF bdKO brains compared with control brains was assayed by RT-PCR using primers located within exons 7, 9 and 10 of Mrtfb. (E) MRTF bdKO mouse (left) and control Mrtfb^{+/+};Mrtfb^{+/+};GFAP-Cre mouse (right) at P14. Note that one copy of Mrtfb or Mrtfb is sufficient for normal development. (F) Average weight of control and bdKO mice at P14. The MRTF bdKO mice are significantly smaller than their control littermates. (G) Expression of Srf transcripts in MRTF bdKO brains. Shown is a quantitative RT-PCR transcript analysis from the cortical regions of MRTF bdKO and Srf^{+/+} mice. Relative expression was normalized to the corresponding transcript levels in control brains.

development
conditional knockout mice to those harboring an Mrtfa-null (Mrtfa−/−) allele (Li et al., 2006) to generate mice lacking both MRTF-A and MRTF-B in the brain. We refer to the Mrtfa−/−;MrtfbF/−;GFAP-Cre mice as MRTF brain double-knockout (MRTF bdKO) mice.

MRTF bdKO mice were born at Mendelian ratios, but showed a significant reduction in body size and weight by P14 and died between P16 and P21 (Fig. 1E,F). Mrtfa−/−;MrtfbF/−;GFAP-Cre and Mrtfa−/−;Mrtfb−/−;GFAP-Cre mice were phenotypically normal, suggesting that a single copy of either Mrtfa or Mrtfb is sufficient to rescue the phenotype.

Interestingly, MRTFs regulate not only Srf activity but also transcription of the Srf gene. Similar to MRTF deletion, ablation of Srf in the brain results in lethality by P21 (Alberti et al., 2005). Hence, we examined the expression levels of Srf in brains of MRTF bdKO mice. Quantitative real-time PCR (qPCR) showed a 25% reduction in the levels of Srf transcripts in the cortical regions of MRTF bdKO mice compared with control mice. Moreover, we compared the mRNA levels of Srf among MRTF bdKO mice and Srf−/− mice, which do not show an obvious brain phenotype. The levels of Srf were comparable between MRTF bdKO brains and Srf−/− brains; suggesting that the lethality of MRTF bdKO mice cannot be exclusively caused by downregulation of Srf at the transcriptional level (Fig. 1G).

**MRTF bdKO mice have severe brain abnormalities**

Histological analyses of brain sections from MRTF bdKO mice at P16 revealed several morphological abnormalities in the hippocampus, corpus callosum, anterior commissures and striatum that phenocopy defects reported in mice with brain-specific deletion of Srf (Alberti et al., 2005). Hematoxylin and Eosin (H&E) staining of sagittal brain sections from MRTF bdKO mice showed a reduction in the size of the striatum and an expansion of the SVZ (Fig. 2A,B). H&E staining of coronal sections from MRTF bdKO mice revealed an absence of both the corpus callosum and the anterior commissures, accompanied by a compressed hippocampus with a deformed dentate gyrus (Fig. 2C,D) (see Fig. S1 in the supplementary material). Nissl staining of hippocampal neurons identified a poorly defined pyramidal cell layer in MRTF bdKO mice (Fig. 2E,F), a phenotype that we confirmed by Golgi staining (Fig. 2G,H). Golgi staining also showed a dramatic decrease in the number of hippocampal neuronal projections compared with control neurons (Fig. 2G,H). We wondered whether the observed abnormalities in MRTF bdKO brains could be explained by glial cell defects. However, immunohistochemistry for the glial cell marker Gfap at P1 and P14 did not reveal any major differences between MRTF bdKO brain and control sections, suggesting that neuronal cell defects were most likely responsible for the observed abnormalities (see Fig. S2 in the supplementary material).

**Defective neuronal migration along the rostral migratory stream**

The accumulation of cells at the SVZ in MRTF bdKO brains could be observed as early as P0. Normally, newborn neurons originating from the SVZ migrate out tangentially along the rostral migratory stream (RMS) towards the olfactory bulbs, where they differentiate into interneurons (Fig. 3A). We speculated that the phenotype we observed in MRTF bdKO mice at the SVZ was due to a neuronal migration defect. This hypothesis was supported by the fact that Mrtfa−/− mouse embryonic fibroblasts (MEFs) failed to arrange their cytoskeleton and migrate to the wound site in an in vitro scratch assay (see Fig. S3 in the supplementary material).

