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MicroRNA-124 Is a Subventricular Zone Neuronal Fate Determinant

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New neurons are continuously generated from neural stem cells with astrocyte properties, which reside in close proximity to the ventricle in the postnatal and adult brain. In this study we found that microRNA-124 (miR-124) dictates postnatal neurogenesis in the mouse subventricular zone. Using a transgenic reporter mouse we show that miR-124 expression is initiated in the rapid amplifying progenitors and remains expressed in the resulting neurons. When we stably inhibited miR-124 in vivo, neurogenesis was blocked, leading to the appearance of ectopic cells with astrocyte characteristics in the olfactory bulb. Conversely, when we overexpressed miR-124, neural stem cells were not maintained in the subventricular zone and neurogenesis was lost. In summary, our results demonstrate that miR-124 is a neuronal fate determinant in the subventricular zone.

Introduction

In the postnatal mammalian brain, neural stem cells (NSCs) reside in the subventricular zone (SVZ) (Doetsch et al., 1999). These cells generate new neurons that migrate via the rostral migratory stream (RMS) to the olfactory bulb (OB). The NSCs, often termed type B cells, are of astrocytic lineage expressing glial fibrillary acidic protein (GFAP) and have the morphology and ultrastructural properties of astrocytes (Doetsch et al., 1999; Laywell et al., 2000; Skogh et al., 2001; Imura et al., 2003; Merkle et al., 2004). Type B astrocytes undergo asymmetric cell division to generate rapid amplifying progenitors (type C cells) that subsequently differentiate into neurons. This cellular transformation is accompanied by transcriptional changes for which the underlying molecular mechanisms remain largely unknown.

MicroRNAs (miRNAs) are small, noncoding, endogenous RNA that bind to and regulate mRNA targets, making them central players of gene regulation (Bartel, 2009). In neurons, miR-124 is one of the most abundant miRNAs (Lagos-Quintana et al., 2002). The expression of microRNA-124 (miR-124) is initiated upon neural differentiation and reaches high levels in mature neurons (Cao et al., 2007; Makeyev et al., 2007; Visvanathan et al., 2007; Cheng et al., 2009; Sanuki et al., 2011). Several in vitro studies suggest that miR-124 plays a role in neuronal fate determination. For example, delivery of miR-124 duplexes to HeLa cells induces a neuronal gene profile (Lim et al., 2005), and forced expression of miR-124 in progenitor cells causes neuronal differentiation (Visvanathan et al., 2007; Yu et al., 2008).

Nevertheless, despite the observed upregulation of miR-124 during NSC neuronal differentiation (Cheng et al., 2009), in vivo blockade of this miRNA by antisense oligonucleotides only resulted in subtle phenotypes, with mild delays in differentiation and no detectable malformation (Cao et al., 2007; Visvanathan et al., 2007; Cheng et al., 2009). Based on these findings, it was concluded, that miR-124 regulates proliferation but does not affect the glia/neuronal fate choice (Cheng et al., 2009). However, these results were obtained using a technique, in vivo infusions of antisense molecules, which only induced a transient inhibition. In addition, targeting of specific cell types, such as type B astrocytes, could not be ascertained since the antisense molecules were not coupled to a reporter.

Here, to study the role of miR-124 in the postnatal SVZ, we generated a transgenic reporter mouse that allows visualization of miR-124 activity in the brain in vivo. We demonstrate that in the SVZ stem cell niche, miR-124 activity is initiated already in transient amplifying progenitors, type C cells, suggesting that it is not linked to cell cycle exit. This finding was substantiated with loss of function studies of miR-124 in the SVZ, demonstrating that stable inhibition of this miRNA does not force progenitors to remain cycling. miR-124 loss of function, rather, blocks adult neurogenesis and induces the formation of ectopic astrocytes in the OB derived from the SVZ. Furthermore, when we overexpressed miR-124 in the SVZ, we found that NSCs lost their stem cell characteristics, resulting in a loss of continuous supply of new neurons to the OB.
Materials and Methods

