



# In-silico profiling of miRNAs against type 2 diabetes mellitus and myocardial infarction associated genes

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## Abstract

Type 2 diabetes mellitus (T2DM) and myocardial infarction (MI) are among top ten leading cause of death, worldwide. miRNA based therapeutic approach may prove an icebreaker to overcome the life-threatening complications of MI and T2DM. Mature miRNAs are endogenous single stranded, non-coding, comprised 20 to 22 nucleotides long sequence which involved in gene silencing at post transcriptional level. It has reported that T2DM affected individuals have more chance to develop MI. Therefore, a single therapeutic approach is required to regulate the common underlying molecular pathways. For this, we found T2DM and MI associated genes by using genetic testing registry (GTR) of national center of biotechnology information (NCBI). To further validate the genes data, we did gene enrichment analysis via ShinyGO database. In order to predict targeted miRNAs (8-mer and species conserved) we used TargetScan, miRWalk and miRBase tools. Data analysis shows that T2DM and MI linked genes have some common targeted miRNAs like miR-128-3p/27-3p/ 181-5p/ 132-3p/ 212-3p/ 30-5p/ 101-3p.1/ 101-3p.2/ 9-5p/ 142-3p.1/ 15-5p/ 16-5p/ 195-5p/ 424-5p/ 497-5p/ 155-5p/ 124-3p.1/ 124-3p.2/ 506-3p that may play a putative role to design a most effective therapeutic strategy. Another set of miRNAs like miR-1-3p/ 206/ 27-3p/ 181-5p/ 7-5p and miR-144-3p/ 135-5p/ 142-3p.2 have selected for T2DM and MI respectively that can target more than one gene in each pathological condition. Taken together, our findings suggest most appropriate miRNAs selection for designing better therapeutic strategy against T2DM linked MI. To check the potential of each miRNA against T2DM and MI, more investigation is needed.

## Background

Type 2 diabetes mellitus (T2DM) and myocardial infarction (MI) are among the top leading cause of death, worldwide(Heron, 2018).

T2DM is a metabolic disorder which is characterized with insulin resistance or insufficient insulin production that result in persistent high-level of blood glucose(Olokoba, Obateru, & Olokoba, 2012). T2DM patients have high chance to be affected with MI(Li et al., 2020). There are many approaches being used like pharmacological drugs and stem cells therapies to overcome these pathological disorders, but still more research is needed(Laakso, 2001). MicroRNAs (miRNAs) are the non-coding single stranded, comprised almost 20 to 22 nucleotide sequence which upon the complimentary basis binds to their target mRNA and cause silencing of proteins expression at post transcriptional level (Bartel 2004, Ha 2011). miRNAs expression monitoring showed that many health disorders like cancer, T2DM and MI have altered expression of different miRNAs and they are involved in regulation of fundamental biological processes of cell (Durczyński et al. 2022). It urged to use nucleic acid base therapy that has immense potential to rescue life threatening diseases like diabetes and cardiovascular diseases (CVDs) (He et al., 2020; Lavenniah et al., 2020; Pérez-Cremades, Chen, Assa, & Feinberg, 2022). Beside this, expression profiling of miRNAs can be used for early detection of chronic diseases(Vasu et al., 2019; Zhou et al., 2018).

## Objective

Profiling of different putative miRNAs that are supposed to have potential to reduce the complications of T2DM and MI. Profiling of most suited miRNAs to design effective therapeutic strategy against T2DM and MI.

## Materials & Methods

Bioinformatic databases like Gene testing registry (GTR) of NCBI and online mendelian inheritance man (OMIM) are used to find out T2DM and MI linked genes. In order to find the 8mer and species conserved (human, rat and mouse) miRNAs, we used targetScan, miRWalk and miRBase by putting the gene names one by one.

