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# Mi RNA's are a Novel Class of Regulatory Genes Associated with Kidney Disease

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***Authors' contributions***

*This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.*

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## ABSTRACT

**Introduction:** Micro RNA's have been associated with chronic kidney disease progression and mortality. However, mi RNA 223 and mi RNA 192 role in CKD is poorly evaluated.
**Aim:** The learning aims to find the part of mi RNA 223 and 192 in CKD patients.

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**Methods:** A cross-sectional observational study that included 450 study subjects out of which, 400 were cases and 50 were controls. Biochemical parameters were assessed by ELISA and mi RNA expression levels were evaluated by quantitative PCR.
**Results:** It was found that mi RNA 223 and 192 were significantly increased in the advancing stages of CKD when compared to controls.
**Conclusion:** mi RNA 192 and mi RNA 223 can be used as diagnostic markers of CKD.

*Keywords: Disease; progression; stages of kidney disease; expression.*

## 1. INTRODUCTION

In the recent past, novel non-coding RNA's have been revealed taking new insights into the process of genetic factor parameters [1]. The size of the RNA's deviates them into short and long non coding RNA's [2]. These non-coding RNA's harmfully control genetic factor appearance by deprivation of their mark mi RNA's [3]. It is increasingly evident that mi RNA's are expressed in usual and compulsive tissue which are intricate in kidney disease [4]. Research on micro RNA's as probable biomarkers in the analysis and progression of diseases has gained traction in the current research field. These mi RNA's play a crucial role in different cellular and regulatory processes like apoptosis, development, differentiation, and proliferation and also in the proper functioning of the kidney [5]. It is also obvious that various mi RNA's are identified in saliva, serum, urine, and plasma. Earlier studies demonstrated that mi RNA's exhibit unique pathology and can be used as potential diagnostic markers [6]. There is a growing demand to explore the part of extracellular mi RNA's in the progression and growth of kidney disease i.e.; CKD [7-9]. However, most of the findings relevant to mi RNA appearance in several organic solutions of CKD are unpredictable.

As the main objective of the present study is to find the connotation of mi RNA with CKD.

## 2. MATERIALS AND METHODS

This cross-section observational learning was shown from 2020 to 2024 in urban and rural health centers of Narayana Medical College and Hospital Nellore, Andhra Pradesh, India. Informed consent is obtained from all the subjects and they were conducted after getting approval from the institutional ethical committee. Patients with CKD are considered in the current study. Patients in the age group 18 to 55 years, having been diagnosed with enduring kidney disease according to kidney disease, result quality initiative criteria were considered for the present study. Patients with a history of epilepsy, hypertensive encephalopathy malignancies, and infections. And 5$^{th}$ stage of CKD patients were excluded from the present study. 5 ml of Venus blood samples were withdrawn from each subject and transferred in Serum vacuums at the sample collection center. The serum is separated using centrifuge at 3000 rpm for 13 actions at room temperature.

300- 500 µL serum sample Was used for micro-RNA extraction using a Mir easy serum/plasma kit. Extracted mi RNA's were converted into c DNA using U6 universal primer Further, each c DNA was quantifier by using Agrose gel electrophorosis and nanodrop reading. Quantified c DNA was used for the quantitative expression analysis of two distinguished micro RNA's, that is, mi RNA 223 and mi RNA 192 in patient samples about control subjects, with real-time measurable PCR and 2 delta q technique.

## 3. RESULTS

A total of 450 subjects comprising 400 CKD patient roles and 50 well controls were comprised in the present learning. The patients in the study were bifurcated into four groups and healthy controls. Four groups of diversion are based on the stages of CKD Phase 1 (n=100); Stage 2(n=100), stage 3(n=100), and Stage 4 (n=100) and healthy controls (n=50). The scientific and biological parameters of the learning subjects are potted as follows. (Tables 1 & 2).

Dual mi RNA's be identified in the samples and serum echelons of mi RNA 192 and miR223 concluded the CKD patients were brief in Figs. 1 & 2.

