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Review Article

MiR-492: A Potent Oncological Biomarker

Priya Rani[1], Shobhit Raj[2], Prashant Singh[3], Ranjeet Kumar[4], Manjula Bhargava[5]

[1]PG Med. Pharmacology, Department of Pharmacology, National Institute of Medical Sciences & Research, NIMS University, Jaipur, Rajasthan, India.
[2]Department of Pharmacy Practice, National Institute of Medical Sciences & Research, NIMS University, Jaipur, Rajasthan, India.
[3]Department of Pharmaceutics, Buddha Institute of Pharmacy, GIDA, Gorakhpur, Uttar Pradesh, India.
[4]Department of Pharmacy Practice, National Institute of Medical Sciences & Research, NIMS University, Jaipur, Rajasthan, India.
[5]Department of Pharmacology, National Institute of Medical Sciences & Research, NIMS University, Jaipur, Rajasthan, India

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Corresponding Author:
Priya Rani, Department of Pharmacology, National Institute of Medical Sciences & Research,NIMS University, Jaipur, Rajasthan, India.
E-mail Id:
doctorpriyaraj@gmail.com
Orcid Id:
https://orcid.org/0000-0002-6202-5700
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A B S T R A C T

Recent studies contribute to an analysis of microRNAs' roles in health and disease and their potential involvement as biomarkers in physiological and pathophysiological processes, including initiation and development of cancer. Encoded with pseudogene, MiR-492 plays a crucial role in particular cells and over-expression in tissue. It has been proposed as a biomarker to manage and diagnose certain cancers, including breast, colorectal, cervical, hepatocellular, retinoblastoma and pancreas cancer, in the early stages. The purpose of this analysis was to summarise MiR-492 evidence to diagnose and treat certain types of similar cancers early.

Keywords: MiR-492, Oncotherapeutics, Cancer Therapy, Cancer Biomarker

Introduction

In the past decade, RNA silencing phenomena have had unexpected impacts on biological processes. The study found a type of small non-coding RNAs, known as microRNAs (miRNAs), between 21 and 25 nucleotide durations to regulate the expression of the multiple aim mRNAs via repression translation and mRNA degradation.[1] In 1993, the first miRNA was identified, and now hundreds of miRNA encoding genes have been identified.[2] Most of these miRNAs can be found in 2-7 gene clusters.[3] Any of these genes are tissue-specific or expressed at a stadium. Transcription: Transcription: Transcription TranscriptionPri-miRNAs are found in the nucleus in the same form as the stem-loop processed through two phases in the cleavage of Drosha and Dicer protein.[3,4] Drosha belongs to the cell nucleus of the RNase III family. Drosha cleavages pri-miRNA in the first nucleus stage and forms pre-miRNA with approximately 70 nucleotides. Exportin-5 identifies pre-miRNA and converts it to the cytoplasm. Dicer, a part of the RNaseIII family that uses the PAZ domain to bind 3' pre-miRNA overhangs on ~22 mature miRNA nucleotides, an essential protein involved in the mechanism.[5] In cell processes such as replication, differentiation, apoptosis, epigenetics, signal transduction and organ development, MiRNAs play an essential role.[7,8] MiRNAs are also relevant. This may contribute to cancer, cardiovascular disease, inflammation, systemic lupus erythematosus, multiple sclerosis and rheumatoid arthritis.[9,10] Their deregulated speech. MiRNAs in tumorigenesis and tumour growth have recently been shown in studies. The material and quantitative expression of miRNA is wholly altered in tumour cells. Some abnormalities, including amplifications, deletions, miRNA gene translocations, are typical in cancer cells.[11] E.g., in patients with chronic lymphocytic leukaemia (CLL), miR15 and miR16 encoded by 13q14 genes are frequently decreased.[12] In particular miRNAs such as miR-

