RESEARCH ARTICLE

MicroRNA expression profiling in neurogenesis of adipose tissue-derived stem cells

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Abstract

Adipose tissue-derived stem cells (ADSCs) are one population of adult stem cells that can self renew and differentiate into multiple lineages. Because of advantages in method and quantity of acquisition, ADSCs are gaining attention as an alternative source of bone marrow mesenchymal stem cells. In this study, we performed microRNA profiling of undifferentiated and of neurally-differentiated ADSCs to identify the responsible microRNAs in neurogenesis using this type of stem cell. MicroRNAs from four different donors were analysed by microarray. Compared to the undifferentiation control, we identified 39–101 microRNAs with more than two-fold higher expression and 3–9 microRNAs with two-fold lower expression. The identified microRNAs were further analysed in terms of gene ontology (GO) in relation with neurogenesis, based on their target mRNAs predicted by computational analysis. This study revealed the specific microRNAs involved in neurogenesis via microRNA microarray, and may provide the basic information for genetic induction of adult stem cell differentiation using microRNAs.

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Introduction

Stem cells have the capacity to self renew and to differentiate into multiple lineages that can be largely divided into embryonic stem cells or adult stem cells (Passier and Mummer[y](#page-12-0) [2003\)](#page-12-0). Embryonic stem cells have the greatest differentiation capability, however there are considerable challenges to the use of these cells for clinical application, including ethical limitations (Borge and Ever[s](#page-12-1) [2003\)](#page-12-1). Adult stem cells have less potency, but higher availability than embryonic stem cells.

Adult stem cells can be obtained from a variety of adult tissues including brain, blood, muscle, skin, bone marrow, umbilical cord blood, amniotic fluid and adipose tissue (Clarke and Frise[n](#page-12-2) [2001;](#page-12-2) Prockop *et al[.](#page-12-3)* [2001;](#page-12-3) In 't Anker *et al[.](#page-12-4)* [2004](#page-12-4); Lu *et al[.](#page-12-5)* [2006;](#page-12-5) Schaffler and Buchle[r](#page-12-6) [2007](#page-12-6); Roh *et al[.](#page-12-7)* [2008\)](#page-12-7). Because of their capacity for differentiation into a variety of cell types including osteoblasts, chondrocytes, myocytes, adipocytes, and neural cells under certain conditions. (Musina *et al[.](#page-12-8)* [2006;](#page-12-8) Chamberlain *et al[.](#page-12-9)* [2007\)](#page-12-9), adult stem cells are now in growing demand in various medical fields, including plastic surgery and regenerative medicine. Among these sources, adipose tissue-derived stem cells (ADSCs) are gaining importance due to their ease of acquisition in large numbers (Mizun[o](#page-12-10) [2003;](#page-12-10) Pansky *et al[.](#page-12-11)* [2007\)](#page-12-11).

Due to the growth in the safe application of stem cellbased cell therapy towards medical treatment, it becomes important to understand more about stem cell biology. Emerging evidence indicates that microRNAs play a critical role in maintenance, differentiation and lineage commitment of stem cells, as they are found to be involved in various cellular and biological processes (Krichevsky *et al[.](#page-12-12)* [2006](#page-12-12); Foshay and Gallican[o](#page-12-13) [2007](#page-12-13)).

MicroRNAs (miRNAs) are short (18–25 nucleotides) endogenous noncoding RNAs that post transcriptionally regulate gene expression (Mallory and Vauchere[t](#page-12-14) [2004](#page-12-14)). miRNAs are generated in several processing steps. Primary miRNA (pri-miRNA) transcripts are produced in the cell nucleus by RNA polymerase II and then cleaved to precursor miRNAs (pre-miRNA) by RNase type III enzyme Drosha (Du and Zamor[e](#page-12-15) [2005;](#page-12-15) Zeng *et al[.](#page-12-16)* [2005](#page-12-16)) The pre-miRNAs are then transported to cytoplasm where they become mature miRNA by another RNase type III enzyme Dicer (Gregory *et al[.](#page-12-17)* [2006](#page-12-17)) The mature miRNA become a component of the RNA induced silencing complex (RISC), which can bind to

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3' untranslated regions (UTRs) of messenger RNAs through partial or complete base pairing (Tang *et al[.](#page-12-18)* [2008](#page-12-18)). The major function of miRNAs is to silence the paired messenger RNAs by degradation or translation repression (Behm-Ansmant *et al[.](#page-12-19)* [2006](#page-12-19)) Although miRNA expression profiling has been performed in embryonic stem cells, the basic information on their expression patterns in adult stem cells has not been fully established yet (Foshay and Gallican[o](#page-12-13) [2007;](#page-12-13) Wang *et al[.](#page-12-20)* [2008](#page-12-20)).