Alternatively, SVZ expansion could result from excessive neuron proliferation at the SVZ. To distinguish between these possibilities, we used BrdU labeling to monitor cellular proliferation and migration from the SVZ towards the olfactory bulb. BrdU pulse labeling for 1 hour at E15.5 did not reveal a difference in the rate of cell proliferation at the SVZ (see Fig. S4 in the supplementary material).

We then chased the BrdU-labeled neurons by analyzing their number and position in P7 mice. In control mice, the majority of BrdU-positive cells had migrated away from the SVZ by P7; whereas MRTF bdKO mice showed a significant accumulation of BrdU-positive cells at the SVZ (Fig. 3A,B). As a consequence of the defective neuronal migration along the RMS, the number of neurons at the olfactory bulbs in the MRTF bdKO brains was significantly diminished compared with control brains (Fig. 3C,D). These results demonstrate that the expanded SVZ we observed in MRTF bdKO mice is due to defective neuronal migration and further support the hypothesis that MRTFs regulate cytoskeletal dynamics in the developing nervous system.
Defective neurite outgrowth in MRTF bdKO neurons

In addition to defects in neuronal cell number, organization and position, we also observed by Golgi staining that the number of projections from hippocampal neurons was dramatically reduced in MRTF bdKO mice at P16 (Fig. 2H). Considering the role of the MRTF/Srf pathway in regulating cytoskeletal genes and the implication that Srf participates in neurite outgrowth (Knoll et al., 2006), we further investigated the role of MRTFs in directing neuronal projections outside the hippocampus. We performed anti-MAP2 (also known as Mtap2 – Mouse Genome Informatics) antibody staining to examine the organization of neuronal extension in vivo. Interestingly, MRTF bdKO mice showed less MAP2 in the striatum and cortical regions of the brain than control animals (Fig. 4A-D). The presence of defective neuronal projections in the cortex was also confirmed by Golgi staining (Fig. 4E,F).

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To confirm that the decrease in MAP2 staining is indeed indicative of a defect in neurite extension, we performed an in vitro neurite outgrowth assay in which hippocampal and cortical neurons were cultured from 

Mrtfa<sup>−/−</sup>; Mrtfb<sup>F/F</sup> P0-P3 mice and infected with GFP-Cre-expressing adenovirus. Only ~15% of the MRTF bdKO neurons formed readily identifiable neurites over the 2-week culture period, as compared with 80% neurite outgrowth in control cultures (Fig. 4G-I). The same assay was used to examine neurite outgrowth in primary cultures of MRTF bdKO neurons over a 1-week culture period. In this assay, 75% of neurons in control cultures formed neurites, compared with less than 20% in the MRTF bdKO neuronal cultures (Fig. 4J-L). Taken together, these studies show that MRTFs induce neurite outgrowth in multiple regions of the forebrain.

Pctaire1 is a novel MRTF/Srf target gene

In order to explore the molecular basis for the abnormalities in neurite outgrowth and migration in MRTF bdKO mice, we performed microarray analysis on cortical samples from control and MRTF bdKO brains at P0 (GEO accession number GSE22117). As expected, the expression of numerous cytoskeletal components and known Srf target genes, such as gelsolin, was diminished in the MRTF bdKO mice (see Table S1 in the supplementary material). We confirmed the downregulation of beta-actin and of the actin-binding protein gelsolin in the hippocampal and cortical regions of MRTF bdKO brains by qPCR (see Fig. S5 in the supplementary material).

In addition to these known Srf target genes, we noted a small set of genes that were downregulated in the microarray, were not known Srf targets, and that function during neuronal development. Among these, Pctaire1 (also known as Cdk16 – Mouse Genome Informatics), which encodes a protein kinase that associates with Cdk5, was one of the most strongly downregulated genes in the microarray. Gene expression analysis by qPCR confirmed downregulation of Pctaire1, but not Pctaire2 (also known as Cdk17), in the cortical and hippocampal regions of MRTF bdKO mice (Fig. 5A). Furthermore, anti-Pctaire1 staining revealed decreased expression of Pctaire1 in the pyramidal cells of the hippocampus and in the cortex of MRTF bdKO mice as compared with control mice (Fig. 5B).

