This diploma thesis focus on disorders of coenzyme Q10, which lead to decrease of its concentration in certain patient`s tissues (CoQ10 deficiency). This thesis introduces two molecular-genetics methods for CoQ10 deficiency analysis. The first one is a screening method - High Resolution Melting Analysis, which is a useful tool for screening of a large group of patiens with possible mutations in PDSS1, PDSS2, COQ2, COQ9, CABC1 and APTX genes, which encode some enzymes of CoQ10 biosynthetic pathway. The second one is direct sequencing of coding sequences of these genes including intron sequences neighbouring exons.

This work also describes a model of CoQ10 deficiency applied in vitro using cultured human skin fibroblasts and HEK293 cells. In this case CoQ10 deficiency is evoked by CoQ10 biosynthesis inhibitor – 4 aminobenzoic acid (concentration 1 mmol.dm-3) . 4 days treatment by 4 aminobenzoic acid caused decrease in CoQ10 level in fibroblasts and HEK293 cells (60 - 70 % of control, resp. 41 % of control in case of HEK293 cells), although cell viability and morfology of mitochondria remained unchanged. Our results declare that there was slightly increased reactive oxygen species concentration after treatment, especially the amount of superoxide radicals; nevertheless the ultrastructure of mitochondria stayed unchanged. Last but not least aim of this work was to study changes in oxidative phosphorylation system (OXPHOS) complexes activity and expression of certain subunits of these enzymes. After treatment we measured decreased coupled activities of complexes I-III and II-III in treated cells. We can say that the measurement of coupled acitivities of I-III and II-III is an opportunity to validate CoQ10 deficiency in patients (beside of CoQ10 concentration measurements in muscle and fibroblasts). No specific changes of OXPHOS subunits expression were observed in this model. The model is still useble for future studies of CoQ10 deficiency.