The appearance levels of mi RNA 192 in females were higher than the males of the study**.**

**Table 1. Medical parameters of the study subjects**

| Variable | Number of cases |
|---|---|
| Mean Age (years) | |
| Males | 54 ± 2.3 |
| Females | 52 ± 3.5 |
| Males | 235 |
| Females | 165 |
| Mean weight (Kg) | 58 |
| Mean Height (m) | 1.64 |
| Mean BMI (kg/m$^2$) | 24 |
| Systolic BP (mm Hg) | 120 |
| Diastolic BP (mm Hg) | 80 |
| Family history of CKD (number) | 120 |
| Smoking (only males) | 168 |
| Chewing betel (both males and females) | 98 |
| Consumption of Alcohol (only males) | 76 |
| History of Hypertension | 89 |
| Diabetes mellitus | 20 |
| History of Malaria | 55 |

**Table 2. Biochemical parameters of the study subjects**

| Biochemical parameters (mean) | Stage 1 CKD | Stage 2 CKD | Stage 3 CKD | Stage 4 CKD | Control |
|---|---|---|---|---|---|
| Urea (mg/dL) | | | | | |
| Male | 37 | 38 | 44 | 46 | 32 |
| Female | 38 | 32 | 42 | 48 | 30 |
| Creatinine (mg/dL) | | | | | |
| Male | | | | | |
| Female | 1.4 | 1.5 | 2.1 | 2.8 | 1.0 |
| | 1.32 | 1.46 | 2.5 | 2.7 | 1.1 |
| eGFR (ml/min) | | | | | |
| Male | 68 | 63 | 42 | 30 | 110 |
| Female | 62 | 62 | 43 | 31 | 108 |
| Glucose (mg/g) | | | | | |
| Male | 79 | 200 | 76 | 15 | 70 |
| Female | 77 | 201 | 74 | 12 | 43 |

