Original Article

DOI: 10.7860/JCDR/2025/80307.21511

Biochemistry Section

Serum Levels of MicroRNA-210 as a Pathogenic Factor in Patients with Diabetes and Diabetic Nephropathy: A Cross-sectional Study

DIVYA SINGH[1], IVVALA ANAND SHAKER[2], ASHISHKUMAR AGRAVATT[3]

ABSTRACT

Introduction: Diabetes Mellitus (DM) is a foremost global health challenge, causing disability and premature death. It leads to severe micro and macrovascular complications, including Diabetic Nephropathy (DN), which affects 20% of patients worldwide. Up to 50% of Chronic DM (CDM) patients get end-stage DN and then require Renal Replacement Therapy (RRT). DN develops gradually and causes proteinuria and glomerulopathy. Oxidative stress, Reactive Oxygen Species (ROS), and abnormal microRibonucleic Acid (miRNAs) are involved in DM progression and complications.

Aim: The study aimed to assess serum miRNA-210 levels in DM patients and those with diabetes nephropathy, as it plays a crucial role in DM along with endothelial cell function.

Materials and Methods: The present Cross-Sectional Study (CSS) included 400 participants, grouped into healthy controls, diabetic patients having nephropathy, and diabetic patients not having nephropathy, matched by age and sex. Inclusion criteria covered adults with known diabetes or DN, while individuals with infections, inflammatory or haematological diseases, and pregnant women were excluded. Ethical clearance was obtained, and informed consent was secured from all participants. Biochemical, renal, inflammatory, and epigenetic markers (including miRNA-210) were measured utilising standard laboratory techniques. Also, statistical analysis was performed using MedCalc, with significance value of $p<0.05$.

Results: Of the 400 study participants, 192 (48.0%) were female and 208 (52.0%) were male. This study discovered noteworthy differences in glycaemic, renal, inflammatory, and epigenetic markers among control, diabetic, and DN groups. C-Reactive Protein (CRP) levels were elevated in both diabetic groups 10.591±7.175 mg/L (diabetic mellitus), and 18.710±7.406 mg/L (DN) ($p<0.001$). IL-10 levels were low in the diabetic mellitus group (8.380±0.801 pg/mL) ($p<0.001$). Fetuin-A levels were 186.90±35.913 in diabetic mellitus ($p<0.001$). Adiponectin levels were highest in the nephropathy group (21.340±7.193 µg/mL), compared to controls ($p<0.001$).

Conclusion: These findings highlight reduced serum miRNAs' potential as a biomarker for early detection and disease progression.

Keywords: Alpha subunit, Gene expression regulation, Hypoxia-inducible factor 1, Kidney disease, Reactive oxygen species, Type 2 diabetes mellitus

INTRODUCTION

Worldwide, DM poses a significant challenge to public health, being a leading cause of disability and early mortality. DM is characterised by noteworthy microvascular and macrovascular problems impacting many organs and systems [1]. About 20% of patients having DM develop DN, one of its commonest and most severe complications [2]. However, reports estimate that from 20 to 50% of CDM patients are likely to develop end-stage DN requiring RRT [3]. It is a slowly progressing disease with long periods of latency, and it leads to proteinuria and glomerulopathy [2].

Despite considerable investigation over the last years, the precise DN pathogenesis however remains unclear. Nevertheless, several pathways and risk factors for DN have been proposed in the literature. Oxidative stress may be a primary factor in kidney failure, since ROS are prevalent byproducts of metabolic problems associated with DM, including hyperglycaemia. ROS may directly affect the glomerulus, causing harm to the endothelial and mesangial cells along with podocytes [4]. Furthermore, ROS may influence DN by activating various other pathogenic pathways [5].