We have been interested in neurogenesis using ADSCs for future clinical application in neurodegenerative diseases. Hence, we attempted to investigate the importance of miRNA expression and function in ADSCs' biology by performing miRNA expression profiling in undifferentiated and neurally-differentiated ADSCs and identified the critical miRNAs in neurogenesis using the ADSCs by analysing the microarray data using computational software and webderived databases.

Materials and methods

Isolation of ADSCs

ADSCs obtained from lipoaspirates of four different donors were washed extensively with sterile phosphate-buffered saline (PBS) to remove contaminating debris and red blood cells (Zuk *et al[.](#page-12-21)* [2001](#page-12-21); Raposio *et al[.](#page-12-22)* [2007\)](#page-12-22). The washed aspirates were treated with 0.075% collagenase (type I; Sigma-Aldrich, Missouri, USA) in PBS for 60 min at 37◦C with gentle agitation, followed by inactivation with an equal volume of DMEM/10% foetal bovine serum (FBS). After centrifugation for 10 min at low speed, the cellular pellet was resuspended in DMEM/10% FBS and filtrated through a 100 μm mesh filter to remove debris. The filtrate was centrifuged as detailed above and plated onto conventional tissue culture plates in control medium (DMEM, 10% FBS, 1% antibiotic/antimycotic solution) and maintained at 37◦C in a $CO₂$ incubator. The ADSCs utilized in this study underwent 3–5 passages. Each donor was fully informed and provided informed consent at the Kangbuk Samsung Hospital prior to study enrollment. The study protocols were approved by the institutional review board (IRB) of Kangbuk Samsung Hospital.

Neurogenesis of ADSCs

The ADSCs used in this study were differentiated into the neural lineage as previously established (Ashjian *et al[.](#page-12-23)* [2003](#page-12-23)) Briefly, the cells were cultured for 2 weeks in neural induction media composed of control medium plus 5 μg/mL Insulin, 200 μM Indomethacin and 0.5 mM IBMX which was replaced every 2–3 days. The successful neurogenesis was confirmed by RT-PCR and immunocytochemistry for the neuron-specific markers including NF-M,

Figure 1. Neurogenesis of ADSCs from four different donors. (A) Microscopic observation of ADSCs that were undifferentiated or neurodifferentiated. The representative images were obtained at 100-fold magnitude. (B) RT-PCR for neuro-specific genes. RNAs were extracted from undifferentiated (C) and neurodifferentiated (donor # 1, 2, 3, 4) ADSCs. After reverse-transcription, PCR was performed using each gene-specific primers and then resolved in agarose gel. Images were obtained by gel documentation system.

NSE, MAP2 and GFAP. Primers used for RT-PCR are as follows: NF-M, forward primer 5'-ggaggaagacatccaccggc-3' and reverse primer 5'-gccggtactcggcgatctct-3'; NSE, forward primer: 5'-atcgcgccagccctcatcag-3' and reverse primer: 5'-ttttccgtgtagccagcctt-3', MAP2, forward primer: 5'-tcagaggcaatgaccttacc-3' and reverse primer: 5' gtggtaggctcttggtcttt-3'. Antibodies for immunocytochemistry were purchased from Millipore (Peenya, Bangalore) (anti-NSE and anti-NF-M antibody; Bangalore, India), SIGMA (St Louise, USA) (anti-MAP2 antibody) and DAKO (Carpinteria, USA) (anti-GFAP antibody).

RNA preparation and qualification

Total RNA was isolated from the cells with TRIZOL reagent (Invitrogen, Carlsbad, USA). Briefly, cells were lysed by suspension in TRIZOL solution and subsequent addition of chloroform. After centrifugation, the clear supernatant

Figure 2. Verification for successful neurogenesis of the ADSCs. Immunocytochemistry was performed to confirm the successful neurogenesis of the four different ADSCs that were undifferentiated or neurodifferentiated. Cells were incubated with antibodies against NF-M (A), GFAP (B) or MAP2 (C), and subsequently Alexa488-tagged secondary antibodies (green colour). The images were obtained by fluorescence microscopy after counter staining with nuclear-staining dye DAPI (blue colour).

