Epigenetic control of hippocampal stem cells: modulation by hyperactivation, glucocorticoids and aging

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New neurons in aging brains: molecular control by small non-coding RNAs

Marijn Schouten, M. Renate Buijink, Paul J. Lucassen and Carlos P. Fitzsimons

Chapter 1

Abstract

Adult neurogenesis generates functional neurons from neural stem cells present in specific brain regions. It is largely confined to two main regions: the subventricular zone of the lateral ventricle, and the subgranular zone of the dentate gyrus, in the hippocampus. With age, the function of the hippocampus and particularly the dentate gyrus is impaired. For instance, adult neurogenesis is decreased with aging, in both proliferating and differentiation of newborn cells, while in parallel an age-associated decline in cognitive performance is often seen. Surprisingly, the synaptogenic potential of adult-born neurons is only marginally influenced by aging. Therefore, although proliferation, differentiation and synaptogenesis of adult-born new neurons in the dentate gyrus are closely related to each other, they are differentially affected by aging. In this review we discuss the crucial roles of a novel class of recently discovered modulators of gene expression, the small non-coding RNAs, in the regulation of adult neurogenesis. Multiple small non-coding RNAs are differentially expressed in the hippocampus. In particular a subgroup of the small non-coding RNAs, the microRNAs, fine-tune the progression of adult neurogenesis. This makes small non-coding RNAs appealing candidates to orchestrate the functional alterations in adult neurogenesis and cognition associated with aging. Finally, we summarize observations that link changes in circulating levels of steroid hormones with alterations in adult neurogenesis, cognitive decline and vulnerability to psychopathology in advanced age, and discuss a potential interplay between steroid hormone receptors and microRNAs in cognitive decline in aging individuals.
microRNAs and regulation of adult neurogenesis

Chapter 1

**Introduction**

In humans, aging is being intensively studied, among other reasons because humans are reaching more advanced ages and the effects of a substantially larger aging population on the society have risen significantly. Aging theories traditionally associate a slow accumulation of loss of function and plasticity in cells and organs with aging. Therefore, factors that control the rates of cellular mitogenesis, differentiation and cell death are considered important regulators of the aging process. Many physical changes take place in our bodies as we age, such as hair loss, endocrine changes, motor deficits and sensory changes resulting in a reduced acuity of vision and impairment in hearing. However, the well-reported age-related decline in cognition and memory is arguably one of the aging symptoms that worries humans the most, possibly because memory is so central to our personal identity and relations.

**Aging and the hippocampus**

The human brain coordinates our cognitive abilities and in particular hippocampal and neocortical areas associated with memory and cognition are highly vulnerable to aging. Early studies have shown that aging results in a decline in hippocampal functions such as spatial navigation. Although the hippocampus has been traditionally evaluated as a single structure, it is now widely accepted that the hippocampus is a complex functional circuit, composed of molecular and functionally diverse regions. Studies in rodents and monkeys have shown selective regional differences in sensitivity to advancing age in the hippocampus. Interestingly, the hippocampal dentate gyrus (DG) is particularly affected by aging. In the following section we will review in more detail literature that link adult hippocampal neurogenesis with cognitive functions that decline with age.

**Adult hippocampal neurogenesis and memory-related cognitive functions**

It is now clearly established that new neurons continue to be generated in the adult brain throughout life by neurogenesis from neural stem cells (NSCs). This phenomenon is largely confined to two main regions: the subventricular zone (SVZ) of the lateral ventricle, and the subgranular zone (SGZ) of the DG. In other adult cortical regions limited neurogenesis may occur, but only under specific conditions. In the SGZ, NSCs give rise to transit amplifying neural progenitors that in turn differentiate into new immature neurons. These newly generated neurons migrate short distances into the granular cell layer of the DG and mature locally into dentate granule cells (GCs) within a period of 4-5 weeks. During maturation, newly generated GCs become functionally integrated into pre-existing hippocampal circuits, receiving synaptic inputs mainly from the entorhinal cortex via the perforant path and extend their axons (mossy fibers) to establish synapses onto CA3 pyramidal cells. Both phenotypic maturation and functional integration are tightly regulated processes and are strongly dependent on cellular activity and connectivity with pre-existing networks.

