MetastamiRs: The Role of MicroRNAs in the Metastatic Phenotype of Prostate Cancer

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Abstract: MicroRNAs (miRNAs) are short non-coding RNAs that posttranscriptionally regulate protein expression. The human genome encodes more than 2,500 miRNAs, with each being able to modulate several targets, act along a variety of cellular pathways, and affect various tissues. They are frequently dysregulated in cancers and, via their protein targets, act as oncogenes or tumor-suppressors. As such, their effects are pervasive—miRNAs have been implicated in various biological processes including apoptosis, epithelial-tomesenchymal transition, and angiogenesis. In this context, miRNA involved in metastasis have been termed "metastamiRs". This chapter focuses on the role of miRNAs in the metastatic processes of prostate cancer. Our primary aims are to

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detail specific biological processes and molecular targets through which miRNAs act and that may serve as therapeutic targets. Secondly, we discuss the potential of miRNAs to serve as biomarkers of tumor aggression and thus potentially guide personalized therapy.

Keywords: metastasis-promoting miRNAs in prostate cancer; metastamiRs; metastasis-suppressing miRNAs in prostate cancer; metastatic prostate cancer; microRNAs in prostate cancer

INTRODUCTION

MicroRNAs (miRNAs) are small non-coding RNAs averaging 22 nucleotides in length that generally function by negatively regulating mRNA expression by binding to the 3'UTR of their targets (1). These molecules are found in all major cellular compartments, and are often exported from the cell, where they may function as signaling molecules (2). An individual miRNA can modulate expression of numerous targets based on sequence complementarity between the miRNA and the 3'UTR of an mRNA (3). Similarly, an individual mRNA transcript may be regulated by hundreds of miRNAs, resulting in a network of interactions between miRNAs, their target genes, and their downstream effectors (3). This interactive network contributes significantly towards the regulation of a plethora of biological processes and cellular pathways. While miRNAs typically act to support the normal function of the human body, aberrant expression of these molecules has been implicated in the pathogenesis of numerous human diseases (4).

An area of interest with respect to the impact of miRNA expression on human disease is cancer progression (5). MiRNAs frequently become dysregulated in human cancers through mechanisms such as amplification or deletion of miRNA genes, aberrant transcriptional control of miRNAs, changes in epigenetic regulation and defects in the miRNA biogenesis machinery (6). It has been shown that miRNA dysregulation has a strong influence on the following aspects of cancer phenotype: proliferative capacity, resistance to apoptosis, evasion of growth suppressors, activation of invasion and metastasis via the epithelial-mesenchymal transition (EMT) pathway, and induction of angiogenesis (6). The miRNAs involved in the overall cancer phenotype have been termed "oncomiRs" (7), and their role in the regulation of these processes depends on their interactions with specific targets. MiRNAs that affect the metastatic phenotype when dysregulated can be characterized as having pro- and anti- metastatic effects depending on their net influence on tumor aggressiveness (8). The collection of miRNAs that are specifically associated with the promotion or suppression of metastatic potential and EMT of cancer cells are known as "metastamiRs" (8).

Research on the role of these metastamiRs in the development and progression of cancer has mainly focused on their association with downstream effectors and patient outcomes. Numerous metastasis-associated signaling pathways have been linked to abnormal expression of metastamiRs (9). For example, metastamiR expression has been identified as a driver of the phosphatase and tensin homolog (PTEN)/phosphatidylinositol-3-kinase (PI3K), EGF receptor (EGFR), transforming growth factor-beta (TGF β), and p53 pathways (9). More generally, miRNAs have been a popular target for translational research approaches such as studying the predictive ability of specific miRNA expression signatures and their utility as non-invasive biomarkers. For example, a study in bladder cancer has elucidated the ability of miRNA panels to distinguish the aggressiveness of the cancer (10). Additionally, miRNA expression levels in the urine (11), serum (12), and exosomes (13) have shown viability as non-invasive biomarkers in cancer diagnostics. This chapter focuses on the role of metastamiRs in prostate cancer, explore their role in prostate cancer metastasis, and their potential in cancer diagnosis and therapy.

