

Current Progress for the Use of miRNAs in Glioblastoma Treatment

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Abstract Glioblastoma (GBM) is a highly aggressive brain cancer with the worst prognosis of any central nervous system disease despite intensive multimodal therapy. Inevitably, glioblastoma is fatal, with recurrence of treatment-resistant tumour growth at distal sites leading to an extremely low median survival rate of 12–15 months from the time of initial diagnosis. With the advent of microarray and gene profiling technology, researchers have investigated trends in genetic alterations and, in this regard, the role of dysregulated microRNAs (highly conserved endogenous small RNA molecules) in glioblastoma has been studied with a view to identifying novel mechanisms of acquired drug resistance and allow for development of microRNA (miRNA)-based therapeutics for GBM patients. Considering the development of miRNA research from initial association to GBM to commercial development of miR-based therapeutics in less than a decade, it is not beyond reasonable doubt to anticipate significant advancements in this field of study, hopefully with the ultimate conclusion of improved patient outcome. This review discusses the recent advancements in miRNA-based therapeutic development for use in glioblastoma treatment and the challenges faced with respect to in vivo and clinical application.

Keywords Glioblastoma · MicroRNA · In vivo · Treatment

Introduction

The term ‘brain tumour’ is a standard idiom for an intracranial solid neoplasm which is located either within the brain

itself or within the spinal canal. Although diagnosis of any form of brain cancer is innately serious and life threatening, patient prognosis and overall survival rates differ greatly with respect to the precise classification of the brain tumour type. Glioblastoma (GBM) is a highly aggressive subtype of glioma, designated as a grade IV astrocytoma by the World Health Organization [1, 2]. This form of glioma is extremely invasive with the worst prognosis of any central nervous system disease despite multimodal therapy. Typically, primary care involves mass surgical resection through open craniotomy; however, the infiltrative nature of the glioblastoma cells typically requires post-operative radiotherapy (RT) and concurrent chemotherapy (temozolomide) treatment [3]. Inevitably, glioblastoma is fatal, with recurrence of treatment-resistant tumour growth at distal sites leading to an extremely low median survival rate of 12–15 months from the time of initial diagnosis [3].

Many aspects of glioblastoma contribute to its poor prognosis including the invasive nature of these abnormal cells [4] and the extreme heterogeneity of this cancer both intratumourally and between patients [5]. In addition, treatment progression has been hindered by challenges including drug delivery across the blood–brain barrier (BBB), not to mention the delicate procedures required to remove such tumours completely in the first instance. Despite the extensive clinical differences between individual patients, current treatment regimens are unilaterally applied with the resulting consequence that many patients do not respond to standard therapy and are not reaching median survival times. In this regard, researchers have begun to focus their studies on identifying genetic biomarkers in the hope of developing individual-based treatment options through patient sample gene profiling and deep sequencing for known mutations; for example, our group has previously identified a subset of glioblastoma patients with gene mutations in alternative lengthening of telomeres and isocitrate dehydrogenase 1 which is indicative of improved survival and drug

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responsiveness [6] or the clinical associate of miR-124a with reduced glioblastoma survival rates as a result of altered invasive potential [7].

With the advent of microarray and gene profiling technology, new studies have allowed researchers to investigate trends in genetic alterations which may provide result in the development of novel therapeutics for GBM patients [4, 8–15]. Assessment of differential gene expression in glioblastoma patient samples led to the discovery that O6-methylguanine-DNA methyltransferase (MGMT) promoter methylation status is a clinical indicator of a patient's intrinsic resistance to temozolomide treatment [16–18]. Temozolomide is an alkylating chemotherapy which causes cytotoxic DNA damage such as O6-methylguanine [19, 20]. MGMT is a DNA repair enzyme responsible for the removal of an alkyl group from the O⁶ position of guanine [21]. MGMT promoter methylation is an epigenetic modification in some glioblastoma resulting in MGMT protein suppression. When expression is silenced, these cancer cells are not capable of repairing the damaging effects induced by alkylating chemotherapy agents thereby rendering them more effective in induction of tumour damage. In phase III clinical trials, MGMT methylation status was shown to be a significant predictive marker of temozolomide (TMZ)/RT treatment response [20, 22]; however, survival rates still remain less than 15 months suggesting that additional genetic biomarkers need to be identified to allow more targeted therapeutic development.