The process of AHN consists of several steps: proliferation of progenitor cells; early selective elimination by apoptosis; fate decision and commitment to a neuronal phenotype; morphological and physiological maturation with the development of functional neuronal characteristics and a second selection by synaptic integration into pre-existing hippocampal circuits. Moreover, AHN generates a whole range of neurogenic cell types that are differentially regulated and may play specific roles in the overall process. During this slow maturation process, many of the newborn neurons are selected and more than 50% of the newborn GCs die within the first few weeks after birth. The rapid decline during early stages results from active elimination by apoptosis. On the other hand, those immature neurons that develop synapses and are recruited into functionally active hippocampal circuits stand a better chance to survive. Thus, survival and death of newborn neurons in the DG are not only closely interconnected, but the balance between these two processes is finely tuned by neuronal activity and cognitive experience. For more information about this topic, we refer the readers to some recent reviews.
Possible contribution of AHN to hippocampus-dependent cognitive functions

Although the exact role of newborn neurons in the DG is still under debate, recent data support a functional role for adult-born neurons in learning and memory processes as reviewed in detail elsewhere. We here focus briefly on DG-dependent memory functions that may decrease with aging. The emerging consensus is that adult-born neurons in the DG play a crucial role in pattern separation, a memory mechanism that permits the differential representation of similar stimuli encoded by hippocampal circuits. In humans, pattern separation can be assessed by a combination of functional magnetic resonance imaging and specific memory tasks. Decreased performance in these tasks has been registered in aging subjects, positioning the DG as a key region in age-associated cognitive decline. Importantly, impairment in tasks associated with pattern separation in humans may be an early indicator of DG dysfunction and possibly of early Alzheimer symptoms as altered performance in these tasks has been associated with changes in the activity of the entorhinal cortex, the main input to the DG, probably affecting newborn GCs survival.

Changes in adult hippocampal neurogenesis associated with aging

A steep decline in AHN associated with aging in the DG is well conserved in mammals and has been extensively reviewed elsewhere. The most dramatic changes in AHN associated with aging in fact take place already early in life, when the decrease in AHN rate is exponential and becomes stabilized in early adult life, remaining active for the rest of the lifespan in rodents. Interestingly, this decrease in AHN associated with aging appears to result from a decrease in proliferation and differentiation and an increase in quiescence of NSCs.

Synaptogenesis of newborn granule cells

Surprisingly, synaptogenesis in newborn GCs is less affected by aging than proliferation. Similar levels of synaptogenesis, as measured by dendritic spine densities in newborn GCs, are found both in old and young animals. As mentioned before and consistent with preserved synaptogenic potential in the aging DG, early-response gene expression and electrophysiological recordings have indicated that newborn GCs are more likely to respond to spatial processing than older GCs. These observations suggest that even in the context of an otherwise declining function associated with aging, adult-born neurons remain functional and excitable and may therefore maintain their role in information processing. Although these are intriguing observations, future studies should have to address whether synapse formation or elimination still proceed at the same pace in the aging. Moreover, studies examining the expression of immediate early genes should be interpreted with care. Although immediate early genes are induced by activity, their expression does not provide a direct indication of information processing because it is unclear whether their activation is due to neuronal firing, synaptic plasticity, or subthreshold depolarizations. Overall, the concept that although in decreased numbers, newborn GCs are still efficiently integrated into hippocampal circuits in the aging DG is consistent with theories proposing that AHN could be a promising substrate to restore function in the aging DG. Moreover, it is in agreement with an earlier hypothesis that AHN may create a neurogenic reserve that buffers age-related cognitive decline.

In order to fully understand the tight selection process newborn GC undergo, it is important to mention that newborn GC exhibit a period of enhanced excitability and plasticity as they are between 2 weeks and 5 months old. Interestingly, this critical period of enhanced excitability and plasticity is associated with a period of intense synaptogenesis. During this period, newborn GCs can bypass apoptosis helped by NMDAR-mediated neuronal activity. They actively compete among themselves and possibly with their pre-existing mature counterparts for survival and connectivity to the network. In this respect, studies aimed to characterize the maturation of synapses in adult-born neurons in the DG have found that they receive a diversity of inputs similar to mature granule neurons. Initially, immature neurons contact preferentially multiple synapse boutons. As new neurons mature, spines form synapses preferentially with boutons devoid of other synaptic partners. These observations indicate that the connectivity of new GCs changes in time and suggest the existence of synaptic competition at the level of glutamatergic inputs into new neurons.
**microRNAs and regulation of adult neurogenesis**

**Chapter 1**

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**A**

**Expansion phase**
- Radial glia-like stem cells activate
- Transiently amplifying progenitor cells proliferate

**Differentiation phase**
- Dendrite extension
- Axon extension
- Increased synaptic plasticity
- Activity-dependent recruitment
- Survival or apoptosis

**Integration phase**
- Maturation of dendritic spines
- Lowered threshold for LTP
- Increased synaptic plasticity

**Markers:**
- GFAP, Sox2, S100b
- GFAP, Nestin-GFP, Sox2, Kir6
- PSA-NCAM, doublecortin, TuJ1
- Calretinin, Calbindin, NeuN

**Apoptotic marker expression:**
- Cell shrinkage, mitochondrial CytC release, cleaved executioner caspases, TUNEL

**Stages, timescale**
- 4 weeks
- Gliogenesis
- Adult hippocampal neurogenesis
  - 1 day
  - 4 days
  - 4-10 days
  - 2-4 weeks
- Integration phase