THE ROLE OF MICRORNAS IN THE METASTATIC PHENOTYPE OF PROSTATE CANCER

Apart from cutaneous malignancies, prostate cancer is the most common cancer among men in the United States (US), with roughly 250,000 new annual cases (14–16). Behind lung cancer, it is the second leading cause of cancer death in American men (14). Due to a multitude of treatment options that often offer curative potential, localized disease generally portends favorable outcomes, with 5-year survival for localized and regional disease being nearly 100% (17). However, despite noteworthy recent progress in therapeutic measures, metastatic prostate cancer still inflicts significant morbidity and mortality, with the preponderance of fatal cases of prostate cancer attributed to metastatic burden (18–20).

With most prostate cancer-related morbidity and mortality stemming from its metastatic spread, it is important to understand the molecular processes involved in this disease. As more than 50% of miRNA genes are in cancer-associated genomic regions, they control the expression level of pro-metastatic genes by targeting mRNAs at the post-transcriptional level, and thus act as central nodal points for metastatic progression (21, 22). Because of the highly aberrant expression levels and, in some cases, aberrant sequences of miRNAs found in prostate cancer, miRNAs have a particularly crucial regulatory role, acting as promoter or inhibitors of metastasis primarily through regulating invasion, migration, and EMT (Figure 1) (18, 21, 23–26). Tables 1 and 2 summarize the product of a vast and continuously expanding-collection of research that has culminated in our current understanding of the role of miRNAs in prostate cancer metastasis. Importantly, there are miRNAs with documented roles in prostate cancer that have not been included in this chapter, largely due to either limited or conflicting evidence surrounding their metastatic role. Although current experimental methods are often powerful enough to detect the abnormal changes of miRNA expression in prostate cancer, it remains difficult to identify downstream effects of these miRNAs. This is due to multifactorial reasons including complexity of the metastatic cascade, the heterogeneity of the primary prostatic tumors, as well as the convoluted relationship between genetic and environmental factors contributing to the progression of prostate cancer (27-29).

Metastasis-promoting miRNAs in prostate cancer

While metastasis-promoting miRNAs have diverse molecular targets and pathways, they generally encompass interaction with transcription factors, cytokines, receptors, and enzymes involved in cellular proliferation or the metastatic cascade.

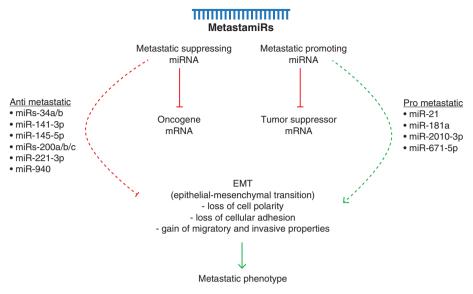


Figure 1. Simplified overview of the role of the effects of metastamiRs on the metastatic phenotype. Metastatic suppressing miRNAs inhibit the metastatic phenotype by attenuating expression of oncogenes that drive epithelial-mesenchymal transition. Conversely, the net effect of metastatic promoting miRNA is to drive epithelial-mesenchymal transition by downregulating the expression of tumor suppressor genes that could otherwise inhibit this process. A few examples of each, prevalent in prostate cancer, are detailed.

Whereas some of these metastasis-promoting miRNAs directly activate oncogenic pathways via known proto-oncogenes, others silence or suppress tumor-suppressive pathways to promote prostate cancer metastasis. For example, Ren et al. demonstrated that miR-210-3p sustains the activation of nuclear factor kappa-B (NF- κ B) signaling by targeting tumor necrosis factor- α (TNF α), which increases the capacity for cellular invasion, migration, EMT, and formation of bone metastases (19, 30). On the other hand, Yu et al. showed that miR-671-5p targets known tumor suppressor SOX6 and inhibits its expression, preventing the transcription of downstream tumor suppressive proteins and thus resulting in cell proliferation, migration, and invasion (26, 31). Table 1 details specific metastasis-promoting miRNAs implicated in prostate cancer, their molecular targets, and function in promoting metastasis (32–46).