Viral vectors. The lentiviral vectors used in this study were third-generation self-inactivating vectors. miRNA target sequences were cloned into the 3′ untranslated region (UTR) of the transgene expression cassette as follows: four tandem repeats of a target sequence perfectly complementary to miR-124 (TTAAGGCACCGGTTGAAATGCACCACGCTGTTTAAAACCCG; sense2: TGGCATTTCACCGGTTGCAATATCGTTAGATCCCAAGGTTAC; antisense1: TTAAGGCACCGGTTGCAATATCGTTAGATCCCAAGGTTAC; antisense2: CGGGTTAACGGCGCGGGTTAATGCTGTTGAAGGCACGCGTGAATGCCATTCGAATTAAGGCACGCGGTGAATGCCA). Sense1 and antisense1, as well as sense2 and antisense2, were hybridized by slow cooling from 95°C down to 37°C, respectively. The resulting double-stranded DNA oligonucleotides could anneal to each other in an ACGCGT sticky end, producing the 119 bp long fragment containing the miR-124 sponge sequence.

For vector injections, 1 μl of concentrated lentiviral vector was unilaterally injected into the right ventricles of NMRI mice at postnatal day 7 (P7) (males and females; Charles River). The pups were placed on ice for 5 min before positioning them in an ice-cold stereotaxic frame. Coordinates from bregma were as follows: AP +0.8, ML −0.8, DV −19.1. Mice were perfused 1, 2, 3, 4, or 8 weeks postinjection. A proportion of the animals were given an intraperitoneal pulse of 50 mg/kg BrdU (Sigma) 2 h before the 4 week time point. We used similar titers for all experiments. We found similar results when analyzing either the ipsilateral or the contralateral hemisphere after vector injection.

Immunofluorescence. Mice were transcardially perfused with 4% paraformaldehyde (PFA) (Sigma), and the brains were postfixed for 2 h and transferred to PBS with 25% sucrose. Brains were coronally sectioned on a microtome (35 μm) and put in potassium PBS. Embryonic brains were fixed in 4% PFA overnight followed by PBS with 15% sucrose and sectioned coronally on a cryostat (14 μm).

Similar procedures were used for both fixed sections and cells, as published in detail previously (Thompson et al., 2005; Sachdeva et al., 2010). A subset of antibodies used were diluted as follows: chicken anti-GFP 1:1000 (Abcam), rabbit anti-GAP 1:1000 (DAKO), goat anti-DCX 1:400 (Santa Cruz Biotechnology), mouse anti-NeuN 1:1000 (Millipore), mouse anti-S100 1:1000 (Sigma), rabbit anti-IBA1 1:1000 (Wako Chemicals), mouse anti-MASH1 1:200 (BD Biosciences), mouse anti-O1 1:1000 (Millipore), and rabbit anti-PERIPHERIN 1:200 (Covance). The dilution factor of the secondary antibodies was 1:500 (Invitrogen) or 1:200 (Jackson Laboratories).

For BrdU staining, the slices were fixed for 20 min in 4% PFA followed by incubation at 65°C in 1 M HCl before addition of the primary antibody (1:500 rat anti-BrdU; Serotec).

Quantification of GFP expressing cells in the OB. Three representative OB sections (35 μm) from each of three control injected, three sponge injected, and three overexpressing injected animals were selected for quantification. Fluorescent images of GFP expression were taken with a confocal microscope (Arcturus). The transgene data (WPRE primer) was normalized with the control, Actin data to give the number of transgenes in the genome of each animal.

For statistical analysis, data were presented as mean ± SEM. An unpaired t test was performed to test for statistical significance.
with minor modifications (Ahlenius and Kokaia, 2010). In brief, half the forebrain from each miR-124.T or GFP control E13.5 fetus was dissected and placed in DMEM/F12 basic medium with trypsin and DNase. The tissue was mechanically suspended by pipetting followed by incubation in 37°C for 30 min. Cells were plated out in DMEM/F12 supplemented with 20 ng/ml EGF and 10 ng/ml bFGF at a density of 100,000 cells/ml and were cultured in a humidified incubator at 37°C with 5% CO₂. Neurosphere cultures were passaged using mechanical dissociation approximately every 7 d. For adult neurospheres, 8 week old wt NMRI mice or 4.3 week old NMRI mice injected with CMV.1000 in the ventricle at P3 were used. The mice were lethally anesthetized, and each brain was removed from the skull. The brain was put in ice-cold L15 media and transferred to a coronal brain matrix, and 1 mm thick sections were cut. From those, the SVZ region was dissected out under a dissection light microscope. SVZ from four different animals was pooled in L15 medium. The tissue was dissociated in HBSS with HEPES, glucose, trypsin, DNase, hyaluronic acid in 37°C for 30 min, followed by titration by pipetting. Adult neurospheres were cultured in Neurobasal basic medium supplemented with EGF, bFGF, and heparin. Cultures were passaged every 7 d using Accutase (Sigma) and mechanical dissociation. FACS analysis of dissociated neurospheres was performed at passages 1–2, as previously described (Jonsson et al., 2009).