**B**

**Neuronal activity**
- GR
- CREB
- BDNF

**Growth factors**
- p300
- MeCP2
- mR-132
- p250GAP
- SIRT1
- LIMK1
- mR-134
- Synaptogenesis

**Figure 1 - miRs are key regulators in all phases of the adult neurogenesis cascade.**

Schematic illustration, adapted from (Lucassen et al., 2010)\textsuperscript{15}, summarizing (A) miRs and targets involved in the regulation of different phases of adult neurogenesis and (B) miRs and targets hypothesized to be involved in the regulation of synaptogenesis during functional integration of adult-born new neurons. (A) The overall picture indicates that regulation by miR is less well characterized in the integration phase as opposed to expansion and differentiation phases. (B) Regulation of synaptogenesis by miR-132 and miR-137 has been studied in AHN and in other contexts as well. From these observations, described in the text, we hypothesize that the regulatory network(s) depicted in (B) could be engaged in fine-tuning synaptogenesis during the functional integration phase of AHN.
Small non-coding RNAs can be classified into several major classes, i.e. small nucleolar RNAs (snoRNAs), endogenous small interfering RNAs (siRNAs), piwi-interacting RNAs (piRNAs), microRNAs (miRs), transfer RNAs (tRNAs), ribosomal RNAs (rRNAs), spliceosomal RNAs, RNase P/MRP genes. Other, less well-characterized small non coding RNAs classes are the small modulatory RNAs (smRNAs), repeat-associated small interfering RNA (rasiRNA) that associate with piRNAs in protective mechanisms against transposable elements in the germ line and the smallest members of the family, the 17-18 nt long transcription initiation RNAs (tiRNAs) and small RNAs positioned at splice sites (spliRNAs), thought to be involved in the regulation of nucleosome positioning. With respect to the regulation of adult NSCs, the small double-stranded RNA (dsRNA) NRSE can trigger gene expression of neuron-specific genes through interaction with the NRSF/REST transcriptional machinery, resulting in the transition from neural stem cells into cells with a neuronal identity. The mechanism of action appears to be mediated through a dsRNA/protein interaction, rather than through RNA interference.

snoRNAs, are derived from protein-coding and non-protein coding transcripts. They are involved in sequence-specific 2'-O-methylation (box C/D snoRNAs) or in the isomerization of specific uridines to pseudouridines (box H/ACA snoRNAs) in target RNAs. Some snoRNAs show tissue- and/or context-dependent expression, especially in the brain and may target other RNAs, including spliceosomal and transfer RNAs. Except for snoRNA MBII-52, involved in the alternative splicing of the serotonin receptor 2C, very little is known about the function of snoRNAs in the brain. Although not directly linked to AHN, an increased expression level of snoRNA host-gene growth arrest specific 5 (GAS5) has been correlated to age-dependent spatial memory deficit in mice. GAS5 is a gene with a complex structure, whose introns encode the snoRNAs SNORD44, 47, 74-81 involved in ribosomal RNA biosynthesis by 2'-O-methylating pre-rRNAs. GAS5’s 5’ end harbors a terminal oligopyrimidine and its exons do not encode a protein. Interestingly, Kino and collaborators have demonstrated that GAS5 is able to block the
transcriptional activity of the glucocorticoid receptor and other steroid hormone receptors\textsuperscript{52}. In line with this crosstalk between GAS5 and steroid hormone receptors, psychogenic stressors and the subsequent release of stress hormone corticosterone, upregulate GAS5 levels in the hippocampus\textsuperscript{53}. Interestingly, treatment of cortical NSCs with ciliary neurotrophic factor (CNTF) induces NSCs to drift into the astrocytic lineage and strongly induces GAS5 expression\textsuperscript{94}. Recently, we have observed that GAS5 is expressed in human hippocampal NSCs in culture (Schouten et al., unpublished data). Future studies will have to address the question whether GAS5 has a regulatory role in steroid hormone responsiveness in hippocampal NSCs.

Endogenous siRNAs
Endogenous siRNAs are substrates of the ribonuclease Dicer and act through the RNA interference pathway, usually by perfect match with the target mRNA, resulting in mRNA degradation. They also seem to be involved in epigenetic regulation of target sequences by yet not well-characterized mechanisms\textsuperscript{85,86}.

piRNAs
piRNAs use the RNA interference pathway as well, but they are not processed by Dicer and are involved in the silencing of transposons, primarily in the germline\textsuperscript{87} and are also involved in epigenetic regulation events such as DNA methylation and histone modification\textsuperscript{88}. Interestingly, recent studies have reported the expression of a restricted group of piRNAs in the hippocampus, with at least one of this piRNAs (DQ541777) being expressed in the dendritic compartment of hippocampal neurons. Suppression of this piRNA by antisense oligonucleotides suggested a role in dendritic spine shape regulation\textsuperscript{89}.