In this regard, over the past decade, the role of dysregulated microRNAs in glioblastoma has been studied with a view to identifying potentially novel mechanisms of acquired drug resistance and allow for development of microRNA (miRNA)-based therapeutics for GBM patients.

MicroRNAs in Glioblastoma

miRNAs are highly conserved endogenous small RNA molecules of approximately 22 nucleotides in length, functioning through complementary messenger RNA (mRNA) base pairing and subsequent gene silencing. Although similar to RNA interference (RNAi), resulting from the use of short interfering RNA (siRNA) or short hairpin RNA (shRNA), complementarity between the target mRNA and the miRNA is not 100 % complete, and therefore, a single miRNA can regulate multiple protein transcripts; unlike an siRNA which is designed to be single-target specific. This mechanism of miRNA function has been referred to as the 'one hit multiple target' mechanism (Fig. 1) [23, 24].

Transport of microRNAs from one cell type to another, to elicit their effect, has recently been associated with bioactive vesicles called exosomes [25]. Studies of these small extracellular vesicles have shown that miRNAs can be functionally transported by such means [26, 27]. Exosomal shuttling of

miRNAs has been identified in glioblastoma and malignant glioma [28], thereby identifying a mechanism by which tumour-derived miRNA-loaded exosomes can target specific proteins in surrounding cell types, effecting processes such as angiogenesis and reduced immune response [29].

Although miRNAs were first characterized in the early 1990s by Lee et al. [30], these molecules were not recognized as a distinct class of biological regulators with defined functions until over a decade later. It is now widely accepted that there are over 1,900 miRNAs in humans, regulating over 30 % of genomic RNA [31]. It was not until 2002, however, that miRNAs were first linked to cancer [10] and it was a further 3 years before altered miRNA expression, specifically in glioblastoma, was assessed [32, 33]. Since that date however, the number of peer-reviewed publications has increased exponentially providing insight not only to miRNA expression patterns in differing GBM cell types and patient samples, but also into the function and mechanisms of several key miRNAs and their potential efficacy in GBM treatment (refer to Table 1). Based on the approach of Möller et al. [34], a Medline/PubMed database search on 'microRNA and glioblastoma' was carried out (search date, 29 November 2012). Publication relevance was determined based on title and abstract content, yielding 313 papers, which were of significance to this publication. Of these, 42 were reviews and 136 research-based papers detailed the pro- or anti-apoptotic or proliferative effects of specific miRNAs on glioblastoma, with a subset of 28 papers including in vivo evaluation of individual miRNAs. Of the original 313 papers, 22 papers dealt with the topic of chemoresistance or sensitization caused or induced by miRNAs in GBM and 173 correlated miRNA profiles to patient outcome and/or diagnosis. Notably, of the 313 papers of relevance, 57 % were published since 2011; most likely, as mentioned previously, due to the advancing techniques and availability of microarray technology.

The pattern of over-expression or suppression of specific miRNAs has been of immense interest to researchers working in the glioblastoma field in the hope that reintroduction of a depleted miRNA molecule, or inhibition of a particular miRNA which is over-expressed, may provide a novel pathway through which targeted therapy may be investigated. miRNA profiles have previously been used to classify tumours based on tissue type and disease state in chronic lymphatic leukaemia, bladder, lung, breast and ovarian cancer [10, 35, 36]. Although still in its infancy with respect to glioblastoma, researchers have highlighted several miRNAs which have been shown to correlate to glioma pathogenesis [20, 37–48] and, as highlighted in Table 1, miRNAs which have been studied in detail have predominantly been shown to be significantly decreased in glioblastoma patient samples or cell lines compared to controls. These miRNAs tend to be encoded in regions of chromosomal loss in glioblastoma patients [49]; for example, miR-34a is encoded at Chr1p36.22, a region with