We analyzed the DNA sequence of the Pctaire1 gene and identified an evolutionarily conserved sequence resembling a CArG box located within the first intron (see Fig. S6 in the supplementary material). We note, however, that the site contains an additional nucleotide in the central region (CC ATTCTAT GG) that differs from the consensus CArG box sequence [CC (A/T)<sub>6</sub> GG]. Nevertheless, gel mobility shift assays showed that this sequence formed a DNA-protein complex with recombinant GST-Srf protein (Fig. 5C). Protein binding was disrupted following mutation of the predicted CArG box but not the empty luciferase constructs. Increased amounts of the Srf were able to activate the Pctaire1-luciferase reporter constructs containing the predicted Srf binding site but not the empty luciferase constructs. (Fig. 5D).

The findings suggested that Pctaire1 might function as an essential effector of the Srf/MRTF pathway during neurite outgrowth. Confirming the potential influence of Pctaire1 on

**Fig. 5. Identification of Pctaire1 as a novel MRTF/Srf target gene.** (A) Decreased expression of Pctaire1 transcripts in MRTF bdKO brains. Quantitative RT-PCR transcript analysis from hippocampal and cortical regions of MRTF bdKO brains. Relative expression was normalized to the corresponding transcript levels in control brains. *P<0.05. (B) Diminished levels of Pctaire1 protein in MRTF bdKO brains. Anti-Pctaire1 antibody staining revealed decreased levels of the protein in the hippocampal and cortical regions of MRTF bdKO mice compared with control mice. (C) Gel mobility shift assays were performed with a labeled Pctaire1 probe and purified GST-Srf or control GST proteins. Increased binding of GST-Srf to the Pctaire1 CArG sequence was detected with increased amounts of recombinant Srf. The use of a labeled mutant probe or an unlabeled probe blocks Srf binding. (D) Responsiveness of Pctaire1 expression to MRTF/Srf signaling. Increased amounts of the Srf were able to activate the Pctaire1-luciferase reporter constructs containing the predicted Srf binding site but not the empty luciferase constructs. Mutation of the predicted CArG box blocks this activation. (E, F) Enrichment of Srf at its predicted binding site within the PCTAIRE1 gene. ChIP assay were performed on chromatin prepared from human 293T cells transfected with either a flag-tagged Srf construct or a control empty construct. The precipitated genomic DNA was analyzed by RT-PCR (E) and by qPCR (F) using primers for the human PCTAIRE1 gene. Shown also is the PCR amplification performed prior to immunoprecipitation as the input control (E). (G) Defective neurite outgrowth in Pctaire1 knockdown neurons. Anti-MAP2 antibody staining from 1-week neuron cultures shows disruption of neurite outgrowth in the Pctaire1 siRNA-transfected but not in control siRNA-transfected neurons. (H) Increased cofilin phosphorylation in Pctaire1 knockdown neurons. Western blot analysis of phospho-cofilin and total cofilin in control and Pctaire1 siRNA-transfected neurons. Gapdh was used as a loading control. Scale bars: 50 µm in B; 5 µm in G.
neuronal cell morphology and neurite outgrowth, knockdown of Pctaire1 using two different siRNAs in primary neuron cultures disrupted neurite outgrowth, phenocopying MRTF bdKO neuronal cultures (Fig. 5G).

Regulation of actin dynamics by MRTFs

Pctaire1 has been reported to interact with Cdk5, a kinase implicated in actin dynamics and neurite outgrowth (Cheng et al., 2002). To assess the potential impact of MRTF signaling on Cdk5 activity, we performed immunohistochemistry against the activated (phosphorylated) form of Cdk5 and observed reduced phospho-Cdk5 accumulation in the hippocampal and cortical regions of MRTF bdKO mice compared with control littermates, with no significant reduction in the total Cdk5 levels (Fig. 6A,B and see Fig. S7 in the supplementary material; data not shown). To further confirm the abrogated activity of Cdk5 in MRTF bdKO brains, we performed a Cdk5 kinase assay with immunoprecipitated Cdk5 from the cortical regions of control or MRTF bdKO mice and used recombinant histone H1 protein as substrate. Indeed, the kinase activity of Cdk5 was significantly reduced in the MRTF bdKO brains as compared with control brains (Fig. 6K).