miRs
miRs are approximately 22 nucleotides long single stranded small non-coding RNAs. miRs are processed by Dicer, bind the RNA-induced silencing complex (RISC) and act through RNA interference by imperfect match recognition of target sites in the 3'UTRs of mRNAs, resulting repression of target mRNA expression. Since their first discovery almost two decades ago, hundreds of miRs have been identified, in a wide range of organisms and are the best characterized members of the small non-coding RNA family. They play important roles in almost all biological processes studied, from development to cell death and metabolic control\textsuperscript{69}. Over 60% of all mammalian mRNAs seem to be under the control of miRs, adding an extra layer of control to the already complex regulatory mechanism of gene expression\textsuperscript{90-92}. The miR seed region (5' region nucleotides 2-8) usually binds to mRNA by almost perfect base-pairing, and the miR 3' region binds mRNAs with less accurate base-pairing. Due to the limited size of miRs and their low mRNA binding specificity, miRs target several mRNAs and one mRNA can be targeted by multiple miRs\textsuperscript{93,94}. In the canonical description of the miR pathway, target recognition by the miR leads to a decrease in the abundance of proteins encoded by the target. This has been explained by several mechanisms including posttranscriptional degradation of the target, translational repression and deadenylation-dependent target decay through partially complementary miR target sites in mRNA untranslated regions\textsuperscript{95-97}. Challenging this canonical view of the miR pathway, recent observations suggest that in quiescent cells, a cellular state that may be relevant for aging, miRs induce upregulation of their targets by induction of protein translation, while in cycling/proliferating cells miRs inhibit translation\textsuperscript{98}.

miR biogenesis
Simultaneously with the regulation that individual miRs exert on their specific targets, the miR pathway is regulated at different levels including miR biogenesis and decay\textsuperscript{99}. The ribonucleases (RNases) III Drosha and Dicer as well as Argonaute 2 (Ago2), appear to be essential for miR biogenesis. In mammals, the presence of Dicer is essential for miR biogenesis, as Dicer-deficient mice die at the embryonic stage\textsuperscript{100}. Therefore, specific Dicer deletion and its consequential loss of miRs have been extensively used to characterize the global role of miRs in neurogenesis. Applying this experimental approach, studies have shown that miRs are essential for survival and differentiation of newborn neurons but not for expansion of neural progenitors during early embryonic neurogenesis\textsuperscript{101}. Using a similar approach in mature hippocampal neurons, more recent studies have demonstrated an essential role for miRs in learning and memory\textsuperscript{102}. Accessory proteins of the miR pathway, such as the DiGeorge syndrome critical
region gene 8 (DGCR8) protein, Exportin-5 (Exp-5), TAR RNA binding protein (TRBP) and fragile X mental retardation protein (FMRP) are important in miR biogenesis as well and are affected in a variety of human pathologies. Interestingly, schizophrenia is associated with an increase in cortical miR biogenesis in the adult CNS. This induction of miR biogenesis is linked to an elevation in primary miR processing and corresponds with an increase in the microprocessor component DGCR8.

miR decay

In contrast to miR biogenesis, miR decay has received much less attention. This is probably because miRs are considered to be highly stable molecules. Nevertheless, several examples of regulation of miR turnover are known. Interestingly, recent studies have shown that neurons actively degrade miRs upon synaptic stimulation. In these studies, blocking glutamate receptors prevented the turnover of miR-124, -128, -134, and -138, while the addition of glutamate accelerated it. Notably, the behavior of miR-132 was opposite to that of the other miRs. Its degradation was induced by blocking glutamate receptors and not by the addition of glutamate. These findings suggest a difference in the mechanisms regulating the turnover of miR-132 as compared to other neuronal miRs such as miR-134 or -138.

Roles of individual miRs in NSCs

The actions of several individual miRs on the proliferation, differentiation and synaptogenesis stages of adult neurogenesis have been intensively studied. For example, Szulwach et al. found that miR-137 targets Ezh2 mRNA, thereby promoting proliferation and inhibiting differentiation of NSCs in the SGZ. miR-137 also inhibits dendrite formation through inhibition of its target Mib1 in newborn immature neurons. Based on these observations it would be possible to speculate that changes in miR-137 levels could be partially responsible for the age-dependent decrease in proliferation of NSCs in the SGZ. In this respect, it would be appealing to investigate whether levels of miR-137 and its targets Ezh2 and Mib1 change with aging in NSCs and immature neurons. On the other hand, assuming that one miR alone would be responsible for regulating NSC proliferation, differentiation and integration may be an oversimplification. Indeed, in addition to miR-137, other miRs have been shown to have a regulatory function in the proliferation stage of AHN (Table 1). For example, miR-let-7b reduces stem cell numbers and self-renewal in NSC of the SVZ through its target Hmga2. Supporting a possible role in aging, Nishino et al. demonstrated that changes in let-7b and Hmga2 expression during aging contribute to decline in neural stem cell function. Moreover, miR-137 and let-7b converge on molecular pathways that involve TLS, a member of the nuclear receptor family central in the control of adult NSC renewal and fate determination. Let-7b regulates NSC proliferation and differentiation by targeting, among other mRNAs, TLX. Interestingly, TLX represses the expression of miR-137 by recruiting the histone lysine-specific demethylase 1 (LSD1) to genomic regions of miR-137, providing a clear example of crosstalk between miRs and epigenetic regulatory mechanisms. A possible interaction between of miR-137 and let-7b in regulating NSC function is interesting for multiple reasons. One is that different miRs could agonize or antagonize on particular NSC functions (i.e. proliferation, differentiation, synaptogenesis), potentiating or counteracting their individual effects. Another reason is that the levels of some individual miRs could be altered by aging, while others would not. In this latter scenario, the potentiating or counteracting effects of two miRs on NSCs would dynamically change with aging. Of course, the same questions could be applied not only to miR-137 and let-7b but to other miRs as well. Therefore, we will discuss in greater detail miRs that regulate adult neurogenesis at different stages, their mRNA targets and the subsequent effects.