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34c, miR-34b, miR-9-1 and miR-9 the hypermethylation is also crucial in the metastatic stage of colon cancer.[13,14] Among the various miRNAs detected, MiR-492, also known as hsa-MiR-492, is found on 12q22 with potential for production by sense strands of keratin 19 pseudogene-2 prominent upregulation of active p53.[15] According to a miRNA database, MiR-492 evolved 39 million years ago and has no mouse or rat orthologue. Studies have shown that variations in the MiR-492 expression are linked with cell biologic activity and could activate normal cells to cancer cells. Control and function of MiR-492 have been established. For instance, MiR-492 with miR-1247 cluster and the production of pancreatic tumours can find altered expression. Measurements of serum MiR-492 correlated to CA19-9 may be a valuable biomarker for diagnosis.[17] The testing of genes and proteins inserted as biological markers in various cancers and plays an essential role in deciding the tumour's molecular mechanism is being created. For the diagnosis, prognosis and treatment of biomarkers, MiRNAs may be used. Yu and Developing Robust Differential Correlation Networks to classify microRNA interactions have shown that MiR-492 targets 107 genes[18] so that the analysis of MiR-492 in multiple cancer cells has helped us understand its mechanisms and can serve as an exciting goal for treating cancer therapies (Table 1).

deficiency or overexpression of these genes. Also, up/down testing of the prometastatic or antimetastaticm iRNAs causes cancer metastasis[20] respectively. The evidence is that SOX7 suppression may result from MiR-492 upregulation and may boost the cell cycle and cell proliferation in breast cancer. The SOX7 gene has a tumour suppressor role. Regulation of particular signalling mechanisms, such as wnt/β, regulates genes related downstream, such as c-Myc, cyclin D1 and p-Rb. Targeting 3'UTR of SOX7 mRNA utilising MiR-492 allows it to control down SOX7 and up cycline, D1, c-Myc, and p-Rb.[22] The c-Myc gene product of the nucleus is a transcription factor that is phosphorylated if specific growth factors are present. Its consistency and oncogenic actions are also enhanced. This indicates that the up-regulation of c-Myc is a significant factor in unprogrammed cell proliferation.[22] According to the above data, MiR-492 has a proto-oncogenic feature. It enables cell proliferation and cell cycle in breast cancer cells and targets MiR-492 as a promising therapy for breast cancer. Yan and coworkers have shown that Hsa circus 0072309 inhibited the formation, migration and infiltration of breast cancer cells by inhibiting MiR-492, thereby observing that the Hsa circuit 0072309-MiR-492 plays a crucial role in the production of breast cancer.[23]

Table 1.New biomarkers to detect ovarian cancer

Function	Target	MiR-492	Type of Cancer
Promotion of the cell proliferation	Sox7 3'UTR	Upregulation	Breast cancer
Resistance of drug	CD147	Upregulation	Colorectal cancer
Formation of Tumour Metastasis	PTEN Metallothionein AFP CD44	Upregulation	Hepatic cancer
Elevation in movement of cervical onco cells to pelvic lymph node Chemo-radiotherapy	TIMP2 P53	Upregulation	Cervical cancer
Biomarkers (Rapid detectors)	----	Upregulation	Ovarian cancer
Rapid diagnosis	-----	Upregulation	Retinoblastoma
Biomarkers as rapid detectors	----	Upregulation	Pancreatic cancer

Breast Cancer & MiR-492

In women after lung cancer, breast cancer is the second most frequent cancer death.[19] An irregular expression of unique miRNAs has been identified consistently in breast cancer tissues. Few miRNAs are found to be tumour suppressants. Some have been identified as oncomiR so that the growth of tumours appears to be induced by

Colorectal Cancer & MiR-492

Colorectal cancer is one of the most widespread females and male cancers in the world.[24] It is considered a heterogeneous disease and has revealed several distinct genetic defects across its pathogenesis. Disrupted production of MiRNA is one of the most prominent anomalies in different colorectal cancer stages. By examining tissue samples

from colorectal cancer patients using the real-time RT-PCR technique, Li et al. showed miR492 has a high degree of colorectal cancer (up to 16 times higher) expression.[25] The degree of expression of miRNA will influence the risk of colorectal cancer through polymorphisms of particular genes encrypting different variants of miRNAs, including pri-miRNA, pre-miRNA or mature miRNA. Recent studies indicate that unique polymorphisms may impact miRNA sites and, in various ways, disrupt biological pathways. SNPs were associated with therapy response and improved disease progression in MiR-492 for colorectal cancer.[26] For patients with C/G and G/G genotypes, MiR-492 (rs 228 9030) was correlated with low survival compared to CC genotypes.[27-29] This SNP will also increase the likelihood of this cancer along with bladder cancer.[30] MiR-492 also deals with colorectal cancer resistance. Drug resistance is consistent with the regulation of marker language such as CD147. CD147 is a transmembrane protein that plays an essential role in recognising intercellular units and has a strong surface expression of the tumour cell. It has critical functions, including cancer chemoresistance, the proliferation of tumour cells and metastasis. Based on the findings, MiR-492 is predicted to increase CD147 levels of expression in colorectal cancer cells, thus raising drug resistance.[29] MiR-492 down-regulation may be used to predict, diagnose and manage colon cancer as a biomarker.

