The path to microRNA therapeutics in psychiatric and neurodegenerative disorders

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The microRNA (miRNA) class of non-coding RNAs exhibit a diverse range of regulatory roles in neuronal functions that are conserved from lower vertebrates to primates. Disruption of miRNA expression has compellingly been linked to pathogenesis in neuropsychiatric and neurodegenerative disorders, such as schizophrenia, Alzheimer's disease, and autism. The list of transcript targets governed by a single miRNA provide a molecular paradigm applicable for therapeutic intervention. Indeed, reports have shown that specific manipulation of a miRNA in cell or animal models can significantly alter phenotypes linked with neurological disease. Here, we review how a diverse range of biological systems, including *Drosophila*, rodents, and primates such as monkeys and humans, can be integrated into the translation of miRNAs as novel clinical targets.

Keywords: microRNAs, psychiatric, neurodegeneration, non-coding RNA, therapeutics, schizophrenia, monkeys, primates

INTRODUCTION

The multi-functional role of RNA as a molecular regulator spans a broad range of classifications as protein-coding and non-protein coding RNA transcripts. Notably, the microRNA (miRNA) class of non-coding RNAs have been implicated in a vast majority of the established signaling cascades (Bartel, 2009). Brain-localized miRNAs are of particular interest for neurological diseases which have a complex etiology and no currently effective therapeutic options. The transcriptomic targets of an miRNA can encompass numerous cellular pathways, consistent with the extensive molecular disruption linked to neurological disease onset. In this review, we discuss how various model systems can be integrated into the translation of miRNAs as novel clinical targets in the treatment of neuropsychiatric and neurodegenerative disorders.

CONSERVED ROLE OF NEURONAL miRNAs

The conserved role of miRNAs in neuronal functions underscores their relevance in the molecular dynamics between normal and pathogenic mechanisms. Indeed, *Drosophila*, rodents, monkeys, and humans have all shown significant sensitivity to microRNA modulation (Jin et al., 2004; Ashraf et al., 2006; Elmen et al., 2008; Hollander et al., 2010). Notably, some core components of the miRNA processing machinery, guided by the RNA-induced silencing complex (RISC), are shared between lower vertebrates and primates, such as the Argonaute-interacting proteins, GW182 (Chekulaeva and Filipowicz, 2009; Chekulaeva et al., 2011) and the 5′ pocket motif of the Dicer-homologs (Park et al., 2011). Furthermore, regulation of long-term memory processes and associated synaptic proteins are controlled by the miRNA RISC pathway in a diverse group of species (Ashraf et al., 2006; Rajasethupathy et al., 2009; Gao et al., 2010; Konopka et al., 2010). Collectively, the previous reports indicate that epigenetic modulation by miRNAs are a principal component to central nervous system development and homeostasis.

Several of the more extensively reported brain-enriched miRNAs, such as miR-9, miR-34, miR-124, miR-128, miR132, miR-219, have predominantly identical mature sequences across species, including humans, monkeys, mice, and *Drosophila* (Kapsimali et al., 2007; Hu et al., 2011; Juhila et al., 2011). The conservation of those miRNAs spans from the 5′ seed region to the 3′ end of the transcript. Moreover, the precursor sequence for some of the brain-enriched miRNAs, including miR-9 and miR-124, are also identical between humans and mice, further supporting a highly conserved function for those transcripts.

miRNA REGULATION IN NEUROPSYCHIATRIC AND NEURODEGENERATIVE DISORDERS

In the past few years, an extensive list of published reports have emerged to support a significant role for miRNAs in the pathogenesis of psychiatric and neurodegenerative disease (Bilen et al., 2006; Lukiw, 2007; Hebert et al., 2008, 2009; Li et al., 2008, 2011; Wang et al., 2009, 2010, 2011; Beveridge et al., 2010; Nelson and Wang, 2010; Nunez-Iglesias et al., 2010; Shioya et al., 2010; Chandrasekar and Dreyer, 2011; Kocerha et al., 2011; Lee et al., 2011; Santarelli et al., 2011; Smith et al., 2011; Liu et al., 2012b). The pathogenic mechanisms underlying the development of psychiatric deficits and neurodegeneration are not always distinct, suggesting they may be ideally suited for therapeutic targeting by pleiotropic miRNAs. Reports have shown that the precursor and mature miRNA transcripts as well as the miRNA processing machinery itself, such as Drosha and Dicer, are all subject to disruption with neurological disease progression (Sun et al., 2009; Beveridge et al., 2010; Babiarz et al., 2011; Fenelon et al., 2011; Schofield et al., 2011). Notably, the miRNA-linked pathology can be provoked through either genetic or non-genetic (sporadic) anomalies (Rademakers et al., 2008; Kocerha et al., 2011).

