

Profiling of targeted miRNAs (8-mer) for the genes involved in type 2 diabetes mellitus and cardiac hypertrophy

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Type 2 diabetes mellitus and cardiac hypertrophy are among the top ten leading cause of deaths, worldwide. Type 2 diabetes mellitus and cardiac hypertrophy are the chronic diseases, have close association and direct life-threatening implications like stroke, myocardial infarction, retinopathy, nephropathy and limb amputation. In addition to other medical approaches, microRNAs -based strategy is considered a game-changer for early detection of these chronic diseases and also has potential for the treatment of Type 2 diabetes mellitus and cardiac hypertrophy like it is being used for cancer in clinical trials. MicroRNAs are the non-coding single stranded, almost 20 to 22 nucleotides sequences which upon the complimentary basis bind to their target mRNA to silencing the protein expression at post transcriptional level. Bioinformatic databases are used like gene testing registry, online mendelian inheritance in man, TargetScan and ShinyGO for validation of disease linked genes and sorting the common microRNAs in both diseases, such as *miR-30-5p/101-3p.2/190-5p/506-3p/9-5p/128-3p/137/96-5p/7-5p/107/101-3p.1, let-7-5p, miR-98-5p/124-3p.2/124-3p.1/15-5p/16-5p/195-5p/424-5p/497-5p/1271-5p*. Aforementioned databases also used for the microRNAs that have more than one disease linked genes target in each pathological condition. Such microRNAs for cardiac hypertrophy are: *miR-19-3p/183-5p.2/153-3p/302-3p/372-3p/373-3p/520-3p/129-5p/144-3p/139-5p* and for Type 2 diabetes mellitus are: *miR-1-3p/206/27-3p/181-5p*. These findings will be of merit after future validation by using their expression analysis, mimic/anti-microRNA approach to check their potential against cardiac hypertrophy and Type 2 diabetes mellitus.