Another miR with important functions in NSCs is miR-184. The Methyl-CpG binding protein 1 (MBD1) regulates gene expression via epigenetic mechanisms and miR-184 is directly repressed by MBD1 in NSCs, providing an interesting example of crosstalk between epigenetic regulation and miRs. Acting through inhibition of its target mRNA Numbl, high levels of miR-184 promoted proliferation but inhibited differentiation of NSCs. Therefore, MBD1, miR-184 and Numbl form a regulatory network that controls the balance between proliferation and differentiation of NSCs.
The miR cluster miR-106b–25 and miR-25 in particular seems to be relevant in the regulation of NSC proliferation, since inhibition of miR-25 expression resulted in decreased NSC proliferation. Brett et al. proposed that miR-25 would regulate NSC proliferation through a number of potential targets involved in insulin/insulin-like growth factor-1 (IGF) signaling, a pathway implicated in aging. Unfortunately, no direct experimental evidence of this regulation was provided in these studies. Still, the concept of miR-106b–25-dependent regulation of insulin/IGF signaling in NSCs is attractive because a direct link between insulin/IGF signaling activation and subsequent increase in NSC proliferation has been demonstrated before.

Two other well-characterized brain-specific miRs regulate NSCs functions. miR-124 overexpression in HeLa cells, resulted in an expression profile similar to that of brain tissue. Moreover, introducing miR-9 and miR-124 into human fibroblasts caused these cells to develop into functional neurons. These two examples illustrate the potential of miR-9 and miR-124 to profoundly drive cells into a neuronal fate. Therefore, it seems reasonable that miR-9 and miR-124 fulfill a similar role in NSCs of the SGZ. Supporting this hypothesis, miR-9 and miR-124 where found to be abundantly expressed in the human hippocampus and were differentially expressed in fetal and normal aged hippocampus. miR-9 has been linked to enhanced proliferation and migration by regulation of its target Statmin in embryonic stem cell derived NSCs. In the embryonic ventricular zone, miR-9 inhibits proliferation and enhances differentiation through regulation of TLX. In the adult SVZ, miR-124, enhances differentiation of NSCs through regulation of its target the transcription factor Sex Determining Region Y-box 9 (SOX9).

As suggested by the examples discussed before, it is important to realize that single miRs could have opposite effects, depending on the presence of their specific targets in a particular cell type. Therefore, in spite of the well-established roles of several miRs in NSCs of different ages and origins, the question still remains whether they have similar functions in any of the various cell types involved in AHN (Figure 1A). In summary, several miRs have been shown to tightly regulate many targets involved in NSC proliferation, differentiation and maturation. In addition, multiple miRs and other small non-coding RNAs are differentially expressed in the aged hippocampus. This makes small non-coding RNAs appealing candidates to regulate various stages of AHN that may be involved in age-related decrease in cognitive functions.

Table 1 - All the stages of SGZ or SVZ neurogenesis are regulated by miRs, repressing their target mRNAs to be translated.