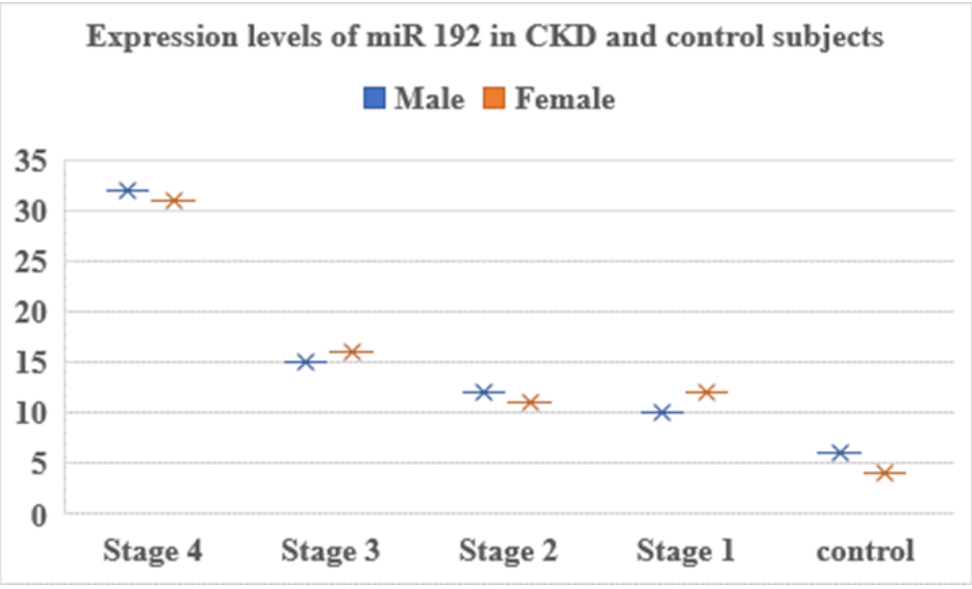


**Fig. 1. Expression of mi RNA 192 in CKD of all stages**

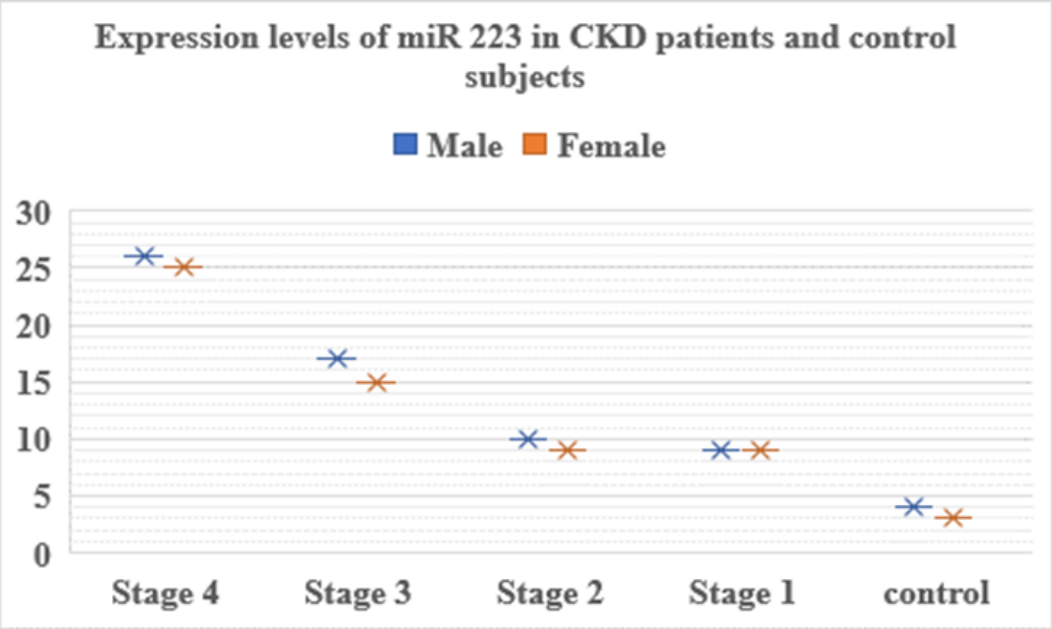


**Fig. 2. Expression of mi RNA 223 in CKD of all stages**

The appearance of mi RNA 223 in males is more advanced than in the females of the CKD - affected individuals.

## 4. DISCUSSION

The current study proved a significant increase in mingling mi RNA 192 and miR 223 in patients with more unadorned stages of CKD.

Glomerular purification rate estimation meanwhile the serum levels of creatinine currently remain the most suitable marker of renal function for average practice and large epidemiological studies [10]. Albuminuria, proteinuria, and serum urea levels are useful indicators of renal character once controlled for urinary creatinine. However, these are not actual complex when detecting the first phases of CKD. Some other markers have been evaluated for their prognostic value of death, cardiac complications, and kidney disease evolution without victory [11-13]. mi RNA's take attention as biomarker candidates to measure kidney disease severity [14,15]. One of the main compensations of mi RNA's is their serac stability which makes them appropriate as a non-invasive biomarker [16]. So, one can hope that minor RNA's might prove to be a dependable marker to be valuable in clinical practice.

Quantification of mi RNA's stages in blood samples is performed by quantitative PCR. Various study squads have depicted the appearance of mi RNA in plasma circulation in CKD advanced stages [17, 18]. A cohort study by Chen et al proved that miR-125b, mi RNA 145, and 155 stages declined as the disease progressed [19]. The plasma levels of cardiac mi RNA's as well decline with eGFR [20].

In difference to the above studies, in the present investigation, there is a growth in the levels of mi RNA 223 and 192 are advanced stages of CKD.

As miR-223 is measured to be a marker of tenderness, it can be used as a marker for detecting CKD [21]. As per our study observations, mi RNA 192 and mi RNA 223 remain as prophetic markers of CKD identification and detection. The present investigation is the first study to identify the raised levels of mi RNA in CKD patients.

## 5. CONCLUSION

To conclude, this is one of the rare studies to prove mi RNA's be used as diagnostic markers in detecting chronic kidney disease. Mi RNA 192 and mi RNA 223 are used as prognostic markers for identifying CKD disease progression.

## DISCLAIMER (ARTIFICIAL INTELLIGENCE)

Author(s) hereby declare that NO generative AI technologies such as Large Language Models

(ChatGPT, COPILOT, etc) and text-to-image generators have been used during writing or editing of manuscripts.

## ETHICAL APPROVAL

As per international standards or university standards written ethical approval has been collected and preserved by the author(s).

## CONSENT

As per international standards or university standards, patient(s) written consent has been collected and preserved by the author(s).

## COMPETING INTERESTS

Authors have declared that no competing interests exist.

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