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# New, sought-after standard for diagnosis within neurology

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For the first time, researchers from Sweden and the US have succeeded in identifying the majority of the detectable proteins in the cerebrospinal fluid (CSF) of healthy human beings. The advance is expected to provide a valuable tool for diagnosis and research into diseases of the nervous system. The study is being published today in *PLoS ONE*.

Mapping the mix of 2,630 identified proteins in the CSF of healthy human beings may represent a turning point for research in neurological diseases. Until now, the lack of a clear picture of normal CSF made it impossible to fully assess how the fluid is affected by different disease conditions.

“Obtaining this tool represents a very important step,” says Jonas Bergquist, professor of analytic chemistry and neurochemistry at Uppsala University in Sweden and a researcher at the Uppsala Berzelii Technology Centre for Neurodiagnostics. “Our findings could serve as a representation of the normal case in connection with research into Alzheimer’s, ALS, Parkinson’s, multiple sclerosis and many other diseases.”

Knowledge of the overall protein composition of human CSF is important to the study of brain diseases. Until now, technological hurdles and a lack of samples from healthy individuals prevented the acquisition of such knowledge. The mapping of the protein composition of normal CSF by researchers at Uppsala University, in collaboration with American colleagues at UMDNJ-New Jersey Medical School and Pacific

Northwest National Laboratory, involved 200 patients in Sweden initially suspected of suffering from neurological diseases but subsequently determined to be healthy and 20 healthy volunteers in the U.S.

A total of 2,630 proteins, 56 per cent of which are CSF-specific (i.e., unrepresented among the 3,654 proteins already identified by researchers in blood plasma) were identified. Multiple samples from ten individuals showed the mix of proteins to be surprisingly stable - no significant variation was found among samples taken from the same individual at different times. The study also identified sequence-specific markers, suitable for international research purposes, for each protein.

“The protein composition of CSF from patients with diseases like ALS and Alzheimer’s had already been determined by our research team and others,” says Jonas Bergquist. “A whole range of uses for the earlier findings will open up now that we have a normal representation that can be used for control purposes.”

The study was carried out using advanced methods (separation by means of immunoaffinity and liquid chromatography and elucidation by means of high-sensitivity/resolution mass spectrometry) at a unique technological platform in the U.S. Similar tools are now being implemented in the context of the SciLifeLab Uppsala project, another undertaking in which Jonas Bergquist is involved.

**More information:** Read the article in PLoS ONE: www.plosone.org/article/info%3Adoi%2F10.1371%2Fjournal.pone.0010980

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