Fluorescence in situ hybridization. LNA-FISH was performed as previously described with minor modifications (Silahtaroglu, 2010). In brief, fresh frozen brain tissue was cut at 14 μm on a cryostat on charged slides and kept at −20°C until use. Upon staining, slides were dried and fixed with 4% PFA for 10 min. The slides were hybridized with a DIG-labeled miR-124 LNA-probe (Exiqon) diluted 1:200 for 1 h at 67°C. Following hybridization, slides were washed in 0.1× SSC at 75°C followed by treat-

Figure 1. miR-124 is a neuron-specific miRNA. A, Illustration of the vectors and experimental approach to generate miR-124.T reporter mice using lentiviral transgenesis. Lentiviral vectors were injected into the perivitelline space of fertilized embryos, which were transplanted into a pseudopregnant mouse. B, The vector-encoded transcript is expressed in both miR-124 expressing cells and nonexpressing cells. In the miR-124-expressing cells, the target site containing transcripts is suppressed, resulting in no GFP expression. C–E, GFP expression in miR-124 T reporter mice was found exclusively in nonneuronal cells throughout the brain. Control mice (PGK.GFP) displayed GFP activity in all cells of the brain. Scale bars, 100 μm. F–H, Confocal analysis of GFP cells in miR-124 T mice showing that neurons (NeuN) do not express GFP while astrocytes (GFAP) and microglia (IBA1) do. Scale bars, 10 μm. cPPT, Central polypurine tract; SIN, self-inactivating.
ment with 3% H2O2. The slides were then incubated with an anti-DIG-antibody (1:100; Roche) overnight and developed using Cy3-tyramide (PerkinElmer) for 2 h. Slides were counterstained with DAPI and coverslipped with polyvinyl alcohol mounting medium with DABCO (Sigma).

LNA-qRT-PCR. Total RNA, including miRNA, was extracted from dissociated neurospheres using the miRNeasy kit (Qiagen) followed by Universal cDNA synthesis kit (Exiqon). LNA–PCR primer sets, hsa-miR-124 and hsa-miR-103 (normalization miRNA), were purchased from Exiqon and were used together with LightCycler 480 SYBR Green I Master (Roche). Standard procedures of qRT-PCR were used, and data were quantified using the \( \frac{\text{Ct}}{\text{H9004}} \) method.

Results

Generation of miR-124 sensor transgenic mice
Studies of miRNA expression patterns in the brain in histological preparations have up to now mostly relied on ISH techniques (Pena et al., 2009). However, ISH requires high stringency, and it is often incompatible with other labeling techniques such as immunohistochemistry. In addition, discriminating between the pre-miRNA and mature miRNA is difficult through ISH, making it complicated to detect potential posttranscriptional regulation, which is thought to play a prominent role in controlling the activity of miRNA (Obernosterer et al., 2006). To circumvent these issues, we decided to generate a transgenic sensor mouse that can report the activity of miR-124.

