

Tear proteomic analysis

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Contact lens-related ocular surface complications occur more often in teenagers and young adults. The purpose of this study was to determine changes in tear proteome of young patients wearing glasses (GL), orthokeratology lenses (OK), and soft contact lenses (SCL). Twenty-two young subjects (10-26 years of age) who were established GL, OK, and SCL wearers were recruited. Proteomic data were collected using a data independent acquisition-parallel accumulation serial fragmentation workflow. This research was highlighted by the following findings:

- Using the diaPASEF approach, we have identified 19 protein groups that showed significant differences in abundance in the SCL group compared to the OK group.
- Eighty-two proteins differed in abundance in the tears of children versus young adults in the GL group.
- Many of the significant proteins are related to inflammation and immunity as well as ocular surface homeostasis.

In this research, machine learning models, such as KNN, SVM, and LDA, were able to predict the study groups by analyzing MS data, and evaluate the importance of proteins in prediction. It was verified that machine learning models performed the best in discriminating children and young adult groups.

The research results indicated that tear proteomes were altered by orthokeratology and soft contact wear and age, which warrants further larger-scale study on the ocular surface responses of teenagers and young adults separately to contact lens wear. Overall, this study provides a deep coverage of tear proteome and suggests the need to investigate ocular responses to contact lens wear separately for teenagers and young adults. We also confirmed that tear proteomic analysis is useful in identifying important proteins in diabetes diagnosis.