Abnormal miRNAs were spotted in diverse human diseases having a significant functional part of disease pathogenesis [6]. It has been found that many miRNAs contribute to the pathophysiology of DM, and include complications such as DN [7]. Several studies have shown that dysregulation of miR-210 is a contributor to DM progression, with a well-established function of promoting angiogenesis by increasing proliferation of vascular endothelial cells [8,9]. But, the serum levels of miRNA-210 in diabetes have never been investigated. Based on the above declared essential role of miRNA-210 in DM along with endothelial functions, this work intended to investigate serum levels of miRNA-210 in patients having DM as well as with diabetes nephropathy.

MATERIALS AND METHODS

The present CSS was done in the Clinical Chemistry Laboratory of General Hospital Bharuch, Gujarat, India from April 2023 to May 2024. Ethical approval for it was secured from the Institutional Ethics Committee of Dr. Kiran C Patel Medical College and Research Institute, Bharuch (Approval No: IECNO:04/2023).

Inclusion and Exclusion criteria: Participants were recruited grounded in the inclusion along with exclusion criteria. Individuals aged above 18 years having an established DM diagnosis were included. Diagnostic criteria for DM included fasting plasma glucose >126 mg/dL, Postprandial 2-hour Blood Sugar (PP2BS) >200 mg/dL, and HbA1c ≥6.5% [10]. DN is a clinical condition defined by persistent albuminuria along with a progressive deterioration in renal function, indicating a characteristic pattern of glomerular disease [11,12] and a reduced estimated Glomerular Filtration Rate (eGFR) as configured utilising the Modification of Diet in Renal Disease (MDRD) formula. Additionally, healthy individuals above 18 years

of age who were willing to participate were included as controls. Exclusion criteria encompassed individuals under 18 years of age, pregnant women, and patients having infectious diseases, haematological disorders, inflammatory conditions, or non-diabetic kidney diseases [8]. All parameter ranges were processed according to the laboratory standards.

Sample size selection: A Convinient sample size of 400 participants was incorporated into the study, matched in age and sex, and categorised into two primary groups, where Group-I (healthy controls, n=200) along with Group-II (diabetic patients, n=200). The diabetic patients were further divided into diabetics with and without nephropathy with 100 subjects in each group.

All participants were given detailed information in their local language about the purpose and procedures of the study, and written informed consent was acquired before enrollment. From each participant, 5-7 mL of venous blood was acquired under aseptic conditions using Ethylenediaminetetraacetic Acid (EDTA), fluoride, and plain vacutainers at designated collection centers. The samples were then processed and analysed at the respective hospital clinical chemistry laboratories.

Study Procedure

Biochemical and inflammatory markers were measured using standard laboratory techniques and instrumentation. Fasting Blood Sugar (FBS) and PP2BS were determined using the Glucose Oxidase-Peroxidase (GOD-POD) method on a semi-automated analyser. Glycated haemoglobin (HbA1c) was measured by immunoturbidimetry on a fully automated analyser. Renal function parameters included serum urea (estimated by the GLDH process) and serum creatinine (measured by Jaffe's kinetic method), both assessed using a fully automated biochemistry analyser. Serum cystatin C was also measured via immunoturbidimetry. The eGFR was calculated utilising the MDRD formula. Inflammatory and molecular markers analysed included CRP, IL-10, adiponectin, fetuin-A, and serum microRNA-210 (miRNA-210). These were analysed by utilising Enzyme-Linked Immunosorbent Assay (ELISA), and absorbance values were recorded using a microplate reader.

STATISTICAL ANALYSIS

Data analysis was conducted utilising MedCalc® software version 12.7.0.0 (MedCalc Software, Ostend, Belgium). Continuous variables were presented as mean±Standard Deviation (SD), and categorical variables were reported as counts and percentages. Also, the Chi-square test was employed to compare categorical variables between groups. All statistical tests remained two-tailed, along with a p-value <0.05 was deemed statistically significant.