<table>
<thead>
<tr>
<th>AHN stage</th>
<th>miR</th>
<th>Cell type</th>
<th>Target</th>
<th>Effect</th>
<th>References</th>
</tr>
</thead>
<tbody>
<tr>
<td>Proliferation</td>
<td>let-7b</td>
<td>Adult SVZ mNSCs</td>
<td>Hn ga2</td>
<td>Inhibits</td>
<td>(Nishino et al., 2008)</td>
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<td>miR-9</td>
<td>Adult forebrain mNSCs</td>
<td>TLX</td>
<td>Inhibits</td>
<td>(Zhao et al., 2009)</td>
</tr>
<tr>
<td></td>
<td>miR-106b–25</td>
<td>hNSCs</td>
<td>Statmin</td>
<td>Enhances</td>
<td>(Delaloy et al., 2010)</td>
</tr>
<tr>
<td></td>
<td>miR-137</td>
<td>Adult forebrain mNSCs</td>
<td>IGF/IGFβ?</td>
<td>Promotes</td>
<td>(Brett et al., 2011)</td>
</tr>
<tr>
<td></td>
<td>miR-184</td>
<td>Adult forebrain mNSCs</td>
<td>Ezh2</td>
<td>Promotes</td>
<td>(Szuwach et al., 2010)</td>
</tr>
<tr>
<td></td>
<td>miR-124</td>
<td>Adult forebrain mNSCs</td>
<td>Numb1</td>
<td>Promotes</td>
<td>(Liu et al., 2010)</td>
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<tr>
<td>Differentiation</td>
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<td>TLX</td>
<td>Accelerates</td>
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<tr>
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<td>Inhibits</td>
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</tr>
<tr>
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<td>Statmin</td>
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<td>Synaptogenesis</td>
<td>miR-132</td>
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<td>P250GAP</td>
<td>Promotes</td>
<td>(Magill et al., 2010)</td>
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<td>Integration</td>
<td>miR-132</td>
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<td>Immune</td>
<td>Promotes</td>
<td>(Luikart et al., 2011)</td>
</tr>
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</table>

mNSCs: mouse neural stem cells, hNSCs: human neural stem cells, regular characters: found in SGZ, italics: found in SVZ, (?) no direct evidence shown
miRNA-132: a key miR for newborn cell integration into hippocampal circuits

After the literature overview presented in the previous section and summarized in Figure 1A, it becomes apparent that many miRs play key roles in the initial phases of AHN. Besides their regulatory roles in proliferation, differentiation and migration (Table 1) some miRs, including the previously discussed miR-137, have also been identified as regulators of synaptogenesis and neuronal integration of newborn immature neurons in the SGZ107. More specifically, by deleting the locus encoding miR-132 Magill et al. demonstrated a dramatic decrease in dendrite length, arborization and spine density of the newborn immature neurons123. Using lentiviral and retroviral reporters of miR-132 activity, Luikart et al. showed miR-132 is “at the right place and right time” to regulate the integration of newborn immature neurons124. In addition to morphological changes, Luikart et al. showed that newly born GCs have impaired synaptic connectivity after miR-132 inactivation. As mentioned before, newborn neurons in the aging DG are as capable of synapse formation and functional integration as neurons born in a younger DG53. Therefore, if miR-132 would be a key factor in maintaining synaptogenic potential in newborn neurons during aging, its levels should be unaffected by aging in these cells. Indeed, recent studies have shown that miR-132 levels remain unchanged in fetal, aged and even Alzheimer’s patient hippocampus119.

Assuming that some of the miR-132’s regulatory capabilities and target networks are conserved between mature and newborn neurons, some of the observations on the function of miR-132 in synaptogenesis of mature neurons could be extrapolated to adult-born neurons in the DG. This assumption has the limitation discussed before for other miRs, i.e., the overall effect of a particular miR may depend on the specific repertoire of targets expressed in the cell type of interest. Yet, in mature neurons much more details are known about the cellular compartments, pathways and networks in which miR-132 functions125 (Figure 1B).

Overexpression of miR-132 in cultured hippocampal neurons revealed that miR-132 modulates short-term synaptic plasticity126, and overexpression in vivo triggers an increase in dendritic spine density and impaired novel object recognition memory127. Besides these relevant functions of miR-132 plays in regulating synaptic plasticity and memory, miR-132 expression is strongly regulated by neuronal activity123,124. Upon activation of cortical neurons, cAMP-response element binding protein (CREB) induces miR-132 expression through the CaMK-MEK/ERK-CREB pathway128, a mechanism probably also present in hippocampal, olfactory bulb and striatal neurons and neurons of the visual cortex129-131. Aging in humans is strongly associated with changes in the circadian clock, resulting in strong sleep alterations in the elderly132. In rodents, sleep deprivation strongly inhibits AHN through HPA axis-dependent and -independent mechanisms133,134. Again, miRs may provide a link between alterations in the circadian clock and human health disorders associated with aging. In particular, miR-219 and miR-132 modulate the circadian clock. From these two, only miR-132 is induced by light via a MAPK/CREB-dependent mechanism, and modulates clock-gene expression and attenuates the entraining effects of light on the circadian clock135. These findings have suggested that approaches to increase the robustness of the circadian clock by controlling miR expression may counteract the fragmentation of the sleep-wake cycle associated with aging136.