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a, b, [∗], probes for different regions of the same miRNA; 5p, 5' side of stem-loop sequence; 3p, 3' side of stem loop sequence.

was transferred to a new tube and mixed with isopropanol, followed by another round of centrifugation. The pellet was washed with 75% ethanol solution and then centrifuged following the same procedures as stated earlier. The final pellet was air-dried and suspended in RNase-free water. The quality of the isolated RNA was evaluated using Agilent's 2100 Bioanalyzer system (Santa Clara, CA, USA), as RNA integrity number (RIN) through migration pattern by electrophoretic trace and peak pattern by electropherogram. RNA with RIN above 7 was utilized in the microarray analysis.

Microarray analysis

To control and test RNAs, the synthesis of target miRNA probes and hybridization were performed using Agilent's miRNA Labelling Reagent and Hybridization kit (Agilent Technology, Santa Clara, USA) according to the manufacturer's instructions. Briefly, each 100 ng of total RNA were dephosphorylated with ∼15 units of calf intestine alkaline phosphatase (CIP), followed by RNA denaturation with ∼40% DMSO and 10 min incubation at 100◦C. Dephosphorylated RNA was ligated with pCp-Cy3

Figure 3. Unsupervised hierarchical clustering of miRNAs. The expression levels of miRNAs were compared between undifferentiated and neurodifferentiated groups, upregulated miRNAs by neurogenesis were shown as red and downregulated miRNAs by neurogenesis were shown as green.

Table 2. miRNAs upregulated or downregulated at over 2 fold after neurogenesis of ADSCs.