Schizophrenia, autism, Fragile X syndrome, depression, addiction, and anxiety are a few examples of psychiatric diagnoses where

altered miRNA profiles have been identified, and a summary of the dysregulated miRNAs and the biological source they were profiled from are outlined in **Table 1** (Jin et al., 2004; Abu-Elneel et al., 2008; Li et al., 2008; Pietrzykowski et al., 2008; Hunsberger et al., 2009; Yang et al., 2009; Zhou et al., 2009; Zhu et al., 2009; Beveridge et al., 2010; Hollander et al., 2010; Im et al., 2010; Sarachana et al., 2010; Saus et al., 2010; Xu et al., 2010a,b; Baudry et al., 2011a,b; Eipper-Mains et al., 2011; Ghahramani Seno et al., 2011; Haramati et al., 2011; Mouillet-Richard et al., 2011; O'Connor et al., 2011; Shaltiel et al., 2012). In schizophrenia, miRNA profiling has now been completed in several patient populations, primarily focused within the cortex (Perkins et al., 2007; Beveridge et al., 2010; Kim et al., 2010; Moreau et al., 2011; Santarelli et al., 2011). Although a majority of the miRNA profiling studies for neurological disease have been performed from brain, miRNA dysregulation has also been observed in other sources such as cerebral spinal fluid

(CSF), plasma, serum, and peripheral blood (Schipper et al., 2007; Cogswell et al., 2008; Gardiner et al., 2011; Ghidoni et al., 2011; Lai et al., 2011). Beveridge and Cairns (2011) recently reviewed the various studies to compare and contrast the collection of miRNA results in schizophrenia. Interestingly, a few of the miRNA families, including the miR-15 and miR-30 families, have consistently shown disruption in several of the population analyses (Beveridge and Cairns, 2011). We examined the bioinformatic mRNA targets of miR-15 and miR-30 with Targetscan and found several mRNAs which are strongly linked with schizophrenia, including neuregulin and synaptotagmin (Kim et al., 2007; Kao et al., 2010).

Psychiatric symptoms can also co-exist in patients with neurodegenerative pathology, such as Huntington's disease (HD), Frontotemporal dementia (FTD), Alzheimer's disease (AD), Parkinson's disease (PD), and amyotrophic lateral sclerosis (ALS),

Table 1 | miRNAs associated with neuropsychiatric disease.