Cdk5 regulates neuronal migration and neurite outgrowth by modulating the activity of a kinase cascade that targets actin polymerization (Dhavan and Tsai, 2001; Smith, 2003). At the base of this cascade is the actin depolymerase cofilin, the activity of which is diminished by phosphorylation (Kuhn et al., 2000; Sarmiere and Bamburg, 2004). Cofilin is a substrate for LIM kinase (LimK), which in turn is a substrate for the kinase Pak1 (Arber et al., 1998). Cdk5 inactivates Pak1 via phosphorylation and promotes actin depolymerization. We speculated that the Pak1-Limk-cofilin cascade is a target of Cdk5 downstream of MRTFs. Indeed, the cortical and hippocampal regions of the MRTF bdKO mice showed diminished Pak phosphorylation and a greater accumulation of phospho-LimK and phospho-cofilin than control brains (Fig. 6C-H; data not shown). Furthermore, immunoblotting for phospho-cofilin and total cofilin showed a dramatic increase in phospho-cofilin in the brains of MRTF bdKO mice compared with controls, without a significant change in total levels of cofilin protein (Fig. 6L and see Fig. S5 in the supplementary material). The total levels of Pak and LimK were unchanged (see Fig. S7 in the supplementary material).

Interestingly, the levels of phospho-cofilin were also increased upon knockdown of Pctaire1 in primary neuronal cultures, further supporting our model and placing Pctaire1 as an upstream regulator of cofilin phosphorylation (Fig. 5H). These results define a mechanistic pathway in which MRTFs induce Pctaire1 and Cdk5 activity, which in turn inactivate the Pak1-Limk cascade to promote the actin-depolymerizing activity of cofilin and neuronal outgrowth.

To verify that MRTF deletion results in dysregulation of actin severing and abrogates actin dynamics, we evaluated the levels of actin polymerization by F-actin staining with phalloidin. Phalloidin staining of Mrtfa/b-null MEFs showed actin cytoskeleton disruptions and a lack of cortical accumulation of actin filaments upon MRTF deletion in MEFs (see Fig. S8 in the supplementary material). The levels of F-actin were also markedly decreased in the cortical and hippocampal regions of MRTF bdKO mice compared with their control littermates (Fig. 6I,J). Quantification...
of phalloidin staining showed ~50% reduction in the levels of F-actin in MRTF bdKO sections compared with control sections (Fig. 6M). MRTFs are thus essential regulators of actin dynamics in neurons.

**DISCUSSION**

The results of this study reveal obligate roles for MRTF-A and MRTF-B as redundant regulators of neurite outgrowth and neuronal migration during brain development in vivo. The abnormalities in brain development resulting from the combined deletion of *Mrtfa* and *Mrtfb* reflect disorganization of the actin cytoskeleton and impairment of actin dynamics. MRTFs couple the Rho and Cdk5 signaling pathways to actin treadmilling and Srf-dependent transcription to regulate neuronal development, as schematized in Fig. 7. Targets of the MRTF/Srf signaling pathway include genes that encode actin and other cytoskeletal components, as well as *Pctaire1*, a negative regulator of actin polymerization.

MRTFs also promote the kinase activity of a second negative regulator of actin polymerization, Cdk5, probably at the post-transcriptional level. Thus, MRTFs function as nodal regulators that couple two downstream signaling pathways that modulate cytoskeletal dynamics, thereby fulfilling a cytoskeletal-transcriptional circuit that governs neurite outgrowth and neuronal development.

**Functions of MRTFs in vivo**

This study is the first to reveal the importance of the MRTF/Srf partnership during brain development in vivo. Potentiation of the transcriptional activity of Srf by MRTFs has been well documented in vitro (Pipes et al., 2006). However, the phenotypes of knockout mice lacking myocardin, *Mrtfa* or *Mrtfb* have not been comparable to those of Srf knockout mice. The remarkable similarities between the neuronal defects resulting from deletion of both *Mrtfa* and *Mrtfb* and those reported for brain-specific Srf knockout mice (Alberti et al., 2005; Knoll et al., 2006) strongly suggest that the actions of Srf in the brain rely completely on its association with MRTFs and argue against the involvement of other transcriptional co-factors in mediating Srf signaling during brain development. The redundancy of MRTF functions in the brain contrasts with the distinct phenotypes observed in *Mrtfa* and *Mrtfb* single-knockout mice (Li et al., 2005; Li et al., 2006; Oh et al., 2005; Sun et al., 2006). Interestingly, neuronal defects were only observed upon deletion of all four MRTF alleles in the brain.