Hepatic Cancer & MiR-492

Hepatic cancer is the world's sixth most common cancer induced by several different forms, including cirrhosis and persistent inflammation from Hepatitis C and B, misuse of alcohol and fatty liver. Causes of cancer and hepatocarcinogenesis may be regarded as genetic and epigenetic alterations.[31] A form of lipid phosphatases, such as phosphatase and tensin homologue, has a controlling function in the PI3K-AKT signalling pathway phosphorylated as a tumour suppressor phosphatidylinositol 3, 4, 5-trisphosphate (PIP3) to PI (4, 5) P2. The AKT pathway plays an essential role in cell proliferation and may contribute to tumorigenesis by inhibiting PTENs in normal cells.[32] Previous experiments have shown that the enhanced expression of MiR-492 is linked to PTEN control. In other words, decreasing the expression of PTEN by MiR-492 plays an essential role in the production of tumorigenesis.[31] Further study has shown that MiR-492 could play a crucial role in metastasising hepatic cancer cells. Genes that are repressed by MiR-492 in the form of functional clusters are connected to the family of metallothionein genes, which are very active in regulating neoplastic cell growth and radiation and chemotherapy resistance. In these clusters, the family members (ALB/AFP/AFa) were also noticeable. These genes are found in the human fetal liver. The findings have shown that MiR-492 overexpression in hepatic cancer could have detrimental consequences on some genes such as metallothionein and AFP. As reported earlier, MiR-492G>C (rs2289030) is correlated with multiple cancers. Previous experiments have shown that the CG and GG genotypes of miR492G>C have a better probability of survival and exposure to care than the CC genotype. Therefore, MiR-492 rs2289030 is a crucial biomarker to assess potential risk patients and bad clinical results.[33] Oncogenic transcription factor PLAG1 in hepatoblastoma is frequently altered (HB). This MIR position has been identified in the HB marker gene keratin 19 (KRT19), a metastatic progression marker for liver progenitors, cancer cells and HCC. PLAG1 will co-regulate expression KRT19 and release MiR-492. In metastatic HB tumour samples, substantially more co-expressed KRT19 and MiR-492 were found, which indicate an essential role in this disease progression.[15] The CD44 gene has been established by Frowein and colleagues and is a precisely regulated target gene that plays a significant role in hepatoblastoma's metastasis.[34] A glycoprotein transmembrane. It acts as hyaluronic, several growth factors and cytokine signals receptors. CD44 may modulate different cellular processes, helping to regulate hepatic cancer cell growth, invasion and migration. CD44 was developed as a direct metastatic progression target for MiR-492. High levels of MiR-492 expression help cell growth and migration by adjusting CD44 expression and EGDR reporting.[34,35] Finally, MiR-492 may be an excellent biomarker for detection and clinical approaches in managing liver cancer.

Cervical Cancer & MiR-492

Cervical cancer is one of the world's most common cancers in women, and about 520000 new cases are reported annually. High-risk Human Papillomavirus (HPV) viral infection is a significant cause of this cancer.[36,37] Some cervical cancer treatment and preventive methods, including chemoradiotherapy and vaccine, although not all are vaccinated. Unfortunately, certain people are immune to chemotherapy or radiation. Many studies have been conducted to understand the resistance mechanism and describe why radiation treatment is not being responded to. Researchers find that the high degree of miR492 expression is linked to a lack of care in patients with advanced cervical cancer.[38] Liu et al. also revealed that MiR-492 is a P53 gene target by analysing human cervical cancer cell lines (SiHa and HeLa cells). In wild cell lines of p53, MiR-492 was upregulated and decreased in P53 mutant cell lines. Thus, P53 activation radiation and chemotherapy will raise MiR-492 expression[39] In contrast, MiR-492upregulation only promotes the migration of cervical cancer cells to the pelvic lymph node. Analysis has shown that MiR-492 is useful for invading cervical cancer cells by controlling the expression of TIMP2 and activating pelvic lymph node cells.[38] Scientists investigated the HPV16, 18 integration location in the host genome and found that the HPV18

genome fused with the host genome at 12q22 at 0.21 MB from MiR-492. This would possibly justify the MiR-492 overexpression of cervical cancer metastasis and perhaps an underlying cause for the progression of HPV18 from early to end stages, including the invasive carcinoma.[40]