Disease	Associated miRNAs	Biological profiling source	Reference
Schizophrenia	106b, 107, 128a, 134, 150, 15a, 15b, 16, 17, 181a, 181b, 195, 199a*, 19a, 20a, 20b, 212, 219, 24, 25, 26b, 27a, 29a, 29b, 29c, 30a-5p, 30b, 30d, 30e, 328, 346, 382, 487a, 9-3p, 92, let-7d, let-7e, 652, 7	Human cortex (temporal and prefrontal)	Beveridge et al. (2008, 2010), Zhu et al. (2009), Perkins et al. (2007), Santarelli et al. (2011)
	219	Cortex from mouse model of schizophrenia	Kocerha et al. (2009)
	137, 30e	Human genomic DNA	Ripke et al. (2011), Xu et al. (2010a)
	30e, 34a, 449a, 564, 432, 548d, 572, 652	Human blood	Xu et al. (2010a), Lai et al. (2011)
Schizophrenia or bipolar disorder	106b, 132*, 132, 133b, 138, 140-3p, 145*, 145, 148b, 151, 154*, 15a, 181a, 186, 190, 192, 193a, 193b, 210, 212, 22*, 22, 27b, 29a, 301, 32, 324-3p, 33, 330, 338, 339, 34a, 425, 454*, 504, 520c-3p, 544, 545, 573, 639, 7, 767-5p, 874, 889, 99a	Human cortex	Moreau et al. (2011), Kim et al. (2010)
Autism	106a, 106b, 128, 129, 132, 140, 146b, 148b, 15a, 15b, 181d, 193b, 21, 212, 23a, 27a, 320a, 381, 431, 432, 484, 539, 550, 598, 652, 7, 93, 95	Human cerebellum	Abu-Elneel et al. (2008)
	103, 106b, 107, 10a, 125b, 132, 133b, 136, 139, 148b, 153-1, 16-2, 182-AS, 185, 186, 189, 190, 191, 194, 195, 196a, 199a-5p, 199b, 199b-5p, 205, 211, 219, 23a, 23b, 25, 29b, 30c, 326, 338-3p, 346, 367, 376a-AS, 451, 455, 455-3p, 486-3p, 486-5p, 495, 518a, 519c, 520b, 524, 577, 650, 93	Lymphoblastoid cell lines	Sarachana et al. (2010), Ghahramani Seno et al. (2011)
Depression	16	Mouse serotonergic raphe nuclei	Baudry et al. (2011a,b)
	182, 30e	Human genomic DNA (blood)	Saus et al. (2010), Xu et al. (2010b)
	101, 10a, 130a, 137, 142-3p, 142-5p, 146a, 148b, 155, 190, 20a, 20b, 27a, 301a, 324-5p, 335, 376a*, 489, 494, 497, 660	Human prefrontal cortex	Smalheiser et al. (2012)
Addiction	212, 132, 124, let-7d, 181a	Brain tissue from rat cocaine addiction model	Hollander et al. (2010), Chandrasekar and Dreyer (2011)
	103, 125b-5p, 127, 138, 181a, 24, 26a, 29a, 29b, 30a, 30c, 30d, 30e, 7a, 7b, 7c, 7c, 9, let-7a, let-7f, let-7g	Brain tissue from mouse cocaine addiction model	Eipper-Mains et al. (2011)
	9	Striatal neuronal cultures for model of alcohol exposure	Pietrzykowski et al. (2008)
Anxiety	132, 34	Brain tissue from mouse model of anxiety	Shaltiel et al. (2012), Haramati et al. (2011)

all of which have shown miRNA disruption and is summarized in **Table 2** (Wang et al., 0000; Hebert et al., 2008; Packer et al., 2008; Hebert and De Strooper, 2009; Williams et al., 2009; Haramati et al., 2010; Jiao et al., 2010; Lau and de Strooper, 2010; Buckley and Johnson, 2011; Gaughwin et al., 2011; Kocerha et al., 2011; Lee et al., 2011; Martins et al., 2011; Minones-Moyano et al., 2011; Smith et al., 2011; Enciu et al., 2012; Mouradian, 2012). A pivotal role for miRNAs in neurodegenerative disease is further supported by numerous reports linking miRNAs with neurogenesis and neurodegenerative signaling cascades, and thus, overall neuronal density (Patel et al., 2008; Boissonneault et al., 2009; Gao, 2010; Magill et al., 2010; Schonrock et al., 2010; Shi et al., 2010; Cho et al., 2011; Shibata et al., 2011; Tao et al., 2011; Han et al., 2012; Persengiev et al., 2012).

Some miRNAs, such as miR-132, have been shown to be dysregulated in both psychiatric and neurodegenerative disease. miR-132 has been linked with schizophrenia (Perkins et al., 2007; Kim et al., 2010), addiction (Hollander et al., 2010), HD (Lee et al., 2011), AD (Cogswell et al., 2008), and progressive supranuclear palsy (PSP; Smith et al., 2011). Indeed, the wide range of neurological diseases in which miR-132 is disrupted is consistent with its principal role in neuronal plasticity and related functions (Magill et al., 2010; Remenyi et al., 2010; Mellios et al., 2011; Shaltiel et al., 2012).