As all miRs, miR-132 targets multiple mRNAs including p250GAP128,137, MeCP2138, SIRT1139, p120RasGAP140 and p300141. miR-132 and its target p250GAP play a key role in activity-dependent structural and functional plasticity in hippocampal neurons137. P250GAP is highly abundant in the postsynaptic density, where it interacts with multiple proteins involved in synaptic plasticity such as the tyrosine kinase Fyn142, β-Catenin143,144, the NR2B subunit of the NMDA receptor and the PSD-95 scaffolding protein145. Other p250GAP partners within the Rho family, including Rac1 and Cdc42 regulate actin cytoskeleton organization146,147. These findings suggest that miR-132 is a central regulator of synaptic plasticity, capable of linking synaptic activity with changes in synaptic structure by repressing p250GAP expression and thereby altering the composition of the synapse in an activity dependent manner.
Another target of miR-132 is MeCP2\(^{138}\), capable of binding methylated DNA and either repressing or activating transcription\(^{148}\). Important in synaptic plasticity, mutations and/or altered levels of MeCP2 have been linked to severe neurodevelopmental disorders such as Rett syndrome, Angelman’s syndrome and autism\(^{148}\). Blocking miR-132 in primary cortical neurons elevates MeCP2 expression and subsequently increases BDNF levels, while loss of MeCP2 reduces BDNF and miR-132 levels, indicating a feedback loop that involves miR-132 and regulates MeCP2 expression\(^{138}\). Importantly, MeCP2 depletion in human and mouse brain causes an increase in expression of two neuronal gene transcriptional repressors REST (RE1 silencing transcription factor), and CoREST and is associated with a change in the histone modification profile to a more active conformation, suggesting that MeCP2 is a central regulator of epigenetic processes in the brain\(^{150}\). This demonstrates another example of crosstalk between epigenetic regulation and miRs that could have a relevant role in AHN, since epigenetic regulation seems to play an important role in AHN and neuropsychiatric disorders\(^{151}\).

**Potential interaction of miR-132 with other miRs**

Highlighting the relevance of the crosstalk between classical epigenetic mechanisms and miRs, MeCP2 is a key regulator of miR-137 expression too\(^{106,152}\). Therefore, miR-132 could regulate miR-137 expression through MeCP2, finally resulting in modulation of the miR-137 target Mib1. This miR-132-MeCP2-miR-137-Mib1 pathway could result in an inhibition of immature neuron maturation (Figure 1B), which would contradict the previously described pro-maturation effect of miR-132. This may not be completely unexpected, as exemplified by several seemingly paradoxical effects of miRs on NSC proliferation discussed before. Nevertheless, one simple explanation could be that miR-132 and miR-137 are not expressed simultaneously during maturation of NSCs. Therefore, in future studies the potential interactions between signaling pathways modulated by miR-132 and miR-137 would have to be carefully validated experimentally.

Pharmacological or genetic upregulation of the sirtuin (silent mating type information regulation 2 homolog) pathway, associated with anti-aging effects of calorie restriction, has shown promising results in laboratory models of aging\(^{155}\). The sirtuin SIRT1, is involved in NSC fate determination and SIRT1 is required for NSCs to adopt an astrocytic fate at the expense of the neuronal lineage under oxidative stress\(^{154}\). Interestingly, SIRT1 has been identified as a target of miR-132\(^{139}\). Moreover, SIRT1 limits the expression of another brain-specific miR, miR-134. SIRT1 deficiency results in miR-134 upregulation and concomitant, downregulation of CREB and BDNF, thereby impairing synaptic plasticity\(^{155}\). Therefore, the miR-132-SIRT1 pathway could connect miR-132 to another regulator of dendritic spine development, miR-134 (Figure 1B).

As miR-132 inhibits SIRT1\(^{139}\), it would relieve SIRT1-mediated repression of miR-134 resulting in increased levels of miR-134 and decreased CREB and BDNF expression and described by Gao et al. Alternatively, miR-134 negatively regulates Limk1, decreasing the size of dendritic spines\(^{156}\). The theoretical anti-synaptogenic effect that miR-132 could exert via both the miR-132-SIRT1-miR-134-Limk1 and miR-132-MeCP2-miR-137-Mib1 pathways, contrasts with the observations made with miR-132 overexpression in vivo, which triggers an increase in dendritic spine density\(^{127}\) and highlights a complex homeostatic balance network in which miR-132 may function by competing or interacting with other miRs to fine-tune expression of relevant targets during synaptogenesis (Figure 1B).

Underlining the complexity of miRs regulation of synaptogenesis, other targets downstream of miR-134, including BDNF and CREB\(^{155}\), complete a complex self-regulatory circle in the following theoretical pathway: miR-132-SIRT1-miR-134-CREB-miR-132. Simpler feedback regulatory loops controlling self-expression are well-characterized features of miR pathways in NSCs\(^{109,157}\). Therefore, further experiments would be needed to verify the proposed interaction between miR-132 and miR-134 through SIRT1 and CREB in NSCs. Notably, an increase in chromatin instability and DNA breaks correlates with aging in mammals. In response to DNA damage, SIRT1 relocates to DNA breaks to promote repair, resulting in transcriptional changes that parallel those observed in the aging mouse brain\(^{158}\). Although SIRT1 levels change with aging in various brain
areas in mice the hippocampus was not analyzed in this study. Extrapolating from observations showing a preserved synaptogenic and functional activation potential of newborn GCs in the aging DG one would predict SIRT1 levels to be unaffected by aging in adult-born immature neurons of the SGZ. This would be in agreement with results discussed before showing that miR-132 expression seems to be unaffected by aging.