RESULTS

Of the 400 study participants, 192 (48.0%) were female and 208 (52.0%) were male. The control group (n=200) had 93 (46.5%) females and 107 (53.5%) males; the DN group (n=100) had 49 (49.0%) females and 51 (51.0%) males; and the diabetic mellitus group (n=100) had an equal sex distribution of 50 (50.0%) females and 50 (50.0%) males. The three groups' sex distribution exhibited no statistically noteworthy variance (p=0.850) [Table/Fig-1]. The mean age of participants in all three study groups- control, diabetic mellitus, and DN- was closely matched and statistically non-significant (p=0.950) [Table/Fig-1]. The control group possessed a mean FBS of 90.8±210.63 mg/dL, the DM group had a mean FBS of 145.64±18.51 mg/dL, and the DN group had mean FBS of 178.96±16.35 mg/dL (p<0.001). PP2BS values were 120.80±12.61 mg/dL, 254.94±39.92 mg/dL, and 295.81±65.01 mg/dL in the control, DM, and DN groups, correspondingly (p<0.001). HbA1c values were 4.386±0.757% in controls, 6.514±1.129% in the diabetic mellitus group, and 8.047±1.680% in the DN group (p<0.001) [Table/Fig-2].

Sex	Group			Total	p-value
	Control group	Diabetic nephropathy	Diabetic melltus		
Female	93 (46.5)	49 (49)	50 (50)	192	0.850
Male	107 (53.5)	51 (51)	50 (50)	208	
Total	200	100	100	400	
Mean age	52.20±14.31	52.30±13.57	52.74±13.36		0.950

[Table/Fig-1]: Demographic profile.

Parameters	Control group (Mean±SD)	Diabetic Nephropathy (DN) (Mean±SD)	Diabetic mellitus (Mean±SD)	p-value
FBS (mg/dL)	90.82±10.63	178.96±16.35	145.64±18.51	<0.001
PP2BS (mg/dL)	120.80±12.61	295.81±65.01	254.94±39.92	<0.001
HbA1C (%)	4.386±0.757	8.047±1.680	6.514±1.129	<0.001

[Table/Fig-2]: Glycaemic parameters levels between groups.

The DN group had significantly elevated mean blood urea levels (74.83±12.95 mg/dL) compared to the control (28.11±7.33 mg/dL) and diabetic mellitus groups (28.96±7.70 mg/dL) (p<0.001). Serum creatinine levels were also higher in the DN group (4.584±1.838 mg/dL) than in the control (0.947±0.824 mg/dL) and diabetic mellitus groups (0.987±0.179 mg/dL) (p<0.001). eGFR was markedly lower in the nephropathy group (38.13±15.39 mL/min/1.73 m^2) than in controls (94.05±3.99) and diabetic patients (94.15±5.29) (p<0.001). Serum cystatin C was also markedly increased in the DN group (14.1382±7.835 mg/L) than in the control (0.8796±0.170) and DM groups (0.9639±0.401) (p<0.001) [Table/Fig-3].

Parameters	Control group (Mean±SD)	Diabetic Nephropathy (DN) (Mean±SD)	Diabetic mellitus (Mean±SD)	p-value
Urea (15-45 mg/dL)	28.105±7.33	74.830±12.95	28.960±7.70	<0.001
Creatinine (0.7-1.2 mg/dL)	0.947±0.824	4.584±1.838	0.987±0.179	<0.001
eGFR (MDRD >60 mL/min/1.73m^2)	94.05±3.99	38.13±15.39	94.15±5.29	<0.001
Cystatin C (0.62-1.15 mg/L)	0.8796±0.170	14.1382±7.835	0.9639±0.401	<0.001

[Table/Fig-3]: Renal parameters levels between groups.

CRP levels were elevated in both diabetic groups compared to controls: 3.077±1.497 mg/L (controls), 10.591±7.175 mg/L (diabetic mellitus), and 18.710±7.406 mg/L (DN) (p<0.001). IL-10 was lesser in the diabetic mellitus group (8.380±0.801 pg/mL) than in controls (16.199±2.731) and the DN group (16.822±4.540) (p<0.001). Fetuin-A levels were 61.61±6.036 ng/mL in controls, 186.90±35.913 in diabetic mellitus, and 102.77±14.161 in DN patients (p<0.001). Adiponectin levels were highest in the nephropathy group (21.340±7.193 µg/mL), compared to controls (6.437±1.581) and diabetic mellitus (8.829±2.058) (p<0.001) [Table/Fig-4].