NON-PRIMATE MODELS AND miRNA THERAPEUTIC DISCOVERY

A selection of cell and animal models have been engaged in the preliminary search for miRNAs with clinical relevance for neurological disease. Cell lines, primary cell cultures, differentiated neurons, and induced pluripotent stem (iPS) cells are a few of the platforms that have effectively been utilized for *in vitro* analyses (Cole et al., 2008; Agostini et al., 2011; Arias-Carrion and Salama, 2011; Kim et al., 2011; Saba et al., 2012). Indeed, cell-based systems have led to successful large-scale screening studies as well as in-depth molecular analysis of functional miRNAs (Vo et al., 2005; Cole et al., 2008; Connelly et al., 2012). For example, the discovery that neuronally enriched miR-132 is regulated by cAMP-response element binding protein (CREB) was initiated through a genome-wide screen in rat PC12 neuronal cells (Vo et al., 2005). Not all miRNAs will have a functional biological role, however, cell-based screens can facilitate the identification of promising candidates.

In parallel with the *in vitro* findings, studies in non-primate animal models have significantly advanced our understanding of miRNA biology in psychiatric and neurodegenerative disorders (Kocerha et al., 2009; Hollander et al., 2010; Lee et al., 2011; Li et al., 2011). Animal studies are a critical step in the progression toward testing of miRNA-based therapeutics in clinical trials. Our group examined the regulation of miRNAs in mice with pharmacological induction of a schizophrenia-associated behavioral phenotype (Kocerha et al., 2009). Likewise, a neurotoxin induced mouse model (1-methyl-4-phenyl-1,2,3,6-tetrahydropyridine; MPTP) for Parkinson's disease (PD) was used to uncover a role for miR-7 in PD pathology (Junn et al., 2009). In addition to pharmacologically treated animal models, transgenic, knock-out and knock-in mice have also been valuable *in vivo*

resources (Lee et al., 2011; Tao et al., 2011). Indeed, transgenic expression of the AD-causative amyloid precursor protein (APP) gene in mice provoked significant disruption in neuronal miRNA expression (Schonrock et al., 2010).

In addition to mice, rats as well as zebrafish and other vertebrate species have been integral in the study of neuronal miRNA pathways prior to testing in primate models (Yang et al., 2011; Tal et al., 2012). Indeed, recent reports identified miRNAs in zebrafish directly linked to neurobehavioral responses and neuronal differentiation (Tal et al., 2012). The exploration of miRNAs which regulate central nervous system functions, however, is not limited to vertebrate species. *Drosophila*, an invertebrate model, have been widely used for many years to examine or further define molecular mechanisms. Moreover, studies in *Drosophila* recently revealed that the conserved miRNA miR-34 mediates aging and neurodegenerative processes (Liu et al., 2012a), further substantiating that all biological models are applicable in the investigation of non-coding RNAs. Additionally, as each miRNA may regulate a number of transcripts and therefore off-target effects may result when altered, animal and cell models may help to filter out those candidates.

PRIMATE MODELS AND miRNA PRE-CLINICAL EVALUATION

Arguably, a principal goal in the field of non-coding RNAs, including miRNAs, is to uncover transcripts which can ultimately lead to advancements in human health. Correspondingly, there are numerous studies which have profiled miRNA expression from humans with and without a disease diagnosis. Although some of those reports have focused on peripheral tissues, a subset of those analyses have specifically examined miRNA transcripts in distinct brain regions (Hebert et al., 2008; Kocerha et al., 2011; Santarelli et al., 2011). Genome-wide association (GWAS) studies and microarray profiling have both been used to identify miRNAs which are potential disease risk factors for neurodegenerative and psychiatric disorders (Rademakers et al., 2008; Hollander et al., 2010; Kocerha et al., 2011; Richardson et al., 2011; Ripke et al., 2011). Furthermore, there can be disruption of a cluster or multiple members within an miRNA family, such as with miR-29. In brain tissue from a cohort of Alzheimer's patients, miR-29a and miR-29b expression were both significantly repressed in patients with increased levels of beta-secretase/*BACE1* (Hebert et al., 2008). *BACE1* is a direct mRNA target for the miR-29 family and has consistently been linked to AD pathology. Therefore, correlation of expression for a miRNA and its targets in the transcriptome, as well as identification of disruption in miRNA families, can all contribute to effective discovery of new treatment alternatives for diagnosed patients.