Lentiviral vectors expressing a reporter gene regulated by four copies of a perfectly matched miRNA target sequence can be exploited to monitor miRNA activity (Brown et al., 2007; Sachdeva et al., 2010). For this study we used a lentiviral vector containing a GFP reporter gene followed by four copies of perfect matching miR-124-target sequences (miR-124.T) (Fig. 1A). When miR-124 is present in the cell, it binds the miR target sequence in the vector-derived mRNA and efficiently inhibits GFP expression. In cells in which miR-124 is not expressed, the mRNA remains active, and GFP expression from the ubiquitous PGK promoter is easily detected (Fig. 1B). We used the miR-124.T-vector to generate transgenic mice through lentiviral transgenesis (Lois et al., 2002; Sauvain et al., 2008). High-concentration lentiviral vectors were injected into the perivitelline space of fertilized single-cell embryos followed by transfer to surrogate mothers (Fig. 1A). We generated mice with either the miR-124.T-containing or control GFP vectors (without miRNA regulatory sites). Noteworthy, the simplicity and high efficiency of lentiviral transgenesis allowed us to generate several founders that each carried multiple copies of the transgenes. We then analyzed offspring from six founders for each construct, all carrying 5–15 copies of the vector, and found no difference in GFP expression patterns among lines. Furthermore, we performed intercrosses between founders that, in theory, further reduce the risk for position-dependent effects, and when analyzing such intercrosses we found the same expression pattern as with F0 generation mice.

Figure 2. Characterization of miR.124.T mice. A, Adult miR.124.T mice display low GFP expression in the brain, while other tissues, here exemplified by lung and heart, display similar GFP levels as control animals. B, The developing brain is almost entirely depleted of miR-124 activity at E13.5, as shown by diaminobenzidine-staining for GFP. Scale bar, 1 mm. C, Confocal analysis of E13.5 peripheral ganglion reveals GFP expression in peripheral nervous system neurons labeled with PERIPHERIN. Scale bars, 100 μm. D, Generation of neurospheres from forebrain of E.13.5 miR.124.T embryos. FACS plots showing that in miR.124.T cultures, ~20% of the cells express GFP at early passages. E, F, FACS sorting of the GFP-expressing cells followed by LNA-qRT-PCR for mature miR-124 reveals that mature miR-124 levels are higher in the GFP negative fraction. G, LNA-ISH for miR-124 reveals high-level expression in neurons (top). There is also an absence of miR-124 expression in the ependymal layer that mirrors the expression pattern in miR.124.T mice (bottom). LV, lateral ventricle. Scale bars, 100 μm. Neg, Negative.
miR-124 activity is detected in all neuronal populations in the adult brain but not in glia

Histological examination of adult brains from miR-124.T mice revealed that all neuronal populations throughout the anterior/posterior axis lack GFP expression (exemplified in Fig. 1C–E by low-magnification images from hippocampus, striatum, and cerebellum). Using double-labeled immunohistochemistry for GFP and the neuronal marker NeuN, we found no evidence for GFP-expressing neurons in any brain region examined (Fig. 1C–F). In contrast, GFP control mice showed abundant GFP expression in NeuN-positive cells (Fig. 1C–E). The GFP-expressing cells found in the brains of the miR-124.T mice had a nonneuronal morphology resembling different glial cell types. Colabeling with GFAP and IBA1 confirmed that astrocytes and microglia do not display miR-124 activity (Fig. 1G, H).

We analyzed grossly dissected organs from the miR-124.T mice and found that the brain was mostly devoid of GFP expression when compared with control GFP mice (Fig. 2A). In other organs such as lung and heart there was no major difference in GFP expression (Fig. 2A). FACS analysis of white blood cells from miR-124.T mice showed similar GFP expression levels as GFP control mice (data not shown). In addition, we analyzed GFP expression in embryos at E13.5 and found that miR-124.T embryos displayed a lack of GFP expression exclusively in the...
miR-124 activity is initiated in neurogenic niches in the adult brain

We then focused our analysis on the SVZ stem cell niche in the adult brain. In the SVZ, we detected GFP-expressing cells (i.e., not expressing miR-124) lining the lateral ventricle (Fig. 3A), and colabeling with S100β confirmed that ependymal cells express GFP, thus not exhibiting miR-124 activity (Fig. 3B). To detect proliferating cells, we injected BrdU 2 h before killing the mice. Only rare GFP/BrdU-positive cells could be found, which were in close contact with the ventricular wall, while the majority (estimated to be >95%) of BrdU-positive cells did not express GFP (Fig. 3C). BrdU primarily labels the rapid amplifying progenitors type C, while only a small proportion of BrdU-labeled cells are type B.