Donor $#1$		Donor#2		Donor $#3$		Donor#4	
miRNA ID	Neu/Con	miRNA ID	Neu/Con	miRNA ID	Neu/Con	miRNA ID	Neu/Con
Upregulated							
hsa-miR-452 $*$	12.3649	hsa-miR-124a	22.3409	hsa-miR-124a	12.8188	hsa-mi $R-373*$	8.99201
hsa-miR-629	12.2515	hsa-miR-335	10.29985	hsa-miR-345	7.047919	hsa-miR-126	7.35977
ebv-miR-BART20-3p	11.18480	hsa-mi $R-373*$	9.718501	hsa-mi $R-584$	6.86552	$hsa-miR-149$	6.12764
hsa-miR-126	11.00000	hsa-miR-452*	9.038787	$hsa-miR-132$	6.157643	$hsa-miR-132$	6.09768
hsa-miR-32	11.00000	hsa-miR-560	7.817356	hsa-mi $R-452*$	6.029531	hsa-miR-452 $*$	5.9293
hsa-miR-124a	8.99336	hsa-miR-629	7.001485	hsa-miR-146b	5.475309	hsa-mi $R-560$	4.72855
hsa-miR-500	8.868321	hsa-miR-345	6.522692	hsa-miR-181a	4.335888	hsa-miR-564	4.46107
hsa-miR-30c	8.591849	hcmv-miR-UL70-3p	6.4893	hsa-miR-801	4.234988	hsa-miR-345	4.23609
hsa-miR-452	7.954802	hsa-mi $R-584$	5.95749	ebv-miR-BART19	4.001035	hsa-mi $R-324-5p$	4.21623
hsa-miR-30b	7.114367	hsa -mi $R-137$	5.812335	hsa-miR-30c	3.868032	hsa -mi $R-191$	3.70129
hsa-miR-532	6.994533	hsa-miR-452	5.726561	hsa-miR-191	3.727272	hsa-mi $R-452$	3.68101
hsa-miR-191	6.761363	hsa-mi $R-126$	5.512305	hsa-mi $R-455$	3.597304	hsa-mi $R-663$	3.58290
hsa-miR-660	6.522535	hsa -mi $R-210$	5.106823	hsa-miR-373*	3.594157	hsa-miR-181a	3.48405
hsa-miR-560	6.406269	hsa-mi $R-630$	4.604335	hsa-mi $R-126$	3.493665	$hsa-miR-30c$	3.25191
hsa-miR-584	6.320209	hsa-miR-34a	4.548903	hsa-mi $R-564$	3.018522	hsa-let-7i	3.16957
hsa-mi $R-324-5p$	5.823898	hsa-miR-128a	4.508485	hsa-miR-452	2.909913	hsa-miR-148b	3.08372
hsa-mi $R-663$	5.741501	hsa-miR-128b	4.507167	hsa-mi $R-324-5p$	2.902999	$hsa-miR-103$	2.93546
hsa-miR-198	5.38616	hsa-miR-191	4.385028	hsa-miR-768-3p	2.87438	$hsa-miR-33$	2.86461
hsa-mi $R-769-5p$	5.381649	hsa-miR-324-5 p	4.30642	hsa-miR-148b	2.787305	hsa-miR-30b	2.82572
hsa-miR-190	5.299296	hsa-miR-34b	4.002358	hsa -mi $R-491$	2.50978	hsa-mi $R-602$	2.79583
hsa-miR-149	5.241024	hsa-miR-660	3.744209	hsa-miR-30a-5p	2.388547	hsa-mi $R-768-5p$	2.72545
hsa-miR-491	5.15773	hsa-miR-32	3.722026	hsa-miR-30b	2.379695	hsa-miR-107	2.68212
hcmv-miR-UL70-3p	5.15466	$hsa-miR-30c$	3.70265	hsa-miR-557	2.362832	hsa-mi $R-630$	2.65980
hsa-miR-345	5.146942	hsa-miR-181a	3.681028	hsa-miR-342	2.336154	hsa-mi $R-652$	2.60935
hsa-mi $R-373*$	5.10286	hsa-miR-30b	3.567784	hsa-let-7i	2.304572	hsa-miR-34a	2.55219
hsa-miR-34a	4.814482	hsa-let-7i	3.519226	hsa-miR-560	2.301989	hsa-mi $R-185$	2.52091
$hsa-miR-30e-5p$	4.673209	hsa-miR-422b	3.507341	hsa -mi R -103	2.284109	hsa-mi $R-768-3p$	2.49794
hsa-miR-34b	4.639537	hsa-mi $R-663$	3.480477	hsa-miR-181c	2.231021	hsa-mi $R-574$	2.49607
hsa-miR-148b	4.638073 4.569371	hsa-miR-196a hsa-miR-198	3.408277	hsa-miR-320	2.202201 2.179526	hsa -mi $R-197$	2.49528
hsa-miR-101 hsa-miR-137	4.536166	hsa-miR-532	3.356802 3.340554	hsa-miR-422b hsa-miR-149	2.150473	hsa -mi $R-101$ hsa-mi $R-629$	2.48669 2.42244
hsa-miR-128b	4.421787	hsa-miR-149	3.282256	hsa-miR-34a	2.147344	$hsa-miR-320$	2.410985
hsa-miR-374	4.360524	hsa-miR-500	3.252840	hsa-miR-500	2.113932	hsa-miR-125b	2.36336
hsa-miR-422b	4.259643	hsa-miR-374	3.214476	hsa-miR-494	2.107529	hsa-miR-146b	2.34493
hsa-miR-10a	4.243414	hsa-miR-574	3.192512	hsa-miR-34b	2.073393	hsa-miR-34b	2.29725
hsa-miR-181a	4.169982	hsa-miR-101	3.155423	kshv-miR-K12-3	2.072254	hsa-miR-584	2.27556
hsa-miR-197	4.134848	hsa-mi $R-107$	3.028175	hsa-mi $R-107$	2.031978	hsa-miR-196a	2.23804
hsa-miR-574	4.036704	hsa-miR-148b	3.027027	hsa-miR-146a	2.020711	hsa-mi $R-572$	2.22798
hsa-miR-630	3.997406	hsa-miR-224	2.988696	hsa-mi $R-532$	2.020271	hsa-mi $R-30a-5p$	2.19691
hsa-mi $R-30a-5p$	3.788593	$hsa-miR-30e-3p$	2.963207			hsa -mi R -181 c	2.18760
hsa-let-7i	3.728025	hsa-mi $R-103$	2.95928			hsa-miR-98	2.18565
hsa-miR-572	3.721510	kshv-miR-K12-3	2.957622			hsa-mi $R-425-5p$	2.18087
hsa-mi $R-768-3p$	3.504502	hsa-miR-601	2.937058			hsa-miR-565	2.16676
hsa-miR-103	3.490409	hsa-mi $R-572$	2.926896			hsa-miR-24	2.14789
hsa-miR-362	3.485242	hsa-miR-30e-5p	2.912391			$hsa-let-7g$	2.13755
hsa-miR-224	3.401972	hsa-miR-10a	2.886910			hsa-miR-23a	2.12465
hsa-miR-107	3.400869	hsa-mi $R-638$	2.859239			hsa-miR-125a	2.10804
hsa-miR-98	3.394763	hsa-miR-98	2.769848			hsa-let-7d	2.08312
hsa-miR-26a	3.331323	hsa-miR-15a	2.754295			hsa-let-7e	2.07814
hsa-miR-148a	3.305013	hsa-mi $R-30a-5p$	2.729208			$hsa-miR-152$	2.06899
hsa -mi $R-210$	3.283549	hsa-miR-185	2.692396			hsa-let-7a	2.06242
hsa-miR-15a	3.178056	hsa-miR-25	2.665933			hsa-miR-32	2.04561
$hsa-let-7g$	3.171610	$hsa-miR-197$	2.662608			hsa-miR-25	2.01883
hsa-let-7d	3.163391	hsa-miR-125b	2.640156			hsa-miR-30d	2.01789
hsa-mi $R-652$	3.152711	hsa-let-7g	2.639784			hsa-miR-532	2.01505
hsa-miR-146b	3.151944	hsa-miR-22	2.622234			$hsa-miR-221$	2.01049
hsa-miR-361	3.129899	hsa-mi $R-365$	2.600721				
hsa-miR-602 hsa-let-7e	3.123897 3.073295	hsa-miR-768-3p hsa-miR-33	2.598262 2.579403				