Metastasis-suppressing miRNAs in prostate cancer

While there are a diverse number of targets detailed within the literature, several of these pathways are represented across multiple miRNAs, highlighting their global influence in the metastatic process. For example, miRs -141-3p, -212, -200, -204-5p, and -532-3p all influence and downregulate the activity of NF- κ B at some operational level, while miRs -33a, -132, -34a, b, -212, and -200 all act on transforming growth factor- β (TGF- β) to inhibit metastasis (47–62). Ultimately, these molecular processes suppress the transformation of localized prostate

TABLE 1Summary of metastasis-promoting miRNAs
involved in prostate cancer, with impacted
pathways, targets, and resulting oncologic
outcomes

miRNA	Targets/Regulators	Function	Reference
miR-9	E-cadherin, SOCS5, StarD13	Promotes migration, invasion, EMT, and spontaneous metastasis	(32, 33)
miR-18a	STK4	Promotes cell motility, migration, and invasion	(34, 35)
miR-21	MARKS, PDCD4, TPM1, AR	Promotes apoptosis resistance, motility, and invasion potential via several molecular mechanisms	(36–38)
miR-32	RAC2, BTG2	Promotes proliferation of prostatic epithelium and inhibits apoptosis.	(39, 40)
miR-181a	TGIF2, LEF1	Promotes cell migration, invasion, and EMT via SMAD2/3 activation and Wnt signaling.	(41, 42)
miR-210-3p	TNIP, SOCS1	Promotes invasion, migration, EMT, and formation of bone metastasis via NF-κB activation.	(19, 30)
miR-429	P27Kipl	Promotes cell proliferation. Restricts arrest in G1 phase of cell cycle.	(19, 43)
miR-454	NDRG2	Promotes cell proliferation and invasion via Wnt/ β-catenin signaling.	(44)
miR-671-5p	SOX6, NFIA-CRYAB axis	Promotes cell proliferation, migration, and invasion.	(31, 45)
miR-629-5p	AKAP13	Drives cell proliferation, migration, and invasion.	(46)

cancer to metastatic disease. Table 2 delineates many of the known metastasissuppressing miRNAs in prostate cancer (63–92).

miRNAs as biomarkers and therapeutics in prostate cancer

The diagnostic standard for prostate cancer is either a transrectal or transperineal biopsy guided by a transrectal ultrasound (TRUS). Indication for biopsy is generally a prostate-specific antigen (PSA) level or change outside of clinically accepted parameters. The classification of prostate cancer is based on Gleason score (gleaned from biopsy results), PSA level, and other clinical considerations, which together inform therapeutic options and prognosis. Recently, prostate genomics has garnered clinical attention, with multiple assays becoming clinically available to help guide clinical decision making. While these assays further elucidate patient-specific risk, currently available resources are still not sufficient to predict true metastatic potential, particularly at the time of metastatic initiation or transition (19, 93–99). In addition, inconsistencies of Gleason score between prostate

TABLE 2Summary of metastasis-suppressing miRNAs
involved in prostate cancer, with impacted
pathways, targets, and resulting oncologic
outcome

miRNA	Targets/Regulators	Function	Reference
miR-19a-3p miR-33a	SMAD2/4, PMEPA1 TGFBRI, EN-2	Inhibits cell invasion and migration. Inhibits cell proliferation, invasion, and colony	(63) (49, 50)
ппк-ээа	IGFDRI, EIN-Z	formation.	(49, 30)
miR-34a,b	CD44, TGF-β/SMAD3	Suppresses tumor migration, clonogenic expansion, invasion, and progression via WNT/ B-catenin, JAK/STAT3, PI3K/AKT pathways.	(19, 50, 61, 64–66)
miR-132	SOX4	Inhibits cell migration, invasion, and EMT via suppression of TGFβ-mediated signaling.	(51, 60)
miR-141-3p	TRAF5-6, RUNX1, MMP2/9	Suppresses cell invasion and migration via inhibition of NF-кB, EMT, and promotes apoptosis.	(47, 48)
miR-145-5p	E-cadherin, fibronectin, HEF1, OCT3, c-Myc, KLF4, WIP1, TWIST1	Suppresses bone metastasis by downregulating EMT via increasing E-cadherin expression and decreasing fibronectin expression. Decreases colony formation, decreases tumor spheroid formation and cellular cloning.	(67–71)
miR-148a- 3p	DNMT1	Induces apoptosis and reduces cellular proliferation.	(72)
miR-152-3p	TMEM97, NOL4	Suppresses cell viability, invasion, and promotes cell-cycle arrest at S and G2/M.	(73, 74)
miR-195-5p	Fra-1, MMP1/9	Inhibits cell motility, migration, and invasion.	(73, 75)
miR-200a, b,c	NF-kβ, SNAI2, ZEB, TGF-β, BRD4	Inhibits cell migration, adhesion, and angiogenesis.	(19, 54–56)
miR-204-5p	NF-kβ, TRAF1, TAB3, MAP3k3, BCL2	Suppresses invasion, migration, and dissemination of cancer cells into bone.	(57, 58)
miR-212	SOX4, BMI-1, EN2	Suppresses proliferation, promotes arrest of cell cycle, and inhibits EMT.	(51–53)
miR-221-3p	VEGFR2, SIRT1	Suppresses cell proliferation, migration, and colony formation.	(76–79)
miR-224-5p	UAP1, HK2, CHIT1, TOP2A, RRM2	Inhibits cell proliferation and migration.	(80, 81)
miR-335	EGR3, eNOS	Reduces cell viability and angiogenesis of the cell line, reducing migration, and invasive capacity.	(82–84)
miR-505-3p	SMAD2/4, PMEPA1	Inhibits cell invasion and migration.	(85)
miR-532-3p	TRAF1,2,4	Inhibits tissue invasion, cell migration, and bone metastasis.	(59)
miR-543	eNOS	Impairs migration and invasive capacity.	(84, 86)
miR-802	FLOT2	Suppresses cell migration, invasion and EMT.	(87, 88)
miR-940	MIEN1	Suppresses migration and invasion. Attenuates anchorage-independent growth ability via the Wnt/β-catenin, MAPK, PI3K-Akt pathways.	(89–91)
miR-3622a	SNAI2, ZEB1	Inhibits EMT.	(92)