In summary, miRs are strategically placed within intrinsic regulatory networks that coordinate AHN. It is evident that levels of some miRs can change with aging, affecting the expression of their specific targets, while levels of other miRs seem to be unaffected. Thus, the next question is which could be the factors regulate expression of specific miRs during aging. In the following section we will discuss the possibility that steroid hormones could be involved in this regulation.

Could an interplay between miRs and steroid hormones be involved in aging-associated cognitive decline?

Healthy aging in humans is associated with a decline in plasma concentrations of several hormones and a gradual loss of function of endocrine systems. Traditionally, the development of physical frailty and a gradual loss in cognitive function that aging brings about, has been considered to be physiological and unavoidable. In recent years, however, it has become evident that it might not be necessary to accept the stereotype of aging as an unalterable process of decline and loss, particularly in terms of cognitive abilities i.e. memory functions, that so profoundly mark our individual experiences and feelings of well-being in late life.

In humans, the adrenal glands synthesize and secrete large amounts the chemical precursors of sex steroid hormones (dehydroepiandrosterone and its sulfate) and neuroactive steroids. More than 30% of total androgens in elderly men and more than 90% of estrogen in postmenopausal women are derived from these precursors. In aging, a progressive and continuous decline in circulating levels of these precursors has been observed, while levels of the glucocorticoid stress hormone cortisol, synthesized primarily in the adrenal glands, show a parallel linear increase in some aging humans. Importantly, estrogens and glucocorticoids are strong regulators of the miR biogenesis pathway. Both hormones have been shown to control the expression of Dicer-1 and other key enzymes in miR synthesis in different experimental systems. These observations suggest that steroid hormones may be crucial in favoring the expression of miR sets or "signatures" involved in the coordination of gene networks.

Although the effects of steroid hormones are strongly tissue and cell type specific, these observations suggest that steroid hormone regulation of miR biogenesis could be involved in the changes in miR expression associated with aging in the brain.

Low levels of circulating estrogens in post-menopause females have been linked to cognitive deficits. In rats, estrogen replacement after ovariectomy increases LTP and dendritic spine density in hippocampal neurons, suggesting a key role of estrogen signaling in synaptic plasticity. The estrogen receptor α (ERα) is a steroid hormone receptor that can be acetylated - and thereby activated - by p300, a target of miR-132. In addition, SIRT1 is found to promote ERα expression. Overall, these data indicate yet another potential pathway regulating synaptogenesis, in which miR-132 could be central.

Alterations in Glucocorticoid levels and possible effects on aging

Cortisol production by the adrenals influences memory and cognition during aging. Higher cortisol levels are associated with a poorer memory performance and a higher likelihood of memory decline, especially in women. These detrimental effects of cortisol seem to be directed at the hippocampus. In healthy elderly individuals, cortisol levels seemed to be associated with cognitive impairment. Therefore, stress and resulting increases in glucocorticoid levels may have important consequences on the degree and speed of decline in memory and other cognitive abilities in the elderly. Although increasing levels of glucocorticoids are not always found in aged individuals, high levels of glucocorticoids are associated
Moreover, glucocorticoids may influence not only cell birth and death, but also pathways that regulate GC differentiation and survival. These glucocorticoid-mediated pathways may involve some miRs with key roles in NSCs. For example, both glucocorticoid and mineralocorticoid receptors are targets of miR-124,121,168,166. Interestingly, recent observations in human NSCs have shown that GR activation inhibits the expression of neuronal differentiation markers. Therefore, in a likely scenario, the gradual increases in miR-124 that takes place during neuronal differentiation of adult NSCs, may help to fine tune GR expression to a physiological range that promotes a pro-neuronal phenotype.

In conclusion, we have reviewed literature that supports a role for AHN in DG-dependent cognitive functions related to memory, and have discussed how alterations in this process may be related to aging-associated cognitive decline. Furthermore, we have described how miRs could be placed among the factors that control the generation of adult-born neurons in the hippocampus. Moreover, we propose that miRs are strategically positioned within regulatory networks that fine-tune at different levels the proliferation, differentiation, survival and synaptogenesis of adult-born neurons. Finally, we reviewed evidence suggesting that aging-associated changes in circulating levels of steroid hormones, in particular estrogens and glucocorticoids, are associated with cognitive decline and proposed that these changes may impact on AHN through signaling networks that involve miRs. In the future, new experimental efforts will address whether this hypothesis holds true and if so, how could we use it to design new therapeutic interventions that may help us reach a successful healthy aging.

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References


66. Michel, B. F. et al. [In Alzheimer’s disease, the clinical expression of behavioral and psychological signs and symptoms is early and specific of neuropathological stages]. Encephale 36, 314–325 (2010).
microRNAs and regulation of adult neurogenesis


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