

Analysis and Identification of Protein Components in Deposits on Worn Contact Lenses by Liquid Chromatography Mass Spectrometry (LC-MS)

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Background: Deposits on worn contact lenses cause eye adverse events for contact lens wearers but the components of the deposits and their role in adverse events are not known.

Aim: The aim of this study is to develop a LC-MS method to analyze and identify protein components in worn contact lens deposits.

Methods: Worn contact lenses were collected from normal adult subjects (> 18 years old) who participated in an inhouse study involving wearing the lenses for 12 hours without using any contact lens care solution. The deposits on the lenses were extracted using a buffer containing 4 M urea and 0.1% SDS. After desalting and concentrating, the samples were digested with trypsin and analyzed by LC-MS. Peak lists were generated by MassLynx (version 4.0 SP1, Micromass) using the Mass Measure program and submitted to the database search program Mascot. Protein identification was based on matches of detected peptides to reference peptides that could be derived from a protein in NCBI database. Ions scores > 50 indicated identity or extensive homology (P < 0.05). Results: Total 11 proteins were identified in the sample. Among them, 5 are identified tear proteins (lysozyme, basic praline-rich proteins, lactoferrin, immunoglobulin J chain and hypothetical protein), 1 is from skin (epidermal keratin type I) and others are from un-known source (Ig alpha-1 chain C region, beta-actin, actin, apolipoprotein and proapolipoprotein). Conclusion: LC-MS is a sensitive method to analyze and identify proteins deposited onto worn contact lenses.

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