The numbers indicate the ratio that was obtained by dividing the signal intensity (expression level) of each probe after neurogenesis (Neu) by that before neurogenesis (Con). Therefore, the more regulated, the upper located at the list.

a, b, *, probes for different regions of the same miRNA; 5p, 5' side of stem-loop sequence; 3p, 3' side of stem loop sequence.

mononucleotide and purified with MicroBioSpin 6 columns (Bio-Rad, Gurgaon, India). After purification, labelled samples were resuspended with Gene Expression blocking reagent and Hi-RPM Hybridization buffer, followed by boiling for 5 min at 100◦C and 5 min chilling on ice. Finally, denatured labelled probes were pipetted onto assembled Agilent's miRNA microarray (15 K) and hybridized for 20 h at 55◦C with 20 RPM rotating in Agilent Hybridization oven (Agilent Technology, USA). The hybridized microarrays were washed as the manufacturer's washing protocol (Agilent Technology, USA).

Data acquisition and analysis

The hybridized images were scanned using Agilent's DNA microarray scanner and quantified with Feature Extraction Software (Agilent Technology, Palo Alto, USA). All data normalization and selection of fold-changed genes were performed using GeneSpringGX 7.3 (Agilent Technology, Palo Alto, USA). The averages of normalized ratios were calculated by dividing the average of normalized signal channel intensity by the average of normalized control channel intensity (Lopez-Romero *et al[.](#page-12-24)* [2010\)](#page-12-24) Functional annotation of genes was performed according to Gene Ontology™ Consortium by GeneSpringGX 7.3 [\(http://www.geneontology.org/index.shtml\)](http://www.geneontology.org/index.shtml).

MicroRNA target predictions and gene ontology (GO)

The human targets of the differentially expressed miRNAs were predicted using public websites such as miRBase Targets [\(http://microrna.sanger.ac.uk/targets/v5\)](http://microrna.sanger.ac.uk/targets/v5). The GO of the predicted targets was analysed using functional items on [http://www.geneontology.org.](http://www.geneontology.org)

Results and discussion

Identification of miRNAs expressed in undifferentiated ADSCs

Although miRNAs are expected to play critical roles in the biological processes of adult stem cells including self renewal and differentiation, there is very little information about them. We performed the human miRNA microarray (see table 1 in electronic supplementary material at [http://www.ias.ac.in/jgenet/;](http://www.ias.ac.in/jgenet/) gene expression omnibus accession number GSE15290), using the extracted RNA from ADSCs of four different donors which were undifferentiated and differentiated into neural lineage. Neurogenesis was

Figure 4. Supervised hierarchical clustering of miRNAs. Supervised clustering was performed for downregulated (A) or upregulated (B) miRNA at over two-fold by neurogenesis.

followed by the method previously reported (Ashjian *et al[.](#page-12-23)* [2003\)](#page-12-23) and verified by microscopic observation and also RT-PCR (figure [1\)](#page-1-0), followed by immunocytochemistry for neurogenic markers (figure [2\)](#page-2-0). The specificity of neurogenesis was confirmed by performing RT-PCR for adipocyte-specific genes (PPARγ , Adiponectin, LPL) (see figure 1 in electronic supplementary material).

