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Quantitative proteomics of tear fluid using multiplex peptide stable isotope dimethyl labeling

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Human tear fluid is a complex mixture containing high concentrations of proteins and is increasingly becoming an important source for studying protein composition of eye-related diseases. An important part of proteomic research is accurate quantification of proteins and this has made the incorporation of differentially stable isotopes in samples widely used. Dimethyl labeling at peptide level is a cost-effective, undemanding and fast labeling procedure that is applicable to nearly any biological sample. In addition, this procedure is capable of labeling sub-microgram to milligrams of sample and all reagents are compatible with LC-MS analysis. Therefore, the aim of this study was to look into the suitability of stable isotope dimethyl labeling for quantitative proteomics on tear fluid. The tear proteins were extracted using a single unit filter-aided method for both sample handling and protein extraction from Schirmer strips. The peptides were reversely labeled with a light label and an intermediate label and mixed before LC-MS/MS analysis. The different stable isotopically labeled peptides showed a known mass difference when looking into the MS specters. Additionally, a clear signal intensity difference between the differentially labeled peptides was observed. These results show that stable isotope dimethyl labeling of tear proteins is both possible and successful and may serve as an important quantification method for tear proteome.

Biography

Cecilie Aass completed her Master's degree in Analytical Chemistry at Oslo University, Norway, in February 2013. She is now on her third and last year of her PhD at the Hormone Laboratory, Oslo University Hospital, Norway. Her research interests are proteomics in tear fluid from patients with eye-related diseases using Schirmer tear test, quantification with dimethyl labeling, and liquid chromatography coupled to mass spectrometry.

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