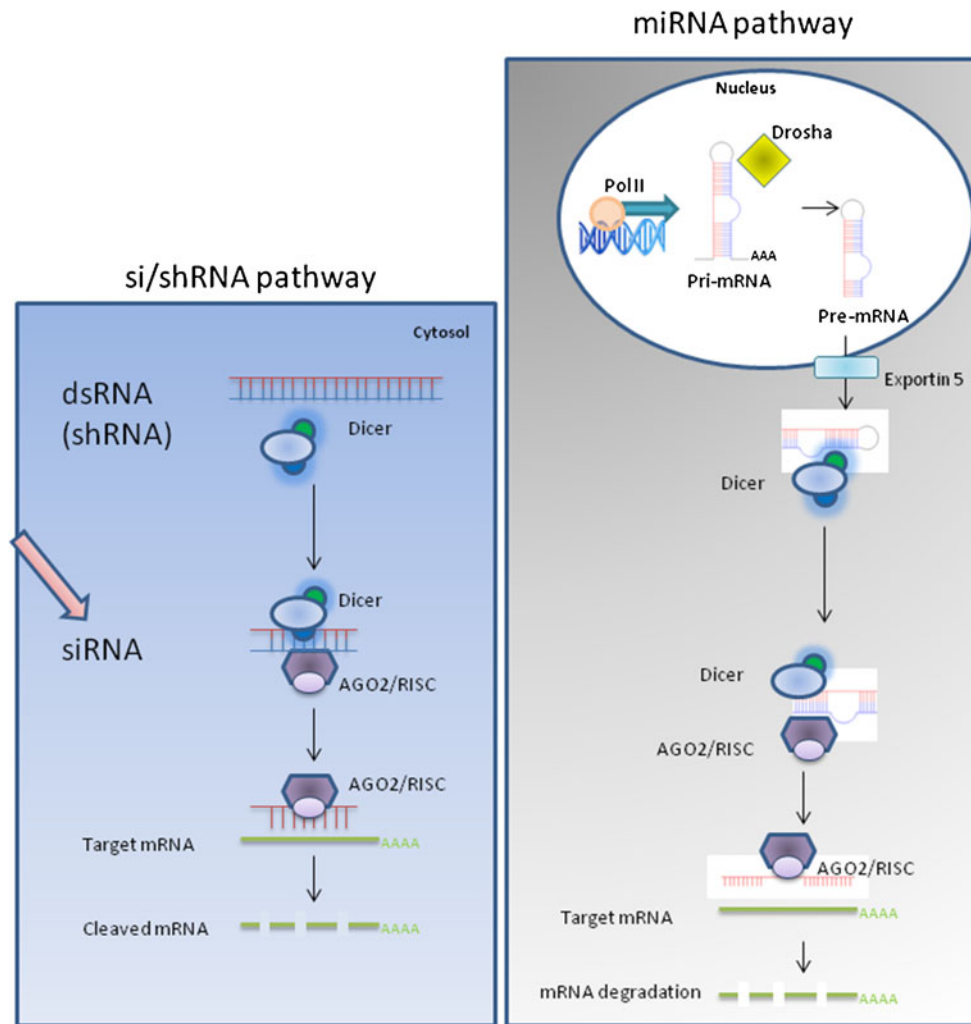


Fig. 1 microRNA and si/shRNA mechanisms of action. RNA interference is a mechanism of gene transcript regulation by transcriptional repression or target transcript degradation. Short interfering RNAs (*siRNAs*), short hairpin RNAs (*shRNAs*) or microRNAs (*miRNAs*) are capable of inducing this mechanism through two similar, but independent, pathways. The microRNA pathway begins with primary microRNA transcripts (*pri-miRNAs*) which are endogenously expressed within the host genome. These *pri-miRNAs* are transcribed by RNA polymerase II

(*Pol II*), processed by Drosha to form precursor miRNAs (*pre-miRNAs*), exported from the nucleus by Exportin 5 and subsequently processed by the Dicer enzyme for loading onto the AGO2–RISC complex. The *pre-miRNA* which is loaded onto RISC has imperfect sequence complementarity; and therefore, the sense strand is unwound leaving a mature miRNA bound to active RISC. This mature miRNA recognizes target sites typically in the mRNA 3'-UTR, leading to direct translational inhibition or mRNA target degradation in processing (P)-bodies

significant loss in many glioblastoma patient samples [50–53].

Re-expression of these miRNAs in glioblastoma cells has been, in some cases, proven efficacious with respect to reduced proliferation, colony formation, migration and invasion, as is the case for miR-34a [45–48]. Conversely, miR-21 has been extensively studied due to its significant upregulation in glioblastoma and the noted observation that miR-21 inhibition induced apoptosis in glioblastoma cells in vitro [32, 54–56] and in vivo [40, 57, 58]. Although such studies used specific miR-21 inhibitors called anti-miRs, alternative approaches to reduce over-expressed miRNAs include sponge modulators [59]. A sponge modulator acts as a competitive inhibitor of the miRNA binding site. They

are transcripts which are expressed from vectors designed with strong promoters and contain multiple binding sites for the microRNA of interest; thereby attracting miRNA binding to the introduced vector as opposed to the native target transcript [60]. This approach has been evaluated by Mei et al. in glioblastoma for the microRNA, miR-146a [61].