First, we analysed the miRNA expression profile of the undifferentiated ADSCs. Of the 550 probes, about 190– 200 miRNAs were found to be statistically significant on analysis, and the results are listed in table [1](#page-3-0) according to their expression level. The comparison between the donors revealed the similar miRNA expression profiling, which have the high expression of mir-29a, mir-125b, let-7a, mir-27a, mir-24, and mir-222 in common. This analysis suggests that undifferentiated ADSCs express the unique set of miRNAs to maintain the stem cell characteristics.

Identification of miRNAs expressed in differentiated ADSCs into neural lineage

Then, we compared the miRNA profiling of the undifferentiated ADSCs with that of the differentiated ADSCs. The unsupervised hierarchical clustering analysis showed that the ADSCs of four donors had the very similar expression patterns for a specific miRNA (figure [3\)](#page-6-0), indicating that ADSCs commonly express a specific set of miRNAs for neurogenesis.

We screened the miRNAs according to the level of expression change by neurogenesis. As compared to miRNAs that were unchanged or not significantly changed at below 2-fold by neurogenesis (see table 2 in electronic supplementary material), table [2](#page-7-0) displays the summarized list of miRNAs that were upregulated or downregulated at over

Figure 5. Measurement of the top changing miRNAs by real-time RT-PCR. Among miRNAs that were differentially expressed during neurogenesis, representative several miRNAs were analysed by real-time PCR using relative quantification method. Data were normalized with a house-keeping gene *RNU48*, and were presented as fold change for each miRNA in 'neuro' sample relatively calculated by 'control' sample.

2-fold by neurogenesis. It was interesting that the number of the upregulated miRNAs (39–101 miRNAs) was much higher than the number of the downregulated miRNAs (3–9 miRNAs). As with the miRNA expression profiling of undifferentiated ADSCs, the miRNA profiling changed by the differentiation that showed the common expression regulation pattern in four donors. As shown in figure [4,](#page-9-0) some miRNAs were upregulated (miR-452, miR-126, miR-560, miR-373, miR-584, miR-149, miR-191, miR-30c etc.) and some miRNAs were downregulated (miR-138, miR-503 and miR-154). To validate the microarray data, we performed real-time PCR for the several top changing miRNA that were differentially expressed during neurogenesis (figure [5\)](#page-10-0). These results demonstrated clearly the different miRNA profiling before and after differentiation, suggesting that the combination of those upregulated or downregulated miRNAs may promote the neurogenic differentiation.

Assortment of miRNAs specifically involved in development of neuron cells

We performed the chemically-induced neurogenesis method to generate all the neural cells including neurons, astrocytes and oligodendrocytes. Thus, we examined whether a specific combination of miRNAs is involved in the generation of each cell type. For this purpose, we predicted the target genes for each miRNA listed in table [2](#page-7-0) using the Sanger database $(\text{http://microma.sanger.ac.uk/targets/v5})$. Then, we assorted the predicted target genes using the GO website (amigo; [http://www.geneontology.org\)](http://www.geneontology.org) by matching them with genes classified according to ontology. First, we obtained the list of miRNAs that are expected to be involved in neuron generation (Ontology search term was 'neuron morphogenesis during differentiation' and 'regulation of neurogenesis') (table [3\)](#page-11-0). Interestingly, most of the top-ranked miRNAs in table [2](#page-7-0) belong to this category (eg. miR-126, miR-373, miR-584, miR-149, miR-191, miR-30c etc.). Some of the miRNAs in this table were well-known miRNAs that are involved in other differentiation processes, such as chondrogenesis (miR-663 and miR-638) and adipogenesis (miR-103 and miR-107) (Wilfred *et al[.](#page-12-25)* [2007;](#page-12-25) Lakshmipathy and Har[t](#page-12-26) [2008](#page-12-26)). In addition, the downregulated miR-503 was previously found to be involved in pancreas development (Joglekar *et al[.](#page-12-27)* [2007\)](#page-12-27).