The brain structure and related functions of humans and monkeys are strikingly similar (King and Wilson, 1975; McConkey and Varki, 2000; Paabo, 2001; Perkins et al., 2010; de Araujo et al., 2012), suggesting that monkeys are a relevant primate model for pre-clinical investigation of miRNAs in neurological dysfunction. Notably, certain key cell types in the brain linked to disease pathology, such as mirror neuron disruption in autism (Perkins et al., 2010), are primarily specific to primate physiology. Moreover, there is extensive conservation in miRNAs between primates, including those which are localized in the central nervous system

Table 2 | miRNAs associated with neurodegenerative disease.

Disease	Associated miRNAs	Biological profiling source	Reference
Huntington's disease (HD)	100, 125b, 127-3p, 135a, 135b, 138, 145, 146, 146a, 148a, 150, 181c, 190, 199a-3p, 199a-5p, 200a, 205, 214, 218, 221, 222, 335, 338-3p, 9*, 9	Huntington cell lines	Ghose et al. (2011), Sinha et al. (2010)
	34b	Human plasma	Gaughwin et al. (2011)
	1-1, 124a, 128, 132, 133a, 135b, 138, 203, 204, 21, 218, 22, 222, 29a, 29b-1, 29c, 330, 344, 346, 674*, 9-1, 9-3	Brain tissue from transgenic HD mice	Lee et al. (2011), Johnson et al. (2008)
	100, 151, 16, 219-2-3p, 27b, 451, 92a, 128, 139-3p, 222, 382, 433, 485-3p, 9, 9*, 29b, 124a, 132	Human brain regions	Marti et al. (2010), Packer et al. (2008)
Frontotemporal dementia (FTLD)	922, 516a-3p, 571, 548b-5p, 548c-5p	Human cortex and cerebellum	Kocerha et al. (2011)
	29b, 107	Cell cultures	Wang et al. (2010), Jiao et al. (2010)
	659	Human genomic DNA	Rademakers et al. (2008)
Parkinson's disease (PD)	1, 126*, 126, 147, 151-3p, 151-5p, 16-2*, 199a-3p, 19b, 22*, 26a, 26a2*, 28-5p, 29a, 29b, 29c, 301a, 30a, 30b, 30c, 335, 374a, 374b	Human blood	Martins et al. (2011), Margis and Rieder. (2011)
	34b, 34c, 133b	Human brain	Minones-Moyano et al. (2011), Kim et al. (2007)
	50, 83, 58, 77, 238, 1, 48, 65, 64, 80, 84, let-7, 236, 51, 241, 230,	C. elegans	Asikainen et al. (2010)
	10a, 10b, 212, 132, 495	Mouse model for PD	Gillardon et al. (2008)
	let-7, 184*	Drosophila	Gehrke et al. (2010)
Amylotrophic lateral sclerosis (ALS)	206	Mouse model for ALS	Williams et al. (2009)
Alzheimer's disease (AD)	137, 181c, 9, 29a, 29b, 34a, 181b	Human blood	Geekiyanage et al. (2011), Schipper et al. (2007)
	137, 181c, 9, 29a, 29b	Human serum	Geekiyanage et al. (2011)
	101, 106b, 107, 125b, 137, 142-3p, 142-5p, 145, 151-5p, 15a, 181c, 184, 185, 194, 197, 19b, 210, 212, 214, 219-2-3p, 22, 223, 26b, 27b, 298, 29a, 29a/b-1, 29b-1, 300, 301a, 320, 326, 330-5p, 338-3p, 338-5p, 361-3p, 363, 382, 424, 425, 509-5p, 511, 516a-5p, 516b, 525-5p, 551b, 576-5p, 583, 9, 93, 98, let-7e, let-7f, let-7i	Human cortex	Wang et al. (2011), Hebert et al. (2008), Shioya et al. (2010), Nelson and Wang (2010), Geekiyanage and Chan (2011)
	9, 125b, 128, 124a	Human hippocampus	Lukiw (2007)
	105, 10a, 10b, 125a, 126*, 126, 127, 135a, 138, 141, 142-5p, 143, 146b, 151, 154, 15b, 181a, 181c, 186, 191, 194, 195, 197, 199a*, 204, 205, 214, 216, 221, 302b, 30a-3p, 30a-5p, 30b, 30c, 30d, 32, 338, 345, 362, 371, 374, 375, 380-3p, 422b, 429, 448, 449, 451, 455, 494, 497, 501, 517a, 517b, 518b, 518f, 520a*, 526a, 7f, 99a	Human CSF	Cogswell et al. (2008)
	125b, 106b, 107, 124, 132, 145, 146b, 148a, 17-5p, 200c, 20a, 210, 212, 26a, 27a, 27b, 30c, 30e-5p, 34a, 381, 422a, 423, 425, 9, 92, let-7b, 100	Human brain	Cogswell et al. (2008), Hebert et al. (2009), Smith et al. (2011), Wang et al. (2008)
	106a, 106b, 125b, 137, 146a, 147, 148b, 153, 17, 17-5p, 181c, 187, 20a, 20b, 21, 212, 26a, 27a, 298, 301, 30b, 30c, 30e-5p, 323-3p, 328, 34a, 361, 365, 376b, 381, 409, 422a, 423, 433, 520c, 644, 655, 664, 700, 7g, 7i, 9, 92	Cell cultures	Long and Lahiri. (2011), Kim et al. (2011), Boissonneault et al. (2009), Patel et al. (2008), Schonrock et al. (2010), Delay et al. (2011), Hebert et al. (2009), Smith et al. (2011)
	34a, 103, 107, 146a, 106b, 16, 34c, 20a, 17-5p	AD mice models	Yao et al. (2010), Li et al. (2011), Wang et al. (2009, 2010), Liu et al. (2012b), Zovoilis et al. (2011), Hebert et al. (2009)
	214, 23a, 23b, 486-3p, 30e*, 143, 128, 27a, 27b, 324-5p, 422a	Bioinformatic single nucleotide polymorphism (SNP) analysis	Mallick and Ghosh. (2011)