Parameters	Control group (Mean±SD)	Diabetic Nephropathy (DN) (Mean±SD)	Diabetic mellitus (Mean±SD)	p-value
CRP (<10 mg/L)	3.077±1.497	18.710±7.406	10.591±7.175	<0.001
IL10 (10-25 pg/mL)	16.199±2.731	16.822±4.540	8.380±0.801	<0.001
Fetuin-A (50-75 ng/mL)	61.61±6.036	102.77±14.161	186.90±35.913	<0.001
Adiponectin (5-12 µg/mL)	6.437±1.581	21.340±7.193	8.829±2.058	<0.001

[Table/Fig-4]: Inflammatory marker levels between groups.

The serum levels of circulating miRNA-210 showed significant differences among the study groups. In the control group, the mean serum miRNA-210 concentration was 213.41±223.00 pg/mL, whereas in the DN group it was significantly reduced to

109.71±12.46 pg/mL. A moderate decrease was observed in the diabetic mellitus group without nephropathy, where the mean level was 132.26±7.60 pg/mL. These variances were statistically noteworthy (p <0.001), suggesting a possible association between decreased serum miRNA-210 levels and disease progression from diabetes to nephropathy [Table/Fig-5].

Measure	Control group (Mean±SD)	Diabetic Nephropathy (DN) (Mean±SD)	Diabetic mellitus (Mean±SD)	p-value
miRNA210 (150-300 pg/mL)	213.41±223.00	109.71±12.46	132.26±7.60	<0.001

[Table/Fig-5]: Serum miRNA210 Levels between groups.

DISCUSSION

The study identified several significant findings among the control, DM, and DN groups. Demographic variables, including age and sex distribution, exhibited no significant differences, thereby ensuring comparability among groups. Glycaemic parameters like FBS, postprandial blood sugar, along with HbA1c, were elevated in DM and further in DN, indicating a progressive deterioration in glucose control. Markers of renal function, including blood urea, serum creatinine, and cystatin C, exhibited significant elevation in the DN group, alongside a notable reduction in eGFR, indicating considerable renal impairment. Inflammatory markers exhibited significant variation; CRP levels were elevated in both DM and DN, IL-10 was diminished in DM but relatively maintained in DN and controls, while fetuin-A was highest in DM and decreased in DN. Adiponectin levels were notably elevated in DN, potentially attributable to impaired clearance or compensatory mechanisms. Serum miRNA-210 levels exhibited a progressive decline from controls to DM and subsequently to DN, suggesting its potential as an epigenetic biomarker for disease progression. The findings highlight the interaction among hyperglycaemia, inflammation, renal dysfunction, and epigenetic changes in the development and advancement of DN.

Almost equal percentage of male and female participants were found in each of the three groups, indicating that gender differences do not obscure the results pertaining to other parameters. The sex distribution's lack of statistical significance suggests that male and female participants were equally represented in each group. This is in line with Romero-Farina G et al., in the field that has not found gender to be a confounding factor when evaluating outcomes related to diabetes [13]. The equal representation of both sexes in the study makes it possible to interpret the results more clearly without having to take into consideration variations in epigenetic marker or other inflammatory and metabolic marker analysis based on sex. The uniformity in age distribution eliminates age as a prospective confounding aspect in the assessment of biochemical and inflammatory markers. Age is a known aspect for development along with progression of T2DM and its complications, including DN [14]. Therefore, ensuring comparable age profiles across groups is essential for the validity of intergroup comparisons.