Assortment of miRNAs specifically involved in development of glial cells

We made a list of miRNAs that are expected to participate in the generation of astrocytes and oligodendrocytes (ontology search term was 'regulation of astrocyte differentiation' and 'oligodendrocyte differentiation') in table [4.](#page-11-1) Two miRNAs, miR-560 and miR-452, were among the top-ranked miRNAs in table [2.](#page-7-0)

Finally, we selected miRNAs that we predicted would be involved in generation of both neuron cells and glial cells

Table 3. miRNAs specifically related to neuron cell generation.

Upregulated	Downregulated
hsa-miR- $373*$	$hsa-miR-503$
$hsa-miR-584$	hsa-mi $R-154*$
$hsa-miR-126$	
$hsa-miR-191$	
$hsa-miR-30c$	
$hsa-miR-132$	
$hsa-miR-149$	
$hsa-miR-148b$	
$hsa-miR-663$	
hsa-miR-34b	
$hsa-miR-137$	
hsa-let-7i	
hsa-miR-30b	
$hsa-miR-630$	
$hsa-miR-103$	
hsa-mi $R-768-3p$	
$hsa-miR-107$	
$hsa-miR-572$	
$hsa-miR-101$	
$hsa-miR-660$	
$hsa-miR-32$	
hsa-miR-652	
$hsa-miR-500$	
$hsa-miR-564$	
hsa-miR-638	
hsa-miR-198	
$hsa-miR-30d$	
hsa-miR-210	
hsa-miR-98	
$hsa-let-7g$	
hsa-let-7e	
hsa-let-7d	
$hsa-miR-557$	
$hsa-miR-152$	

Table 4. miRNAs specifically related to glial cell generation.

(table [5\)](#page-11-2). In this list, we noticed that miR-324-5p and miR-181a were among the top-ranked miRNAs in table [2.](#page-7-0) As both, neuron cells and surrounding glial cells should cooperate to accomplish their biological functions, we propose that miRNAs in this list may provide an important role in clinical and therapeutic aspects for the treatment of neuron-degenerative diseases.

In this study, we used the neurogenesis method developed by Ashjian *et al[.](#page-12-23)* [\(2003](#page-12-23)) for generation of neuro-progenitor cells using ADSCs (Ashjian *et al[.](#page-12-23)* [2003\)](#page-12-23) We assumed that there might be some variations in miRNA profiling according to neurogenesis method, by method and by stem cell origin. Nevertheless, this study provides the first clue that a unique set of miRNAs play a role in specific differentiation of ADSCs.

A recent study reported the miRNA expression profiles of human embryonic stem cells that were undifferentiated and differentiated into endodermal lineage. This study also proposes the possibility of a potential role for specific miRNAs in endodermal differentiation of hESC (Tzur *et al[.](#page-12-28)* [2008\)](#page-12-28). Another study found that the modulation of a single miRNA could promote the formation of adipocytes from precursor cells (Esau *et al[.](#page-12-29)* [2004](#page-12-29)) Consistent with those studies, our study provides attention to the fact that stem cells can be differentiated to neural cells by a single or combined treatment of the miRNA(s) revealed in this study.

Most of the miRNAs in this study have not been previously reported in relationship to neurogenesis. Among the miRNAs distinctly-regulated in neuron cells, miR-373, miR-126, and miR-30 are only known to be related to tumour cell biogenesis, such as metastasis stimulation or suppression, and structural change of the extra-cellular matrix (Duisters *et al[.](#page-12-30)* [2009;](#page-12-30) Huang *et al[.](#page-12-31)* [2008](#page-12-31); Tavazoie *et al[.](#page-12-32)* [2008](#page-12-32)). These miRNAs are the first to be reported towards the neurogenesis of ADSCs, and may play significant roles in regulating neurogenic differentiation using these cells. Several miRNAs including miR-532, miR-574, miR-124, miR-342 and miR-33 were not found in the GO database related to neurogenesis and cannot be sorted by miRNAs to any of the GO categories.

Since there is a possibility of some changes to the results if a different normalization protocol is used, we need further studies to confirm the vast scale of information touched upon in this study. Nevertheless, this study suggests the specific set of miRNAs that may possess a potential role in neurogenesis and thereby provides a possibility about a new strategy using miRNAs in clinical application of ASCs for neurodegenerative diseases by demonstrating the unique set of miRNAs in undifferentiated and neurally-differentiated ADSCs.

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