(Brameier, 2010; Hu et al., 2011). One recent study reported that of the 413 miRNAs expressed in human brain, 366 of those transcripts are also detectable in rhesus macaque brain (Hu et al., 2011). Correspondingly, a number of those miRNAs are also detectable in mouse cortex and hippocampus by microarray and sequencing efforts, such as miR-9, miR-124, miR-128, and miR-132 (Juhila et al., 2011), suggesting that mouse models can be effective prior to testing in primates.

There have been considerable technological advancements in recent years with primate focused research, including with non-coding RNA biology. Groups have successfully delivered modified-antisense oligonucleotides (ASO) into monkeys to inhibit the function of specific miRNAs with minimal off-target effects (Elmen et al., 2008; Petri et al., 2009; Lanford et al., 2010). To date, the ability to modulate miRNAs in primates is restricted to peripheral administration, however, delivery of potential therapeutics across the blood brain barrier could be a future attainable milestone. Progress has also been made in other capacities with primates, including with the generation of transgenic monkeys. Our group established the first transgenic rhesus macaques in 2001 (Chan et al., 2001), which subsequently led to the development of a cohort for HD transgenic monkeys (Yang et al., 2008), a resource directly applicable to assess miRNA functions in a primate model of neurodegenerative disease. Moreover, from the HD monkeys we derived iPS cells which display a progressive cellular phenotype (Chan et al., 2010), providing an *in vitro* platform to complement the *in vivo* analyses for therapeutic and biomarker discovery, including non-coding RNA targets.

In primates, the progression of neurodegeneration and psychiatric deficits is typically gradual, developing over years, rather than weeks or months. Correspondingly, longitudinal analyses of molecular and neurobehavorial changes are fundamental to the monitoring and subsequent discovery of new treatments (Insel, 2009; Thompson et al., 2011). Indeed, longitudinal studies are readily implementable in primate species such as monkeys and humans, including collection of peripheral blood samples for molecular analysis throughout disease progression and parallel correlation with brain morphology by magnetic resonance imaging (MRI; Thompson et al., 2011; Waber et al., 2012; Zhang et al., 2012). The correlation of miRNA expression with disease trajectories may help identify functional non-coding RNA transcripts involved in neuronal pathogenesis.