Chemoresistance and miRNAs in Glioblastoma

An additional aspect of miRNA study in glioblastoma is the evaluation of miR-based therapeutics as an adjunct therapy in an attempt to improve patient response to current chemotherapeutics. Several groups have evaluated the effect of miRNA

Table 1 Review of experimental miRNA-related papers

miRNA	Expression profile in GBM	Noted effect in vitro	Noted effect in vivo	Reference
524-5p	Decreased	<ul style="list-style-type: none"> • Expression inhibits cell proliferation, decreases invasion and induces apoptosis 	<ul style="list-style-type: none"> • Subcutaneous tumours reduced after direct injection in lipofectamine 	[82]
451	Decreased	<ul style="list-style-type: none"> • Expression inhibits cell migration but increases proliferation, reduces apoptosis. Expression associated with high glucose levels 		[129]
328	Decreased	<ul style="list-style-type: none"> • Expression suppressed cell proliferation 		[130–132]
326	Decreased	<ul style="list-style-type: none"> • Expression reduces ATP levels through targeting of PKM2. PKM2 siRNA led to reduced colony formation and invasion 		[133]
296-3p	Decreased	<ul style="list-style-type: none"> • Expression leads to reduced proliferation and invasion in GBM cells and increased sensitivity to chemotherapeutics 		[134]
181d	Decreased	<ul style="list-style-type: none"> • Expression induces apoptosis, G1 cell cycle arrest and inhibits proliferation through K-ras and Bcl2 targeting 	<ul style="list-style-type: none"> • Subcutaneous tumours reduced after direct injection in lipofectamine. Once every 3 days for 15 days 	[92]
146-5p	Decreased	<ul style="list-style-type: none"> • Expression reduced invasion and migration but proliferation effect required several days before a significant effect was noted 		[135]
146a	Decreased	<ul style="list-style-type: none"> • Expression enhanced neuronal differentiation, inhibited proliferation, increased cell cycle exit and reduced sphere formation 	<ul style="list-style-type: none"> • Pre-treatment with miR-146a prior to orthotopic implantation of GBM cells lead to increased survival and reduced tumour burden 	[61]
145	Decreased	<ul style="list-style-type: none"> • Treatment of GBM cells with PU-PEI-miR-145 reduced proliferation, invasion and soft agar colony formation. Enhanced sensitivity to radiation and TMZ/cisplatin treatment • Expression of miR-145 as an adjunct therapy to AAV mediated suicide gene therapy (Ad5CMVSVtk retrovirus) 	<ul style="list-style-type: none"> • Pre-treatment of cells or intracranial injection of miRNA reduced tumour growth in orthotopic tumour model. Enhanced sensitivity to radiation and TMZ/cisplatin treatment • In vivo work was done via intracranial administration of 'drug' (Hsvtk + miR-145) showing significant reduction in GBM tumour growth 	[63, 96, 136, 137]
128	Decreased	<ul style="list-style-type: none"> • Expression reduced proliferation in GBM cell lines, with a decrease in cells in S phase but no change in apoptotic G0 phase 	<ul style="list-style-type: none"> • Subcutaneous tumour burden reduced in miR-128 U87 cells • Pre-treatment of cells with miR-128 in subcutaneous model and also a H-RasV12 induced transgenic model of glioma. miR-128 was significantly decreased in these tumours • When H-RasV12 is intracranially injected, miR-128 is co-expressed. Reintroduction of miR-128 significantly increased survival 	[138]
125b	Decreased	<ul style="list-style-type: none"> • Expression resulted in reduced proliferation, sphere formation through direct E2F2 targeting 		[139, 140]
124 and 137	Decreased	<ul style="list-style-type: none"> • Expression of miR-124 and miR-137 enhances neuronal-like differentiation of adult mNSCs and inhibition of proliferation in GBM cell lines 		[141]
124/124a	Decreased	<ul style="list-style-type: none"> • Expression of miR-124 led to reduced sphere formation and inhibition of invasion through SNAI2 reduction • Ectopic expression of miR-124a led to reduced invasion and retrospective association with reduced survival rates 	<ul style="list-style-type: none"> • Subcutaneous injection of pre-treated cells showed that miR-124 lessened tumour burden 	[7, 93]

