Integrative in Silico Analysis of miRNA and mRNA Expression Profiles in Left Ventricle of Diabetic Rats

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Introduction: Diabetes is characterized by chronic hyperglycemia that induces several inflammatory processes including diabetic cardiomyopathy (DCM). DCM is a diabetic complication with high incidence and prevalence rate in worldwide diabetic patients. DCM is characterized by myocardial hypertrophy, systolic and diastolic dysfunction in the left ventricle. In the last decades, several molecular mechanisms involved in DCM pathophysiology have been reported by epigenomic studies; however, these mechanisms are not fully understood. **Objectives:** In silico analysis was used to investigate the differential expression of mRNAs and miRs-related to cardiotoxicity in strepzotocin (STZ)-induced diabetic rats and to identify potential biomarkers for DCM. **Material and Methods:** Data from microarray experiments that have evaluated mRNA and miR expression profiles in ventricles of rats have been downloaded from GSE4745 and GSE44179 datasets, respectively. Gene Expression Omnibus 2R software was used to construct lists of top 250 differentially expressed mRNAs and miRNAs. The Ingenuity Pathway Analyses software was used to select cardiotoxicity-related mRNAs in all periods evaluated of GSE4745 dataset. MICRORNA web dataset was used to detect regulatory miRNAs of cardiotoxicity-related mRNAs. An integrative analysis was carried out between miRNAs of GSE44179 and the MICRORNA-detected miRNAs that act in regulation of cardiotoxicity-related mRNAs. **Results and Discussion:** Four miRs (miR-122, miR-214, miR-9 and miR-186) had correlation when to compare all miRs lists. The *PLA2G2A* and *HK2* mRNAs were up and downregulated, respectively, in days 3 and 42 of GSE4745. Also, their regulatory miRNAs, miR-122 and miR-214 (*PLA2G2A*) and miR-186 and miR-9 (*HK2*), were down and upregulated respectively, in GSE44179. **Conclusions:** The present results indicated that the *PLA2G2A* mRNA may be regulated by miR-122 and miR-214 and the *HK2* by miR-9 and miR-186 in DCM disease. Therefore, this in silico study suggest that these miRNAs and their target mRNA may represent potential biomarkers to diagnosis and treatment of DCM.

Keywords: Biomarkers; Diabetic Cardiomyopathy; Genomic analysis.

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