Ovarian Cancer & MiR-492

Usually, postmenopausal women are affected by ovarian cancer.[41] Molecular features of ovarian cancer are misunderstood, but analysis has shown that the pathogens are essential in microsatellite instability and microRNAs. Due to delays in the last stage evaluation and the absence of traditional care responses, mortality has risen to 70%. Consequently, it may be a smart idea to find new biomarkers to detect ovarian cancer rapidly. Studies of microRNA ovarian cancer cell profiles have shown that expressions of particular miRNAs are changed, and MiR-492 is more visible. MiR-492 has the oncogenic feature and is a prognostic biomarker for early cancer. As previously mentioned, the activation of p53 protein raises MiR-492 levels.[42]

Retinoblastoma & MiR-492

Retinoblastoma is a rare tumour in the eyes, usually due to the inactivation of both RB1 genes of children. Another inherited retinoblastoma is induced by amplification of the MYCN gene. RB1, as a tumour suppressor gene, has a significant and essential role in cell growth, cell division, proliferation, and processes of differentiation. The first tumour suppressor gene RB1 has been discovered, and studies have shown that lack of RB1 may induce tumorigenesis. MicroRNAs profile indicates that miR492 expression has improved in tumour tissue.[43,44] Sun and collaborators' studies on the influence of MiR-492 on the proliferation and invasion of RB cell lines found that MiR-492 down regulation significantly decreased RB cell proliferation and consequently reduced the charge of the RB cells.[45] They find that kinase 2 (LATS2) in RB cells is a precise target gene of MiR-492. Inhibition of MiR-492 may avoid RB malignancy by attacking LATS2. Targeting MiR-492 may be a practical therapeutic approach for patients with RB.

Pancreatic Cancer & MiR-492

Pancreatic Cancer (PC) is the fourth most frequent cause of death in the country. Several risk factors have been established, but the fundamental reason for this remains unclear. Historic smoke, fat, asthma and blood form will raise the likelihood of disease. Some reports have found that in families with four infected participants, the pancreatic cancer incidence is 57 times greater than in families with no affected members.[46] Słotwiński et al. also observed that MiR-492, is on the top list of microRNA in 170 pancreatic adenocarcinomas by analysing 664 microRNA levels.[47] The pancreatic cancer survival rate is about 6%, although early detection can hit 15 to 40 percent. Thus, early diagnosis of illness significantly decreases the death risk of pancreatic cancer. Although several tumour specific molecular modifications, such as CA19-9, K-ras, P53, and mucins, have shown promise as biomarkers for PC and may quickly diagnose pancreatic cancer, due to low precision and low sensitivity, they are not adequate. Less intrusive, cost-effective strategies are also required to display PC early. Wang and his colleagues also showed that a mixture of CA19-9 levels in patients might be a reasonable target for the anticipation and treatment of pancreatic cancer by testing MiR-492 expression levels.[17,48-50] Lin and co-workers have shown that serum levels MiR-492 will lead 75.5 percent to PC discrimination.[21] Also found that MiR-492 deregulated in PC tissue.[48] Schultz et al.

Conclusion

New cancer screening techniques are critical because patients diagnosed cannot be helped by any medication advantages at the final level. In several experiments in recent years, cancerous tissues have been used to analyse and classify miRNAs that substantially modify the expression. Overexpression of MiR-492 affects various genes CD44, CD147, SOX7, PTEN and MZF1 could influence microRNA-related cancer growth, metastasis and resistance to treatment. These results rendered MiR-492 a potential antiangiogenic target and indicated that MiR-492 played a function in modulating the pro-angiogenic secretion factor. Assessing these microRNA expression levels will help diagnose and manage the disease before metastasis.[49,50]

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