**MRTFs as regulators of actin cytoskeleton dynamics**

Precise control of the neuronal actin cytoskeleton governs multiple events during brain development, such as neurite outgrowth and neuronal migration. Such control could be exerted by direct regulation of the expression of G-actin and by regulation of the activity of actin-binding proteins, which influence actin dynamics. In a recent report, Stern et al. made use of several actin mutants to show that actin filaments can induce neurite outgrowth in neuronal cultures and that regulation of neurite length by actin filaments is mediated by the activity of Srf (Stern et al., 2009). Our finding that deletion of *Mrtfa* and *Mrtfb* disrupts the assembly of actin filaments accounts for the defective neuronal migration and neurite outgrowth in the brains of MRTF bdKO mice.

Genetic ablation of MRTF-A and MRTF-B also results in decreased expression and activity of the two major actin-severing proteins gelsolin and coflin. Unlike gelsolin, which does not require phosphorylation for activity, the actin-severing activity of coflin is inhibited through phosphorylation by LIM kinases (Kuhn et al., 2000; Sarmiere and Bamburg, 2004). Interestingly, gelsolin and coflin are also dysregulated following deletion of Srf in the brain (Alberti et al., 2005), further supporting the role of MRTFs as essential Srf activators. Both proteins are enriched at growth cones and are required to maintain a high concentration of G-actin for continued actin polymerization during cell migration and neurite outgrowth (Cunningham et al., 1991; Furnish et al., 2001; Gurniak et al., 2005; Meberg, 2000; Meberg and Bamburg, 2000). Interestingly, rather than increasing actin filament assembly, the striking phosphorylation and inactivation of coflin in our MRTF bdKO mice were accompanied by diminished actin polymerization. This observation is not surprising because, in addition to promoting actin depolymerization, coflin has been shown to promote the assembly of actin filaments in certain cellular contexts (Chan et al., 2000; Ghosh et al., 2004; Zebda et al., 2000). Recent mechanisms addressing coflin function propose that the actin-severing activity of coflin creates new barbed ends, which are used to nucleate polymerization of new actin filaments. Therefore, aberrant actin severing could explain the defective organization of the actin cytoskeleton in the brains MRTF bdKO mice.
Identification of Pctaire1 as a novel MRTF/Srf target gene in the brain

We show that the MRTF/Srf pathway regulates Pctaire1 kinase in the brain. Pctaire1 is an atypical Cdc-like kinase in that it does not require cyclins for activation and is not involved in cell cycle regulation (Bessel et al., 1998; Graeser et al., 2002; Okuda et al., 1992). It is expressed at low levels in most cell types, but is particularly abundant in postmitotic neurons (Bessel et al., 1999). Two lines of evidence link Pctaire1 function in neurons to the regulation of neurite outgrowth, the first showing regulation of neurite outgrowth by Pctaire1 in Neuro-2a cells (Graeser et al., 2002) and the second reporting the interaction between Pctaire1 and the Cdk5 pathway (Cheng et al., 2002), which is implicated in the regulation of neuronal actin dynamics. We show here that MRTF/Srf activates Pctaire1 expression through a CArG-like box within the first intron of the gene, and that knockdown of Pctaire1 blocks the growth of neurites in primary neuron cultures, mimicking the effect of MRTF deletion.

Cdk5 kinase drives neuronal differentiation, actin remodeling, neuronal migration and neurite outgrowth (Dhavan and Tsai, 2001). Cdk5 phosphorylates and inhibits Pak1, linking the activity of Cdk5 to the regulation of the actin cytoskeleton (Dhavan and Tsai, 2001; Smith, 2003). Pak1 increases the phosphorylation activity of LimK towards cofilin, which blocks its depolymerizing activity and thereby inhibits actin turnover (Arber et al., 1998; Yang et al., 1998). Interestingly, we show that genetic deletion of MRTF-A and MRTF-B in the mouse brain disrupts this cascade of protein kinases, resulting in inactivation of cofilin.

Overall, our findings and those of others demonstrate the essential role of the MRTF/Srf signaling system in the coupling of cytoskeletal dynamics to nuclear gene transcription in the nervous system. Given the importance of MRTF/Srf in the control of cytoskeletal gene expression in other cell types, especially muscle cells, it will be interesting to determine whether the Pctaire1/Cdk5 pathway identified in this study also modulates the actin cytoskeleton downstream of MRTF/Srf in other cell types.

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Competing interests statement

The authors declare no competing financial interests.

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