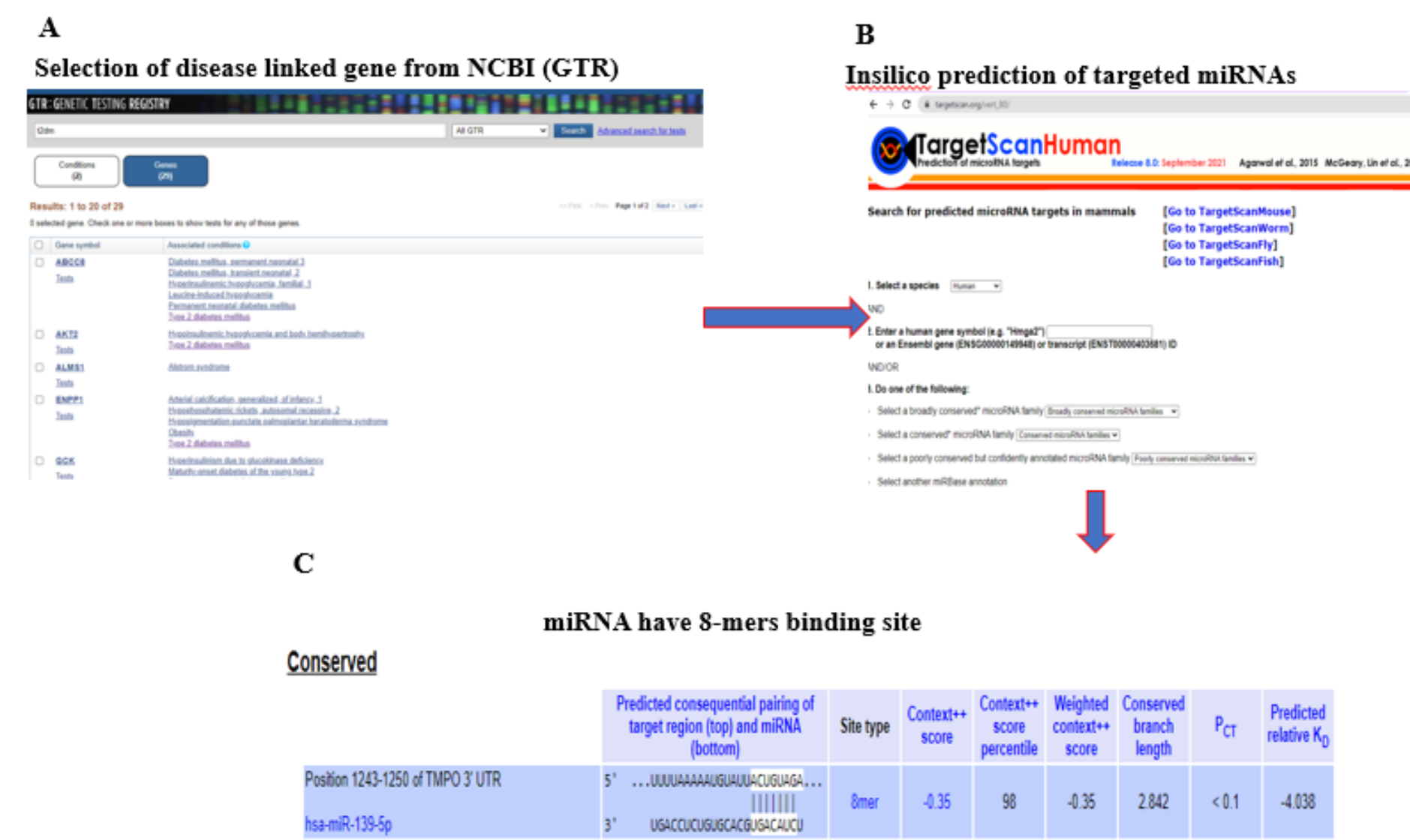


Figure 1: Bioinformatics tool analysis A) selection of disease linked genes from NCBI (GTR) B) miRNA prediction by targetScan C) 8mer and species conserved miRNA selection.

## Results

Our study interestingly showed that some important 8-mers , species conserved miRNAs are common target of T2DM and MI linked genes. Some miRNAs can affect more than one genes in each pathological condition. Our study pave a way to choose most effective miRNAs as therapeutic strategy for T2DM and MI. Red colored genes are linked with T2DM, and green name of genes are associated with MI as shown in figure 2.