This concept was further confirmed by the finding that GFAP-expressing cells in the SVZ coexpressed GFP while both MASH1-expressing cells, which identifies type C cells, and doublecortin (DCX)-expressing cells, which correspond to early migrating neuroblasts, type A cells, were GFP negative (Fig. 3D–F). Moreover, we performed a pulse-chase experiment in which BrdU was injected 4 weeks before the animals were sacrificed. In these animals we found that the majority of the rare remaining BrdU-cells in the SVZ, corresponding mostly to slowly proliferating stem cell-like cells, were GFP positive (Fig. 3G). In contrast, the BrdU-positive cells in the OB that correspond to adult generated neurons were GFP negative (data not shown). We also derived neurosphere cultures from the adult SVZ of miR-124.T mice. These neurospheres had a spotty appearance, with GFP-expressing cells intermingled with non-GFP-expressing cells (Fig. 3H). One percent to 2% of the neurosphere in early passage culture consisted of GFP-expressing cells, resembling the number of expected self-renewing cells in neurosphere cultures (data not shown). Finally, we investigated the expression pattern of JAGGED1 (JAG1), which is a target gene of miR-124 (Cheng et al., 2009; Liu et al., 2011). In our miR-124 reporter mice, we detected JAG1 expression in cells lining the ventricle and in the SVZ. These cells colabeled with GFP, confirming that miR-124 activity and JAG1 expression do not overlap, providing in vivo evidence of miR-124 suppression of JAG1 in the SVZ niche (Fig. 3I).

When we analyzed miR-124 activity in the dentate gyrus (DG) of the hippocampus, which is the second neurogenic niche in the adult brain, we found that GFP-expressing cells had an elaborate morphology with a prominent radial process resembling what has previously been described for neural progenitor cells in the DG. A proportion of BrdU cells were GFP positive, while neuroblasts expressing DCX did not express GFP. This suggests also that in the DG, miR-124 activity is rapidly initiated once the cell exits the self-renewing state (Fig. 4A, B).

Together, these findings demonstrate that miR-124 activity is absent from the actual NSC populations in the adult brain but is initiated as soon as the cell is determined to become a neuron. An interesting aspect is that in the SVZ this corresponds to type C cells that rapidly undergo several cell cycles. Thus, miR-124 initiation does not correlate with cell cycle exit.

Figure 4. GFP expression in hippocampus in adult brain. A. In the DG we found GFP-expressing cells with morphologies resembling what have previously been attributed to progenitor cells. Confocal analysis revealed that a proportion of the GFP-expressing cells incorporated BrdU. It is worth noting that the proportion of BrdU-incorporating cells that expressed GFP was higher in the DG when compared with the SVZ, which reflects differences in the proliferation of progenitors in the two niches. B, GFP-expressing cells did not colabel with DCX. Scale bars, 20 μm.
Inhibition of miR-124 activity impairs neurogenesis

Having found that miR-124 is absent from the GFAP-expressing and BrdU-label retaining stem cells but is upregulated in rapid amplifying progenitors, we hypothesized that miR-124 plays a critical role in fate determination during SVZ neurogenesis. We investigated this by stably inhibiting miR-124 in the SVZ stem cell niche using a lentiviral sponge strategy.

To achieve efficient targeting of the SVZ niche, including all relevant cell types, we injected lentiviral vectors into the lateral ventricles of P3 mice. At this time point, the ependymal layer is not fully developed and the vector can therefore efficiently transduce all cell types in the niche. Using a control CMV.GFP vector, without miRNA sponge sequences, we found that injection of lentiviral vectors into the lateral ventricles of P3 mice allows efficient targeting of the SVZ stem cell niche. At 1 week postinjection, cells lining the ventricle expressed a high level of GFP (Fig. 5A). At 4 and 8 weeks after injection, we found that there were still numerous GFP-expressing cells in the ventricular zone, and colabeling demonstrated that ependymal cells (S100β) and astrocyte-like cells (GFAP) were expressing GFP (Fig. 5B–D). Eight weeks after vector injection, there were GFP-expressing cells in the RMS coexpressing DCX, demonstrating a continuous supply of cells from the SVZ (Fig. 5E). In the OB there was an increasing number of GFP-expressing interneurons that with time colabeled with NeuN (Fig. 5F). To further confirm stable genetic modification of SVZ stem cells, we performed a pulse chase experiment in which animals were injected with BrdU 4 weeks after vector injection and then sacrificed 4 weeks later, at 8 weeks of age. We found GFP-expressing neurons in the OB that colabeled with BrdU. This demonstrates that cells dividing 4 weeks after vector injection still retain the GFP transgene, showing that slowly dividing stem cells are targeted. Scale bar, 10 μm, w, Weeks.