biopsy and radical prostatectomy are frequent. Moreira Leite et al. (100) found Gleason score was underestimated in 29% of cases, and it was overestimated in 14% of cases. As such, there remains an urgent clinical need for alternative biomarkers to improve the diagnosis and prognosis of prostate cancer. miRNAs have considerable potential to fill this diagnostic, prognostic, and potentially therapeutic void (19, 101, 102).

Due to the relative abundance of miRNAs in various biological fluids and their stability and resistance to degradation in diverse storage media, miRNAs are considered strong candidates as molecular biomarkers for prostate cancer (19, 89, 91, 95, 96, 101). There are two distinct theoretical approaches concerning their utility: diagnostics, in which miRNAs can indicate presence or absence of disease; and prognostics, in which miRNAs aid in risk stratification and therapeutic guidance. Concerning the first application, numerous pre-clinical studies have investigated miRNA expression trends in those with prostate cancer compared to non-malignant controls in various isolated body fluids (such as serum, plasma, urine, and semen) in order to identify miRNAs that predict the presence of disease. While individual miRNAs are often studied, the utilization of miRNA panels has bolstered diagnostic value as well (76, 103–106). However, this field requires further development, as much of the current data is complicated by a lack of consistency between miRNA signatures and reproducibility. Proposed sources of these limitations include diversity of sample types (primary tumor, metastatic tissue, blood, urine, serum, plasma, etc.), study design, patient selection, study size, and most importantly, the intrinsic molecular heterogeneity of the disease (19, 101). Nevertheless, the idea of a miRNA panel as a non-invasive disease marker continues to make great headway, in hopes of a clinical application in the near future.

Concerning the utility of miRNA as a disease prognosticator, proposed clinical applications include the prediction of biochemical recurrence after primary treatment, the likelihood of transition to castration-resistant prostate cancer, and a generalized assessment of response to future therapy (101). Biochemical recurrence risk is an important clinical factor, as de-novo rise in serum PSA after treatment can be predictive of metastatic spread. Multiple studies have investigated the role of miRNAs in this prediction, with various miRNA panels showing promising results (37, 107–115). Of particular interest is a miR index quote (miQ) proposed by Larne et al., which utilized four miRNAs (miRs -96-5p, -183-5p, -145-5p, and - 221-5p) to predict tumor aggressiveness in early organ-confined stages and was able to predict recurrence after radical prostatectomy with greater accuracy than PSA, with an AUC of 0.78 (115).

Progression of disease after androgen deprivation therapy is known as castration-resistant prostate cancer and is a significant contributor to prostate cancer morbidity and mortality. Multiple miRNAs have been documented as predictive of castration resistance and many are associated with the androgen receptor pathway as either direct or indirect regulators (40, 116, 117). While several studies have demonstrated differential expression patterns of miRNA between castrate-sensitive and castration-resistant prostate cancer, miRNA-based modeling that predicts a transition from castrate-sensitive to castrate-resistant disease will require further development and refining (36, 40, 77, 116, 118, 119).