Table 1 (continued)

miRNA	Expression profile in GBM	Noted effect in vitro	Noted effect in vivo	Reference
101	Decreased	<ul style="list-style-type: none"> • Expression of miR-101 target (EZH2) induced glioma proliferation, migration/invasion and angiogenesis • Inhibition by a peptide inhibitor (DZNep), comparable to miR-101 activity reduced GBM growth 	<ul style="list-style-type: none"> • IV injection of DZNep reduced subcutaneous GBM tumour growth 	[90, 91]
34a	Decreased	<ul style="list-style-type: none"> • Expression of miR-34a inhibited cell proliferation, colony formation, induced cell cycle arrest and inhibited transwell invasion of glioblastoma cells 	<ul style="list-style-type: none"> • Pre-treatment of GBM cells with miR-34a lead to reduced orthotopic brain tumour burden 	[50–53]
23b	Decreased in migratory GBM	<ul style="list-style-type: none"> • Expression of miR-23b inhibited migration in 4 GBM cell lines tested, whereas anti-miR23b enhanced migration 		[142]
18	Decreased	<ul style="list-style-type: none"> • Forced miR-18 re-expression reduced CTGF expression, mediated through Smad3 		[143]
7	Decreased	<ul style="list-style-type: none"> • Expression reduced migration and invasion in GBM cells 	<ul style="list-style-type: none"> • Reintroduction inhibited subcutaneous tumour formation and reduced lung metastasis 	[88, 144]
26	Increased	<ul style="list-style-type: none"> • MiR-26a directly targets the 3'UTR of PTEN, and also EZH2 and SMAD1. Inhibition of miR-26 leads to partial inhibition of GBM proliferation and growth but not as much as PTEN deletion 	<ul style="list-style-type: none"> • Reintroduction leads to partial reduction in tumour latency 	[86]
21	Increased	<ul style="list-style-type: none"> • MiR-21 inhibition induced apoptosis, and the presence of taxol enhanced this effect further, depressing viability and increasing caspase-3 expression. Also miR21 inhibition +/- taxol resulted in reduced invasive potential 	<ul style="list-style-type: none"> • Pre-treatment and intracranial injection lead to reduced tumour burden in glioma cells where miR-21 was inhibited. Inhibition of miR-21 allowed re-expression of Pcdcd4, and reduction in tumour growth in subcutaneous model of GBM 	[32, 40, 54, 56–58]
21 30b/c	Increased	<ul style="list-style-type: none"> • Expression of miR-21 and 30b/c induced resistance to TRAIL and anti-miR-21 or anti-miR-30b/c induced sensitivity to TRAIL. MIR21 acts directly on Tap63 and miR-30b/c on caspase 3 		[55]
10b	Increased	<ul style="list-style-type: none"> • Inhibition reduced cell growth, led to cell cycle arrest and apoptosis through Bim, TFAp2c, p16 and p21 targeting • As an alternative to miR-10b inhibition, a 'decoy vector' which had 13 repeats of the miR-10b binding site was generated. Inhibition of miR-10b decreased invasiveness of the U87-2MI cells, decreased angiogenicity and enhanced apoptosis 	<ul style="list-style-type: none"> • Subcutaneous tumour burden reduced after 3 intratumoural injections (1 per day for 3 days) and reduced proliferation (Ki-67) and increased TUNEL positive cells • Pretreatment with miR-10b decoy versus control vector reduced GBM cell invasion, growth and vascularisation 	[84, 87]

modulation in enhancing glioblastoma chemosensitivity to temozolomide [62–64], taxol [56, 65] and cisplatin [66], reducing the intrinsic resistance of glioblastoma cells to current therapeutics. Although this approach would benefit patients from the point of initial diagnosis, acquired resistance remains a major obstacle to improvements in current glioblastoma treatment. As mentioned previously, distal tumours often occur in these patients after primary TMZ/RT treatment which are refractory to additional chemotherapy; and although several hypothesis have been proposed as to why such a resistance occurs after initial treatment [67], there are currently no biomarkers or molecular indicators to suggest genetic predisposition to acquired resistance in glioblastoma. Initial studies have assessed the differential expression of miRNAs in acquired resistance *in vitro* providing potential avenues of miR-based targeting to improve patient treatment response [68, 69].