Higher HbA1c levels, as seen in this study, are not only signs of long-run glycaemic control but are also separately linked to the advancement of DN [15]. Higher FBS and PP2BS values in nephropathy patients reflect the difficulty in controlling blood glucose as renal function declines, which may also be compounded by insulin resistance and changes in drug pharmacokinetics resulting from impaired renal clearance there by reveling a significant loss in renal function among individuals with DN, which is linked to Chronic Kidney Disease (CKD) progression in people having long-standing diabetes [16]. Elevated blood urea, creatinine, and cystatin C levels, along with a drop in eGFR, indicate a decline in filtration and higher nitrogenous waste retention [17]. The study also highlights the importance of cystatin C in the form of a sensitive biomarker for early renal dysfunction, as creatinine may not accurately reflect glomerular function in diabetic patients. Interestingly, both control and diabetic groups without nephropathy showed normal renal function values. The study reveals significant dysregulation in inflammatory and metabolic markers in patients having diabetes along with DN. Elevated CRP levels in both diabetic groups, particularly in the nephropathy subgroup, indicate chronic low-grade inflammation that underlies diabetes and its vascular complications. CRP is a predictor of cardiovascular risk and renal progression in DM, and progressively higher levels from control to nephropathy groups suggest a correlation across systemic inflammation and disease severity [18].

IL-10, an anti-inflammatory cytokine, was significantly reduced in diabetic mellitus patients but preserved in controls and patients having nephropathy. Fetuin-A, being a hepatic glycoprotein involved in insulin resistance and vascular calcification, showed an unexpected trend, with elevated levels in both diabetic groups, especially in those without nephropathy [19]. Adiponectin, an anti-inflammatory adipokine, was markedly increased in DN patients, aligning with studies showing elevated adiponectin levels in response to renal impairment and metabolic stress. Lower levels in the diabetic mellitus group may reflect insulin resistance and central adiposity in earlier disease stages. Research has indicated the elevation of miRNA-210 in response to hyperglycaemia, hypoxia, and oxidative stress, which are indicative of diabetes and its consequences. miRNA-210, recognised as a hypoxia-inducible microRNA, is essential for the regulation of mitochondrial metabolism, angiogenesis, and cellular survival during stress conditions [20]. Prior studies conducted by Zaccagnini G et al., and Qadri MMF et al., have shown that hyperglycaemia stimulates miRNA-210 expression as an adaptive protective response in diabetic tissues and vascular settings. [20,21]. This investigation demonstrated significantly low levels of serum miRNA-210 in both DM and DN groups relative to controls (p<0.001), contradicting previous findings. This disparity may arise from various sources. Initially, the sample comprised individuals with enduring, chronic diabetes and nephropathy, in contrast to previous studies that predominantly investigated early-stage disease or in vitro models. Chronic oxidative stress and inflammation may diminish miRNA-210 expression over time due to feedback inhibition or depletion of the hypoxia response pathway. Secondly, it is essential to consider the differences in sample type-whereas numerous studies have examined tissue-specific miRNA expression, our data originated from circulating serum, which may not accurately represent local tissue expression due to factors such as degradation, exosomal packaging, and renal filtration.

Thirdly, chronic hyperglycaemia may cause epigenetic silencing of miRNA-210 or disrupt its transcriptional regulation. Furthermore, renal impairment in DN may affect miRNA clearance and circulation. Methodological discrepancies, including quantification methods and changes in study populations, may also lead to conflicting findings. Moreover, its reduced levels in diabetic individuals without apparent nephropathy indicate that miRNA-210 may function as a predictive marker for the advancement of microvascular damage before the clinical onset of renal impairment, highlighting its diagnostic and prognostic importance in diabetes management.

Limitation(s)

This study presents several limitations; the cross-sectional design restricts the capacity to infer a causal relationship between biomarker levels and disease progression. The findings of this single-centre study may lack generalisability to larger or more diverse populations. The overall sample size was sufficient; however, the subgroup sizes (n=100 for both DM and DN) may diminish statistical power for identifying subtle differences. The lack of data regarding the duration and severity of diabetes, along with other confounding variables such as BMI, lifestyle, medications, and co-morbidities, may influence the interpretation of results. Only a single epigenetic marker, miRNA-210, was assessed without functional validation or comprehensive profiling, limiting understanding of the underlying molecular mechanisms.