To inhibit miR-124 we used a lentiviral sponge vector expressing eight copies of an imperfect miR-124 target sequence driven by a strong CMV promoter (Fig. 6A), a design that has been optimized to inhibit miRNA activity in vivo (Gentner et al., 2009). The vector contains a GFP reporter gene that is only detectably expressed when miR-124 is inhibited or in cells lacking miR-124, allowing for simple detection of sponged cells (Gentner et al., 2009). We validated the functionality of the miR-124 sponge construct by demonstrating its ability to de-repress transcripts controlled by miR-124 using a luciferase reporter assay as well as by performing qRT-PCR for endogenous target genes (Fig. 6B, C). When we inhibited miR-124 expression in the SVZ using miR-124 sponge vectors, we found that transduced GFP sponge-expressing cells displayed reduced OB neurogenesis 4 weeks after vector injection (n = 7). In the OB there were very few GFP sponge-expressing neurons when compared with CMV.GFP-injected animals, and all these neurons expressed a low level of GFP (Fig. 6D, E). These low GFP-expressing neurons most likely correspond to cells in which the sponge is expressed at low levels due to low copy number, resulting in insufficient miRNA inhibition. However, even after amplification of the GFP signal using immunohistochemistry, these cells corresponded to <10% of GFP cells when compared with control injection animals. In the SVZ we found numerous GFP-expressing cells lining the ventricle (Fig. 6F). In the RMS we could not find any DCX-GFP-expressing cells (Fig. 6G). Careful examination of transduced cells in the SVZ and RMS revealed that they were expressing either S100β or GFAP but never DCX (Fig. 6H, I). When we pulsed with BrdU 2 h before sacrifice, we only detected very few GFP-expressing cells that were BrdU positive in the SVZ.
miR-124 inhibition affects the transition from type B stem cells into rapid amplifying progenitors, type C cells, and subsequent neuronal differentiation. It is worth noting that ependymal cells (not expressing miR-124) expressed high levels of the sponge (GFP) at all time points investigated (1, 4, and 8 weeks) and displayed a normal phenotype throughout, indicating that there is no toxicity associated with the miR-124 sponge per se. Interestingly, we found GFP-expressing cells in the RMS with a glial-like morphology that colabeled with S100β 4 weeks after miR-124 sponge injection (Fig. 6K). Adding to this, we detected cells with an astrocyte-like morphology in the OB expressing GFP. These cells colabeled with both GFAP and S100β (Fig. 6L,M). The number of GFP-expressing astrocytes corresponded to ~10 cells/section and could be found in all cell layers of the OB (Fig. 6F). In animals injected with the CMV.GFP vector or a sponge vector targeting the unrelated miR-125b, we never detected GFP/S100β or GFP/GFAP-expressing cells in the RMS or the OB (Fig. 6D,E,N).

Together, these results show that miR-124 inhibition reduces neurogenesis and increases gliogenesis, leading to the formation of ectopic glial cells in the OB. This demonstrates that miR-124 plays a critical role in regulating the molecular machinery that governs the cellular transformation from an SVZ astrocyte-like stem cell into an OB neuron.

Overexpression of miR-124 in the SVZ leads to loss of self-renewing NSCs

Since miR-124 regulates postnatal neurogenesis, we furthermore decided to investigate the consequence of miR-124 overexpres-
sion in the SVZ niche. To this end, we generated a lentiviral vector containing a 484 bp genomic fragment containing miR-124 –1 (miR-124OE) that allowed high-level expression of mature miR-124 and a GFP marker (Fig. 7A).