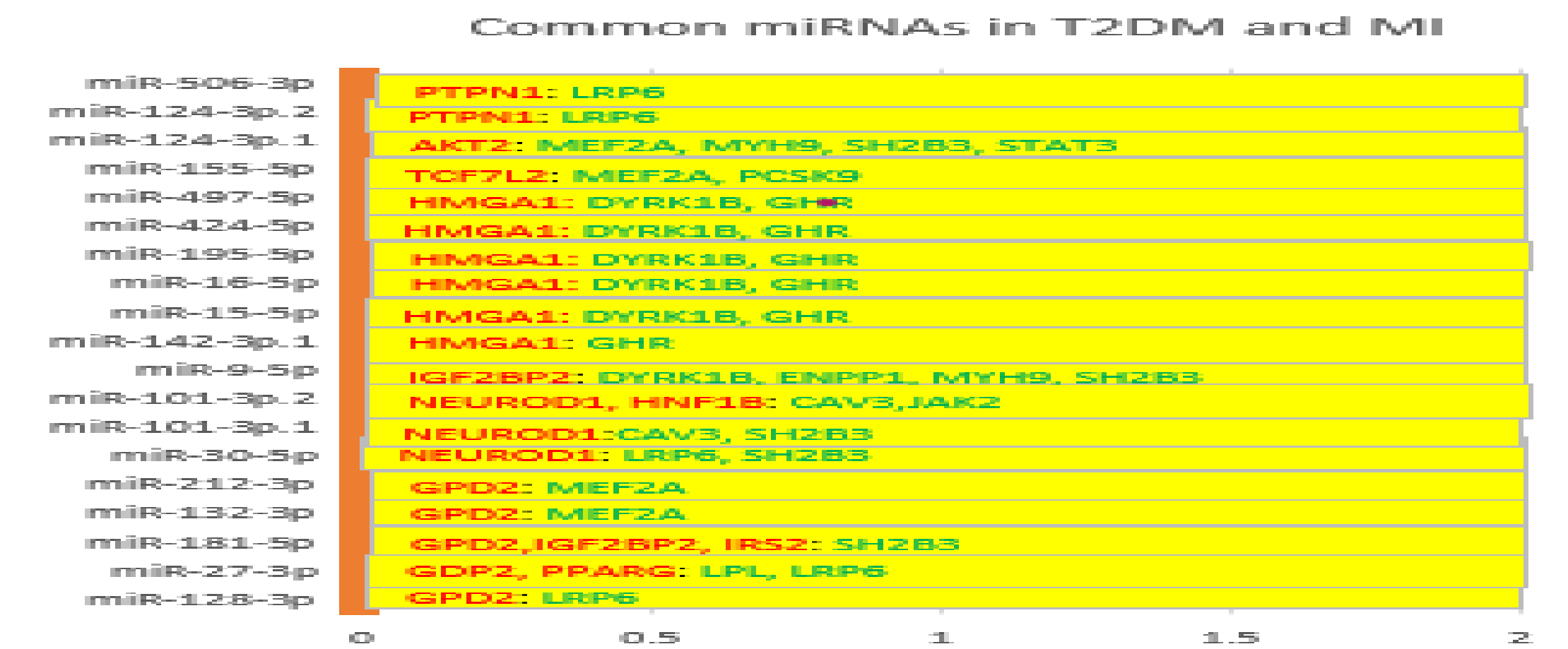


Figure 2: list of common 8 mers miRNAs and their targeted genes associated with T2DM and MI.

## Discussion

Type 2 diabetes mellitus (T2DM) and myocardial infarction (MI) are among the top leading cause of death, worldwide(Heron, 2018). miRNAs can regulate the more than one genes. miRNAs based study showed that it has immense potential to use as therapeutic approach against such life-threatening diseases like T2DM and MI. Beside this it has also potential to use as early detection of different chronic diseases.

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