Abstract

The ever-increasing incidence of coronary artery disease (CAD) in Czech Republic and worldwide is one of the most important health problem today. Obesity and type 2 diabetes mellitus (DM2T) are risk factors for the development of CAD. Lipid metabolism is greatly affected by these diseases and adipose tissue, previously considered a mere energy store, also plays an important role in these changes. Today adipose tissue is discussed also as an endocrine organ, which effect whole body metabolism significantly. Lipidomic analysis is an effective tool for monitoring lipid metabolism. Lipidomics combines the advantages of determining a large number of analytes and a small amount of sample and its rapid preparation.

In the first part of study, I optimized the HPLC-MS method of untargeted lipidomic analysis in adipose tissue. Then, this method was used to compare subcutaneous and epicardial adipose tissue. Finally, I evaluated the effect of CAD and DM2T on the lipid profiles of subcutaneous and epicardial adipose tissues.

Optimization of the pre-analytical phase enabled the analysis of 206 lipid molecules (in total) in both types of adipose tissue. Compared to subcutaneous adipose tissue, epicardial adipose tissue contained a higher proportion of phosphatidylcholines (e.g. PC(32:0), PC(32:1), PC(36:4)) and lower amounts of triacylglycerols (e.g. TAG(18:1,18:2,18:1)).

The results suggest that the size of lipid droplets is smaller in epicardial adipose tissue, which may be due to the protection of tissue against lipotoxicity in myocardium. CAD is manifested by mitochondrial dysfunction in adipose tissue. During the DM2T development, insulin resistance arises in insulin-sensitive tissues, including adipose tissue. Changes observed in lipid molecules are probably consequences of mitochondrial dysfunction and insulin resistance.

The HPLC-MS method is suitable for the analysis of lipid molecules in adipose tissue. Lipid profiles varied depending on tissue location and the disease development in the patient.