SUMMARY

Hypertrophic cardiomyopathy is one of the most common inherited diseases of the cardiovascular system. Although this disease is known for a long time, a suitable diagnostic procedure uncovering its early stages in patients with negative or unknown family history is still lacking.

A development of the method for targeted proteomic analysis in combination with subsequent quantification of chosen hypothetical markers of hypertrophic cardiomyopathy was the main aim of this thesis. This method is able to detect very small amounts of chosen markers in the minimum amount of complex biological material. Moreover, in combination with properly used standards, targeted proteomic analysis enables quite precise quantification of many analytes in a relatively short time.

Several previously described protein markers of hypertrophic cardiomyopathy were assayed and quantified using unique proteomic technique. Concurrently, a new potential protein marker – soluble fibronectin – was described. Protein concentrations were validated using enzymoimmunoanalytical method and obtained results were compared with targeted proteomic analysis findings.

In the presented thesis, a new short method was developed for detection and quantification of potential markers of hypertrophic cardiomyopathy. The main objectives of this dissertation thesis were successfully fulfilled. Nevertheless, an area of the protein quantification using mass spectrometry offers many points of view on these targeted analyses, which should be further studied, critically considered, developed and correctly interpreted.

Key words: hypertrophic cardiomyopathy, protein markers, targeted proteomic analysis, quantification