

## **ABSTRACT**

**Charles University**

**Faculty of Pharmacy in Hradec Králové**

**Department of Biochemical Sciences**

**Candidate:** Tereza Lukavská

**Supervisor:** Assoc. Prof. PharmDr. Iva Boušová, Ph.D.

### **Title of Diploma Thesis: The expression analysis of detoxification enzymes in rat**

Metabolic dysfunction-associated steatotic liver disease (MASLD) represents the most common liver disease and is closely linked to oxidative stress, which plays a key role in its progression. The impact of oxidative stress is largely regulated by the activity of detoxification enzymes, expression of which can be influenced by both genetic predisposition and external factors such as diet. The aim of this thesis was to analyze the expression of ten selected genes encoding detoxification enzymes in the liver of three rat strains. For this purpose, male rats of the following strains were selected: Wistar-Kyoto (WKY), Prague hereditary hypertriglyceridemic (HTG), and Sprague-Dawley (SD), which were fed either a low-fat (LF) diet or a high-fat, fructose, and cholesterol (FFC) diet for six months. The analysis of the relative mRNA expression of selected genes was performed using RT-qPCR. The results showed that both the genetic background of the strains and the type of diet significantly affected the expression of the studied detoxification genes. Differences were observed between the strains, especially in the mRNA expression of phase I drug-metabolizing enzymes (*Cyp1a1/2*, *Fmo3*, *Fmo5*, and *Nqo1*), while the expression of the studied antioxidant enzymes was practically the same between strains. Administration of the FFC diet led to a significant decrease in the expression of *Cyp1a1/2* and *Cat* in all three strains. The most changes in expression were found in the SD strain, while the least were observed in the HTG strain. For most genes, a reduced expression was observed in the liver of rats fed the FFC diet compared to those on the LF diet. The results of this study may contribute to a better understanding of the molecular mechanisms involved in the development of MASLD.