When overexpressing miR-124 in the SVZ, we were unable to detect GFP-expressing cells in the SVZ or RMS 4 weeks after delivery of the miR-124 overexpression vector although we did detect GFP-neurons in the OB (Fig. 7B–D). These data suggest that miR-124 overexpression is not compatible with the maintenance of type B stem cells, leading to a loss of continuous supply of new neurons to the OB via the RMS. To investigate this phenomenon in detail, we killed mice 1, 2, and 3 weeks after miR-124OE vector injection (Fig. 7E–G). At 1 week postinjection, miR-124 overexpressing GFP cells were found in the SVZ and the RMS, and we also found cells with immature morphology that had entered the OB (Fig. 7E) (data not shown). Starting at 2 weeks and even more so at 3 weeks postinjection, there was a gradual loss of GFP-expressing cells in the SVZ and in the RMS (Fig. 7F, G). These data suggest that overexpression of miR-124 results in only a single wave of GFP-expressing cells reaching the OB, which is in contrast to the constant supply of new GFP neurons when using control vectors. In control experiments, in which we used a lentiviral vector with a similar design overexpressing the unrelated miR-125b, we found GFP-expressing cells in the SVZ, RMS, and OB 4 weeks postinjection demonstrating a continuous supply of new neurons (Fig. 7H).

The number of GFP-expressing neurons detected in the OB 4 weeks after miR-124OE injection were fewer and arranged differently when compared with control injected animals (Fig. 7I–K). When we analyzed the distribution of GFP cells in the different cell layers in the OB, we found that miR-124 overexpression led to an increased integration into the GCL, with fewer cells integrating into the glomerular layer compared with the control GFP cells (Fig. 7J). Furthermore, the miR-124 overexpressing cells were primarily found in the inner parts of the GCL (Fig. 7K).

In summary, these data suggest that overexpression of miR-124 in NSCs leads to loss of neural stem cells while it does not impair migration of progenitors from the SVZ to the OB.
In this study we show that miR-124 is expressed and active in all neuronal populations of the adult brain. We also demonstrate that miR-124 activity is rapidly initiated once NSCs, type B cells, transit to rapid-amplifying progenitors, type C cells. When the upregulation of miR-124 expression is blocked, type C cells are not generated, leading to a subsequent inhibition of neurogenesis. On the other hand, if miR-124 expression is forced in type B cells they lose their stem cell characteristics.

Our strategy to detect miR-124 activity relies on the generation of a GFP reporter transgenic mouse. The detection of GFP expression only in glial cell types, including astrocytes and microglia, demonstrates that miR-124 is active only in neurons and cells destined to become neurons. This is in contrast to a recent study in which miR-124 was reported to be expressed in resting microglia (Ponomarev et al., 2011). This discrepancy is most likely explained by the ability of the reporter mouse to detect the activity of miR-124 at single cell resolution whereas the study by Ponomarev et al. (2011) solely relies on PCR-based techniques that are limited to measure expression levels. The possibility that we would detect GFP expression in cells that are also displaying miRNA activity is very unlikely. A false signal could be potentially caused by loss of the miR.T sequence, but this would occur in a random fashion and not specifically in astrocytes and oligodendrocytes, and the fact that we see similar expression patterns in different founder mice further rules out this possibility. Alternatively, a false signal could be caused by a lack of sensitivity of the miRNA reporter system in detecting low levels of miRNA. Still, such a low level of miRNA expression is most likely not relevant for endogenous miRNA targets either (Brown et al., 2007; Mukherji et al., 2011).

We found the reporter mouse particular useful when analyzing neurogenesis since it allows for straightforward colabeling with relevant markers such as BrdU, which otherwise would be complicated to combine with standard miRNA detection techniques such as LNA-ISH. The GFP reporter also permits morphological analysis, which is not possible when using ISH-staining to detect miRNA. In future studies, the miR.124.T mice generated here could be used in studies to monitor changes in miR-124 levels in models of stroke, neurodegenerative disorders, and brain cancer. Additionally, the simplicity of lentiviral transgenesis should allow for the generation of a large number of this type of miRNA reporter mice, which would greatly enhance our understanding of miRNA expression patterns in the brain.