MicroRNAs have also been promoted as biomarkers to guide personalized therapy by tailoring therapeutic options and monitoring for response. To this end, several studies have investigated miRNAs as predictors of both chemo- and radio-sensitivity and have proposed models that are able to predict response rates to both systemic chemotherapy as well as radiation (101, 120–129). While these studies show promise, investigations into radio- and chemo- sensitivity have largely taken place in a non-clinical, *in vitro* setting, and further research is needed to determine if these trends are clinically transferable.

CONCLUSION

There remains a need for prostate cancer markers beyond what is currently available, and miRNAs have the potential to serve as both diagnostic and prognostic biomarkers. For example, as the diagnosis of prostate cancer requires invasive and often repetitive biopsies, utilization of miRNAs as binary markers of the presence or absence of disease would both reduce morbidity associated with prostate cancer workup and healthcare-associated procedural costs (130–133). Further, as current prognostic algorithms lack the ability to truly predict metastatic risk in prostate cancer, miRNAs may refine clinical decision making (19, 93, 94, 96, 98). While further research is needed to bring the utilization of miRNAs as disease biomarkers to their full clinical potential, they remain a promising tool to improve diagnostics and prognostics in urologic malignancies.

miRNAs also have the potential to reach therapeutics, which would be clinically impactful. Since a single miRNA can regulate several separate targets involved in oncologic molecular pathways, targeting the miRNA may be beneficial on multiple molecular levels, thus providing redundancy in a therapeutic mechanism. Pre-clinical studies hope to take advantage of this redundancy with the development of novel therapeutic approaches. These methodologies generally fall under two categories: miRNA mimics or miRNA inhibitors (19). Mimics replace lost or downregulated tumor-suppressive endogenous miRNAs and promote their downstream anti-oncogenic effects via targeting the 3'-UTR of the targeted oncogenes. miRNA inhibitors are antisense oligonucleotides, or anti-miRNAs, that inhibit endogenous tumor-promoting miRNAs via direct binding to the small RNA species within the RNA-induced silencing complex, thus reversing their downstream effects (19). While the therapeutic benefit of this approach is intuitive, it is functionally complicated by the necessity of effective delivery strategies. Two primary approaches include intra-tumoral therapy and systemic therapy, with particular attention focused on the latter as this would have the greatest effect on metastatic tumor burden. Proposed delivery methods include cationic-lipid transfection, polyethyleneimine or magnetic nanoparticles, atelocollagen, or viral vectors. (66, 134–140). While the majority of current research remains at the pre-clinical level, some miRNAs have reached early clinical development. For example, Hong et al. conducted a Phase 1 clinical trial into a miR-34a mimic MRX34, but the trial was discontinued due to its side effect profile (141). Certainly, further research is needed to further develop these therapeutic options, but in vitro and in vivo studies thus far show great promise for the future clinical application of miRNA as a therapeutic avenue in cancer.

While the subject of this chapter is miRNAs, an understanding of an increasingly popular area of research—long non-coding RNAs (lncRNAs)—is necessary to understand the context of miRNA within this realm. These RNAs are an emerging class of transcripts that are coded by the genome but not translated into protein. While not translated, ongoing research has uncovered their crucial roles in cellular and physiologic functions including chromatin dynamics, gene expression, growth, differentiation, and development (142–144). Unsurprisingly, emerging studies have shown that lncRNAs play an important regulatory role alongside metastamiRs in prostate cancer. For example, Huang et al. reported that lncRNA SNHG1 was upregulated in prostate cancer cells and had roles in regulating proliferation, migration, invasion, and inhibition of apoptosis via repression of miR-383–5p (145). Certainly, this growing body of research suggests that the true processes occurring *in vivo* surrounding oncomiRs and metastamiRs are far more complex than their individual targeting pathways alone, and that further research is required to fully comprehend these relationships.

While discrepancies and inconsistencies remain, studies continue to better elucidate the vast and often redundant mechanisms through which they exert their oncologic effects to regulate characteristics of metastasis such as angiogenesis, cellular proliferation, migration, invasion, and EMT. Though this research is still in its infancy from a clinical perspective, efforts toward a more refined understanding are underway, with hopes of soon reaching the full clinical potential of oncomiRs and metastamiRs in combating prostate cancer and metastasis.

Conflict of Interest: The authors declare no potential conflict of interest with respect to research, authorship, and/or publication of this chapter.

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