Furthermore, although the distribution of sex and age was balanced, the absence of subgroup analysis limits the investigation of possible demographic effects on biomarker patterns. The identified limitations indicate the necessity for larger, longitudinal, multi-centre studies that incorporate comprehensive clinical and molecular profiling to validate and expand upon the existing findings.

CONCLUSION(S)

This study reveals distinct biochemical, inflammatory, renal, and epigenetic alterations in individuals having T2DM, DN, along with healthy controls. Despite the same demographic profile between the groups, the metabolic, renal, and inflammatory profiles differed, highlighting the systemic impact of diabetes and its progression to nephropathy. It was found a decrease in circulating miRNA-210 levels, suggesting a potential pathogenic and predictive role of this epigenetic marker. These findings highlight the multifactorial nature of DN, driven by hyperglycaemia, inflammation, renal impairment, and epigenetic dysregulation. The data suggest that serum miRNA-210 could be a useful marker for detecting and tracking diabetic kidney disease early on. More research over time is needed to confirm the miRNA-210 for predicting outcomes and its treatment effects in people with diabetes.

REFERENCES

[1] Huang D, Refaat M, Mohammedi K, Jayyousi A, Al Suwaidi J, Abi Khalil C. Macrovascular complications in patients with diabetes and prediabetes. Biomed Res Int. 2017;2017:01-09.
[2] Samsu N. Diabetic nephropathy: Challenges in pathogenesis, diagnosis, and treatment. Bellini MI, editor. Biomed Res Int. 2021;2021(1):01-17.
[3] Yarahmadi A, Shahrokhi SZ, Mostafavi-Pour Z, Azarpira N. MicroRNAs in diabetic nephropathy: From molecular mechanisms to new therapeutic targets of treatment. Biochem Pharmacol. 2021;189:114301.
[4] Duni A, Liakopoulos V, Roumeliotis S, Peschos D, Dounousi E. Oxidative stress in the pathogenesis and evolution of chronic kidney disease: Untangling ariadne's thread. Int J Mol Sci. 2019;20(15):3711.
[5] Pérez-Morales Rosa E, del Pino M, Valdivielso J, Ortiz A, Mora-Fernández C, Navarro-González Juan F. Inflammation in diabetic kidney disease. Nephron. 2018;143(1):12-16.
[6] Vienberg S, Geiger J, Madsen S, Dalgaard LT. MicroRNAs in metabolism. Acta Physiologica. 2016;219(2):346-61.
[7] Sharma S, Mathew AB, Chugh J. miRNAs: Nanomachines that micromanage the pathophysiology of diabetes mellitus. Adv Clin Chem. 2017;82:199-264.
[8] Zheng Z, Liu L, Zhan Y, Yu S, Kang T. Adipose-derived stem cell-derived microvesicle-released miR-210 promoted proliferation, migration and invasion of endothelial cells by regulating RUNX3. Cell Cycle. 2018;17(8):1026-33.
[9] Naderi R, Mohaddes G, Mohammadi M, Alihemmati A, Khamaneh A, Ghyasi R, et al. The effect of garlic and voluntary exercise on cardiac angiogenesis in diabetes: The role of MiR-126 and MiR-210. Arq Bras Cardiol. 2019;112(2):154-62.
[10] Sathish T, Chandrika Anton M. Newly diagnosed diabetes in patients with mild to moderate COVID-19. Diabetes Metab Syndr. 2021;15(2):569-71.
[11] Selby NM, Taal MW. An updated overview of diabetic nephropathy: Diagnosis, prognosis, treatment goals and latest guidelines. Diabetes Obes Metab. 2020;22(Suppl 1):03-15.
[12] Onalan E. The relationship between monocyte to high-density lipoprotein cholesterol ratio and diabetic nephropathy. Pak J Med Sci. 2019;35(4):1081-86.
[13] Romero-Farina G, Aguadé-Bruix S, Cuellar-Calabria H, Pizzi MN, Roque A, Candell-Riera J. Gender differences in outcome in patients with diabetes mellitus. J Nucl Cardiol. 2020;29(1):72-82.
[14] Natesan V, Kim SJ. Diabetic nephropathy - a review of risk factors, progression, mechanism, and dietary management. Biomol Ther (Seoul). 2021;29(4):365-72.
[15] Lee MY, Huang JC, Chen SC, Chiou HY, Wu PY. Association of HbA1C variability and renal progression in patients with type 2 diabetes with chronic kidney disease stages 3-4. Int J Mol Sci. 2018;19(12):4116.
[16] Pugliese G, Penno G, Natali A, Barutta F, Di Paolo S, Reboldi G, et al. Diabetic kidney disease: New clinical and therapeutic issues. Joint position statement of the Italian Diabetes Society and the Italian Society of Nephrology on "The natural history of diabetic kidney disease and treatment of hyperglycaemia in patients with type 2 diabetes and impaired renal function." Nutrition, Metabolism and Cardiovascular Diseases. 2019;29(11):1127-50.
[17] Singh D, Patel N, Malapati BR, Shaker IA. A study of serum cystatin C as a marker of diabetic nephropathy among patients with type 2 diabetes mellitus: A systematic review and meta-analysis. J Med Sci Res. 2022;10(4):237-42.
[18] Stanimirovic J, Radovanovic J, Banjac K, Obradovic M, Essack M, Zafirovic S, et al. Role of C-Reactive protein in diabetic inflammation. Mediators Inflamm. 2022;2022:3706508.
[19] Donate-Correa J, Ferri CM, Sánchez-Quintana F, Pérez-Castro A, González-Luis A, Martín-Núñez E, et al. Inflammatory cytokines in diabetic kidney disease: Pathophysiologic and therapeutic implications. Front Med (Lausanne). 2021;7:628289.
[20] Zaccagnini G, Greco S, Voellenkle C, Gaetano C, Martelli F. miR-210 hypoxamiR in angiogenesis and diabetes. Antioxid Redox Signal. 2022;36(10-12):685-706.
[21] Qadir MMF, Klein D, Álvarez-Cubela S, Domínguez-Bendala J, Pastori RL. The role of MicroRNAs in diabetes-related oxidative stress. Int J Mol Sci. 2019;20(21):5423.