Multidrug resistance proteins (MRPs) are ATP-binding cassette transporters (ABC transporters) which have previously been identified to play a significant role in drug resistance in several forms of cancer [67, 70, 71], and in 1994, Abe et al. identified a potential role for MRP transporter proteins in drug-resistant glioma cells [72], specifically over-expression of MRP1, 3, 4, 5 (ABCC1, ABCC3, ABCC4 and ABCC5, respectively) and ABCG2 [71, 73]. Although small molecule inhibition of the MRP1 transporter has been evaluated with respect to other forms of cancer such as neuroblastoma [74], and although high grade glioblastoma patients exhibit vascular permeability [75], effective delivery across the BBB in glioblastoma has yet to be evaluated. Although there is no absolute cut-off with respect to molecular size of compound transport across the BBB [76, 77], passive transport is facilitated in molecules under 500D, with low hydrogen bonding capability and lipophilicity, criteria which many current chemotherapies fail to achieve [78]. As a means of evaluating alternative anti-cancer molecules, with potential of crossing the BBB, miRNAs which have altered expression in glioblastoma have been identified and studied. With respect to ABC transporters, miRNA-328 targeting of ABCG2 [79] or miR-9 effect on ABCC3 [80] was assessed in an attempt to improve glioblastoma cell exposure to chemotherapy treatment. Notably, however, such studies were carried out *in vitro*.

In Vivo Research of miRNAs in GBM

In reviewing several papers detailing the effects of miRNAs in glioblastoma, it was obvious that many of these studies are focused on *in vitro* work, and the *in vivo* applications of many of these regulatory molecules in glioblastoma progression have not yet been evaluated. Of significant importance is the fact that those publications which did undertake *in vivo* research focused on evaluation of subcutaneous tumour

formation subsequent to glioblastoma cell inoculation [40, 58, 81–95], orthotopic intracranial injection of glioblastoma cells which were pre-treated with a particular miRNA [52, 53, 57, 61, 63, 96] or direct intracranial injection of a chosen miRNA to an orthotopic model of glioblastoma [57, 63]. A single study evaluated the effect of systemic delivery of a miRNA target protein (EZH2) inhibitor (DZNep), as a comparative molecule to the miRNA (miR-101) itself, with respect to orthotopic glioblastoma tumour formation [91]. This approach, however, eliminated the multi-gene target effect which miR-101 may possess in glioblastoma.

Major limitations in using microRNAs for *in vivo* therapeutics are their rapid degradation in serum conditions, their lack of reliable delivery to the intracellular space [97] and, when combined with the intrinsic challenges of delivery across the BBB, many researchers have focused on direct, rather than systemic, administration of miR-based therapeutics [57, 63]. Notably, the angiogenic and migratory potential of glioblastoma cannot be reflected in subcutaneous tumour models due to the absence of the brain microenvironment which is known to play a significant role in glioblastoma pathogenesis and drug resistance [98–105]. Therefore, translational research requires the use of orthotopic models of glioblastoma in combination with systemic delivery of a potential therapeutic. In a clinical setting, systemic intravenous delivery of potential therapeutics to glioblastoma patients is more favourable with respect to willing involvement in clinical trials due, in part, to the minimal disruption experienced by the patient as the drug of interest may be administered in conjunction with currently established chemotherapy treatment regimens.

When questioning the potential which miR-based therapeutics holds for chronic diseases such as cancer, attention must be drawn to the recent initiation of a phase IIa clinical trial using an anti-miR-122-based drug, miravirsin (SPC3649), in patients with hepatitis C [106] by Regulus TherapeuticsTM; also additional research into miR-21 for hepatocellular carcinoma, kidney fibrosis, miR-33 for atherosclerosis and miR-10b for glioblastoma research progression is the primary focus within this company's therapeutic pipeline [107]. Similarly, Mirna TherapeuticsTM focuses its research on miRNAs which affect solid and blood-borne tumours, such as hepatocellular carcinoma, non-small cell lung cancer, colorectal cancer and pancreatic carcinoma, with MRX34 (miR-34a mimic) due to progress to clinical development in 2013 [108]. Additionally, Miragen TherapeuticsTM has several miRNAs which are nearing the end of preclinical assessment in a variety of chronic and cancer-related conditions. Although such commercialized research shows translational promise for miR-based therapeutics, a major challenge for such therapeutics however, as with many drugs, will be stability, and in the case of miR-10b for glioblastoma, successful delivery across the BBB.

