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Research Article

Serum microRNA-122 as a potential biomarker for early detection and monitoring of type 2 diabetes mellitus: a cross-sectional study

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Abstract

Introduction: MicroRNAs (miRNAs) are small noncoding RNAs with transcriptional repressive properties. Type 2 diabetes mellitus (T2DM) is closely associated with endothelial dysfunction and altered molecular signaling. Although microRNA-122 (miR-122) is highly abundant in the liver and contributes to lipid homeostasis, its significance in predicting long-term metabolic disease risk remains insufficiently understood.

Materials and methods: Circulating miR-122 levels were quantified in 85 patients with T2DM, stratified into: group 1: manifest T2DM (n=50), and group 2: T2DM diagnosed according to WHO criteria (n=35). Results were compared with 47 healthy controls. To assess the long-term predictive value of miR-122, findings were further compared with data from the prospective Bruneck study (n=810, baseline 1995). Multivariable Cox regression models were used to evaluate the association between log-transformed miR-122 levels and incident T2DM over a follow-up period of up to 15 years.

Results: Circulating miR-122 was significantly associated with T2DM status, with patient groups demonstrating altered expression patterns suggestive of its potential involvement in metabolic dysregulation. Notably, reduced miR-122 levels in patient groups emerged as a possible indicator of T2DM. In the Bruneck cohort, each 1-standard deviation (SD) increase in log(miR-122) was associated with a 37% higher risk of developing T2DM (HR=1.37, 95% CI: 1.03–1.82, p=0.021) during the 15-year follow-up.

Conclusion: Decreased miR-122 levels may characterize individuals with existing T2DM, elevated long-term levels were predictive of future diabetes onset in a population-based cohort. These results underscore the utility of miR-122 as a promising biomarker for early identification of individuals at increased risk for T2DM.

Keywords

diabetes mellitus, insulin resistance, microRNA-122

Introduction

MicroRNAs (miRNAs) are a class of small noncoding RNAs that have transcriptional repressive properties.[1,2] They can control the transcriptional suppression or destruction of their target mRNAs by attaching via standard pair to a complement site in 3 untranslated regions of this transcript. Angiogenesis, oncogenesis, stress responses and development all show important roles for miRNAs.[3]

Additionally, there is growing evidence that miRNAs play a major role in the cardiovascular system. For example, miRNAs regulate endothelial cell function, inflammatory response and angiogenic potential.[4,5] These miRNAs are encapsulated in microvesicle that protects them from