PARTICULARS OF CONTRIBUTORS:
1. PhD Scholar, Department of Biochemistry, Parul Institute of Medical Sciences and Research, Parul University, Waghodia, Gujarat, India.
2. Professor, Department of Biochemistry, Swaminarayan Institute of Medical and Research, Swaminarayan University, Kalol, Gujarat, India.
3. Associate Professor, Department of Biochemistry, PDU Medical College, Rajkot, Gujarat, India.

NAME, ADDRESS, E-MAIL ID OF THE CORRESPONDING AUTHOR:
Divya Singh,
Limda, Tal. Waghodia, Gujarat, India.
E-mail: divyarana005@aol.com

PLAGIARISM CHECKING METHODS: [Jain H et al.]
- Plagiarism X-checker: May 19, 2025
- Manual Googling: Jun 13, 2025
- iThenticate Software: Jul 26, 2025 (9%)

ETYMOLOGY: Author Origin

EMENDATIONS: 8

AUTHOR DECLARATION:
- Financial or Other Competing Interests: None
- Was Ethics Committee Approval obtained for this study? Yes
- Was informed consent obtained from the subjects involved in the study? Yes
- For any images presented appropriate consent has been obtained from the subjects. NA

Date of Submission: **May 09, 2025**
Date of Peer Review: **Jun 03, 2025**
Date of Acceptance: **Jul 29, 2025**
Date of Publishing: **Sep 01, 2025**