Potentials for miRNA Delivery Across BBB

Several studies have been undertaken to assess the delivery of exogenously administered microRNAs in various forms of cancer. In most cases, miRNAs have been encapsulated in lipid- or nanoparticle-based molecules. The system of choice for miRNA, or anti-miR, delivery plays a critical role in the delivery of an effective molecule capable of modulating gene expression. Studies involving siRNA molecules have found that delivery systems possessing an external cationic charge can lead to stimulation of the host immune system [109]. Additional studies have shown that certain delivery systems such as polypropylenimine dendrimer encapsulation may lead to induction of particular ‘gene signatures’ not normally present within the target cell, thereby leading to an increased potential of off-target effects of the siRNA or miRNA being delivered [110–112]. The choice of an efficient delivery system is also dependent upon controlled release of the miRNA/siRNA molecule into the intracellular cytosol without degradation in endosomes or lysosomes [113]. Similar to previously described studies using miRNAs, or anti-miRs, for brain tumour research, CNS delivery of siRNA has been through localised intratumoural or intrathecal injection [114] due to challenges in BBB penetration and biodistribution after systemic administration. Notably, the first and only clinical trial for RNAi-based treatment of inoperable brain tumours required invasive surgery and direct injection of the siRNA to the brain [115], although several studies have been evaluated *in vitro* as reviewed by Guo et al. [116].

More recently, scientific studies have been undertaken to evaluate the potential use of nanoparticles for a variety of applications including cancer imaging [117, 118] and molecule delivery [119]. Several studies have used nanoparticles which have been modified to enable encapsulation of miRNAs for tumour-specific delivery and cancer cell death in numerous cancers including neuroblastoma [66, 120–122], lymphoma [123] and head and neck squamous cell carcinoma [124]. Such encapsulation of miRNAs, or indeed anti-miRs, within biodegradable nanoparticles may be applied to numerous miRNAs of interest in glioblastoma research. The chemistry of nanoparticle composition plays an important role with respect to cargo encapsulation, transport across the BBB and successful endocytosis, content release and degradation within the tumour cell. As discussed previously, exosomes are naturally occurring RNA nano-vesicles which may be harnessed for miRNA transport across the BBB. Alvarez-Erviti et al. delivered Cy5-labelled siRNA molecules contained in immunological inert exosomes to brain regions in an *in vivo* model of Alzheimer’s disease after systemic administration [125]. Loading of exosomes may potentially be exploited for efficient systemic delivery of miRNAs to an orthotopic model of glioblastoma. Hwang do et al. carried out a study using cysteine residue-modified polyethyleneimine

(SSPEI) to transport miR-124 to the brain *in vivo*. This study was focused on the delivery of a functional miRNA molecule across the BBB after systemic administration via tail vein injection. Notably, this study utilized an isomer of sorbitol (Mannitol) which temporarily shrinks the endothelial cells of the BBB, stretching the tight junction between them [126], facilitating temporary ‘opening’ of the BBB. This study proved that SSPEI-miR124 was successfully transported across the BBB to the brain parenchyma *in vivo* [97]. Alternative methodologies including siRNA targeting of the tight junction protein, claudin-5, have been used to deliver small peptide-based molecules into the brain [127]. To date, however, nanoparticle delivery of miRNA molecules in glioblastoma has only been assessed *in vitro* [56].

The aggressive progression and dismal prognosis associated with glioblastoma diagnosis have led clinicians and researchers alike to explore new avenues of potential treatment for these patients. MicroRNAs are involved in crucial biological processes, not only in healthy cells but also in cancer cell biology, including differentiation, proliferation and apoptosis. As detailed in Table 1, exogenous altered expression of several miRNAs in glioblastoma leads to significant effects on glioblastoma cell morphology, invasiveness and tumorigenicity. The findings of such studies yield great promise to the hypothesis that miRNAs may be used to target specific traits of glioblastoma cell biology, for example migration and invasion potential, angiogenic capabilities, heterogeneity and resistance to current treatment regimes [128] (refer to Table 1). The advent of nanoparticle-mediated delivery and recent progression in RNAi- molecule delivery across the BBB to both CNS disease and cancer models proves encouraging to the progression of miR-based therapeutic efficacy in this debilitating disease. Considering the development of miRNA research from initial association to glioblastoma [32, 33] to commercial development of miR-based therapeutics [106–108] in less than a decade, it is not beyond reasonable doubt to anticipate significant advancements in this field of study, hopefully with the ultimate conclusion of improved patient outcome.

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