APPROACHES FOR miRNA MODULATION AND CLINICAL TRANSLATION

As discussed above, a considerable number of *in vitro* and *in vivo* models are increasingly becoming available for miRNA functional studies. In conjunction, there have also been significant advances in the approaches to modulate or detect specific miRNAs. Viral and antisense-mediated targeting of non-coding transcripts are routinely applied to alter expression levels, however, technical improvements have allowed for increased effectiveness and efficacy. For example, locked nucleic-modified antisense oligonucleotides (LNA-ASO) significantly enhance the specificity and stability of miRNA silencing (Elmen et al., 2008; Stenvang et al., 2008; Kocerha et al., 2009; Hollander et al., 2010; Obad et al., 2011).

Notably, the LNA-ASO can be administered *in vivo* to animal models through different routes, such as intracerebroventricular (icv) delivery to penetrate multiple brain regions (Kocerha et al., 2009; He et al., 2010), or local stereotactic injections for site-specific miRNA silencing (Gao et al., 2010; Hollander et al., 2010). LNA-modified probes also intensify the detectability of non-coding RNAs for *in situ* localization (Havelda, 2010), which facilitates examination of less abundant transcripts. There are other chemical modifications available for ASO, such as 2′-*O*-methyl RNA, 2′-*O*-methyloxyethyl RNA, and phosphorothioate RNA (Ruberti et al., 2011), some of which have also been successfully utilized in the context of *in vivo* silencing (Cheng et al., 2009).

In addition to viral and antisense methods, nanoparticle delivery of neurogenic miRNAs provide a means for brain distribution of selected transcripts. Just recently, reports showed that rabies virus glycoprotein (RGV)-labeled nanomaterials resulted in specific delivery of miR-124 to neuronal cells (Hwang do et al., 2011). Nanotechnology has also been employed to silence miRNA function, such as with miR-122 conjugated to gold nanoparticles in myeloma cells (Crew et al., 2012), suggesting this technology is effective in the repression or stimulation of miRNA expression.

Importantly, silencing of miRNAs in animal embryos have also provided significant insight to their role in brain development. Recent reports have shown that injection of morpholinos to block miR-9 activity in the embryos of *Xenopus tropicalis* (Bonev et al., 2011) or zebrafish (Tal et al., 2012) substantially altered neuronal functions in the developing animals. Furthermore, overexpression or silencing of miR-9 via electroporation in mouse embryos revealed that Cajal Retzius neuronal cell differentiation is regulated through Forkhead box protein G1 (FOXG1; Shibata et al., 2008). Collectively, these reports indicate that miRNA activity can be modulated *in vivo* at various developmental stages to assess their implications in brain functions.

Overall, the technical developments in miRNA biology mentioned above facilitate the translation of select miRNA transcripts for future clinical intervention. Indeed, there are human trials currently being conducted to assess miRNA-modulation in disease pathogenesis, including the use of LNA-ASO (Seto, 2010; Montgomery and van Rooij, 2011). To date, the reported human trials have focused on miRNA regulation in peripheral organs, however, therapeutic targeting of the brain remains a future objective. Polymer (Cheng and Saltzman, 2012), lipid (Shi et al., 2012), and polylysine (Jin et al., 2012) based nanoparticle modulation of miRNAs has also been reported. Although a majority of the nanodelivery methods for miRNA studies have focused on non-neuronal cells, there is great potential for their application to the central nervous system.

CONCLUSION

The discovery and development of miRNA-based therapeutics, as well as the diverse range of molecular cascades they can regulate, offer a new approach for treating diseases with a heterogeneic or epigenetic origin. There are numerous psychiatric and neurodegenerative diseases with no effective treatments due to their

complex etiology and therefore may be ideally positioned for clinical targeting of pleiotropic miRNAs.

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