

Profiling of MicroRNA expression in obese and diabetic-induced mice for biomarker discovery

ABSTRACT

MicroRNAs (miRNAs) are short (~22 nucleotides) regulatory RNAs involved in many fundamental biological processes. They are involved in post-transcriptional regulation of gene expression. Dysregulated expression of microRNAs has been associated with a variety of diseases, including obesity and diabetes. Obesity is a potential risk factor contributing to the development of type 2 diabetes. Meanwhile, diabetes is one of the most prevalent chronic diseases, affecting 6.4% of the world's adult population. The aim of this study is to identify microRNAs that are differentially expressed in obese, diabetic and control C57BL/6 mice by using small RNA sequencing. Total RNAs were extracted from the serum of the target groups of animals. Next, the small RNAs were sequenced using the TruSeq small RNA Library Prep Kit in a MiSeq Illumina sequencer. A total of 52 up-regulated and 54 down-regulated miRNAs were identified based on the comparison of the log₂ fold change of obese and diabetic (with normal mice as control; FC ≥ 2). The obese groups showed 22 up-regulated and 25 down-regulated microRNAs. Meanwhile, in the diabetic group, 32 microRNAs were up-regulated and 29 were down-regulated. This finding will help better understand the mechanism of metabolic disorders and may influence future approaches for the diagnosis and treatment of obesity and diabetes.