Proteomic screening of cerebrospinal fluid

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Proteomic screening of cerebrospinal fluid: Candidate proteomic biomarkers for sample stability and experimental autoimmune encephalomyelitis

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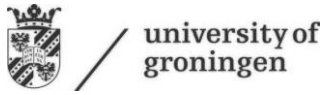

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Scope of the thesis

This thesis handles the whole proteome/metabolome screening of cerebrospinal fluid (CSF). The main focus is the unraveling of the importance of correct sample handling by the study of stability markers in porcine and human CSF as well as the exploration of disease markers connected to experimental autoimmune encephalomyelitis (EAE), modeling the human central nervous system (CNS) disorder multiple sclerosis (MScl).

Chapter 1 is an introduction to the EAE model. Here the model is described, and the importance of animal models and biomarker studies is discussed. The chapter gives an overview of current literature handling proteomic biomarker studies performed on the EAE model and the translational possibility to the human disease multiple sclerosis.

In **Chapter 2** sample handling procedures are investigated. The proteome of porcine CSF as well as the metabolome and free-amino acids are screened for discriminatory differences in abundance after different sample handling procedures. To mimic a possible clinic situation CSF was left at room temperature for up to two hours without cellular elements removed. CSF samples were also exposed to a number of freeze-thaw cycles to mimic the real situation of sample handling in the laboratory. To imitate the auto-sampler environment, digested CSF was left at 4 °C and analyzed after various time spans to investigate the quantitative effect on peptides.

Chapter 3 describes a stability study on the proteome, metabolome and free-amino acids of human CSF left at room temperature for up to two hours after centrifugation and removal of cellular traces.

Chapter 4 portrays a proteomic biomarker study on CSF from an acute EAE model in rats. The proteome was screened for disease related markers. The study was performed on two different platforms with two different data processing techniques applied on each of the both data sets.

In **Chapter 5** a continuation of the study presented in chapter 4 is described. Here the effect of the tetracycline derivate minocycline is tudied on previous detected biomarker candidates. The thesis is summed up with conclusions and future perspectives.