Our loss-of-function and gain-of-function experiments suggest that miR-124 is an essential part of the neuronal network. This is in agreement with previous studies in which it has been shown that overexpression of miR-124 in HeLa cells induces a broad neuronal gene profile (Lim et al., 2005). Furthermore, two recent reports demonstrate that overexpression of miR-124 contributes to direct conversion of fibroblasts into functional neurons (Ambasudhan et al., 2011; Yoo et al., 2011). Together, these studies and ours indicate that miR-124 is a factor necessary for the induction of the neuronal gene program. However, our results contrast, to some extent, a previous study by Cheng et al. (2009) in which the authors concluded that miR-124 does not influence neuron/glia fate decisions in the SVZ. The difference between the studies lies primarily in our lentiviral strategy, which leads to stable targeting of the type B stem cells, whereas Cheng et al. (2009) used infusions of 2’OMe-RNA antisense molecules that are limited to a transient, nontargeted inhibition of miR-124 most likely occurring primarily in rapid-amplifying progenitors.

An interesting observation in our study is that at least a proportion of the cells in which miR-124 was inhibited continued to migrate to the OB without obtaining neuronal characteristics. These data suggest that intracellular gene programs other than those inducing a neuronal fate governs migration to the OB.

Our data show that ectopic expression of miR-124 in the SVZ is not compatible with continuous neurogenesis. Rather, we observed a single wave of neurogenesis when miR-124 was overexpressed. This "washout" of GFP-expressing cells follows a similar temporal profile to what has been observed when injecting MLV retroviral vectors into the ventricles of newborn rodents (Rogelius et al., 2005). MLV vectors target primarily the rapidly proliferating type A and type C cells, suggesting that overexpression of miR-124 in type B cells caused forced differentiation into neural progenitors without self-renewing capacities. Alternatively, it is possible that the loss of self-renewing GFP cells after miR-124 is at least partly due to cell death. We have analyzed our material for cell death markers but have not been able to detect dying cells (data not shown). However, during the first postnatal weeks the SVZ is a dynamic and expanding region, and cell death in response to the overexpression may not be detectable. Still, the presence of GFP-expressing cells in the SVZ, RMS, and OB at different time points after the injection of miR-124OE demonstrates that miR-124 overexpression does not always cause cell death. Furthermore, our observations after miR-124 overexpression are in line with in vitro experiments in which miR-124 has been overexpressed in cultured cells with neural progenitor characteristics (Makeyev et al., 2007; Silber et al., 2008; Cheng et al., 2009; Liu et al., 2011). In these studies, overexpression of miR-124 led to reduced proliferation associated with forced neuronal differentiation. These studies and our findings indicate that miR-124 may in part act by the downregulation of genes that are associated with stemness.

Of particular interest is the identification of the Notch-ligand receptor JAG1 as a miR-124 target (Cheng et al., 2009; Liu et al., 2011). Recent studies demonstrate a critical role for the Notch pathway not only in regulating NSCs, but also in maintaining ependymal cells in a nonproliferating state (Carlen et al., 2009). The consequences of miR-124 overexpression in the SVZ are very similar to Notch inhibition, suggesting that miR-124 is a crucial player in this network. However, the molecular machinery controlled by miR-124 appears to be complex; an mRNA target prediction algorithm suggests >1000 potential targets, and several of those have been experimentally validated (targetscan.org). In the adult SVZ, miR-124 has, in addition to JAG1, been demonstrated to regulate SOX9, which is a transcription factor that controls adult neurogenesis, as well as DLX2, a transcription factor mediating neuronal subtype specification (Cheng et al., 2009). In light of this, it will be interesting to identify the complete set of miR-124 targets in neural progenitor cells. Recent studies demonstrate that a combination of computational approaches, loss-of-function experiments, and experimental determination of either mRNA-Ago2 complexes (PAR-CLIP) or miRNA-mRNA interaction is necessary to obtain a reliable list of true miRNA targets (Lal et al., 2011; Lipchina et al., 2011). The application of such approaches to a small cell population in vivo is challenging but will be a focus in our future work.
References


