Effects of Contact Lenses on Tear Protein Profiles of Non-Dry Eye Users



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Introduction

The regular use of contact lenses (CL) can result in inflammation, dry eye symptoms and ultimately tear film alterations. Not much is known about the underlying mechanistic changes in the tear proteome associated with CL use. The purpose of this study was to investigate the effects of rigid gas permeable (HARD CL) and soft contact lenses (SOFT CL) on the tear proteome of users without dry eye disease.

 In hard CL users, 56 tear proteins were differently expressed compared to non-CL users. In soft CL users, even 71 tear proteins differed in their expression level from the non-CL user group. An overlap of 30 proteins was found between both hard and soft CL users (Fig. 2).

HARD_A SOFT_A 30 41 71 tear 56 tear proteins proteins

Fig. 2: Proteins that differed in their expression level from control.

- A significant upregulation of proteins involved in inflammatory responses and cell injury was observed CL users of both groups.
- The altered expressions of some proteins were exclusive to a particular CL type (**Fig. 3A & 3B**).
- Many of the differentially expressed protein levels were restored to near normal following renouncement of both CL types (Fig. 3C).
- However, in both CL groups some protein clusters did not revert back to normal levels following renouncement (Fig. 3D).

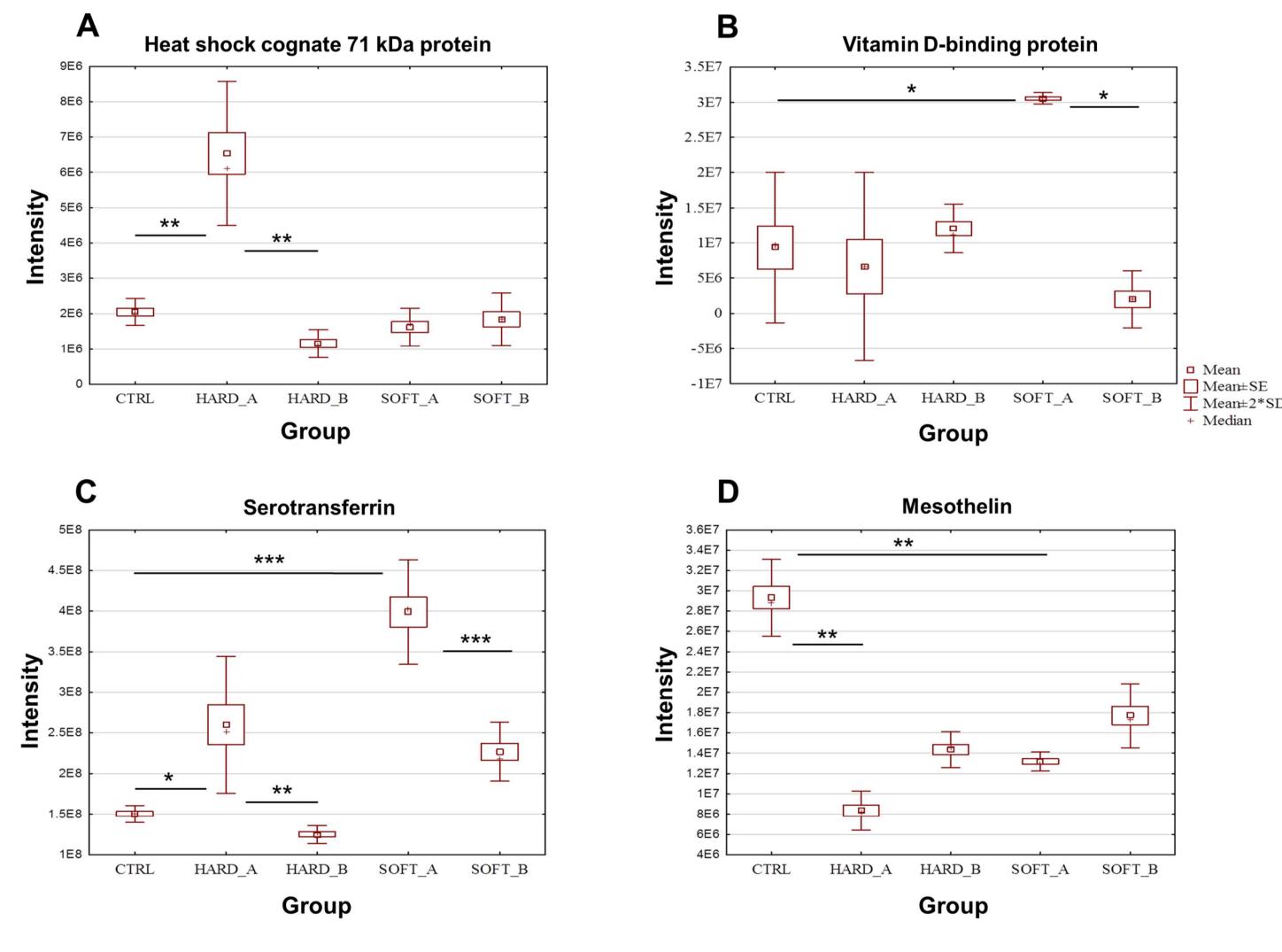


Fig. 3: Box plots showing the regulation profiles of exemplary differentially expressed proteins in tears of hard CL and soft CL users before and after CL renouncement. The y-axis represents the mean absoltute LFQ intensities.

Methods

Results

Samples

1) Non-CL users (n=22): (CTRL)

2) Hard CL (n=16): (HARD_A) Before CL renouncement

(HARD_B)

After CL renouncement for 5 d Before CL renouncement

(SOFT_A)

After CL renouncement for 5 d (SOFT B)

Schirmer test I: ≥ 10mm/ 5 min

No dry eye symptoms

3) Soft CL (n=18):

Protein extraction and one dimensional gel electrophoresis (1DE) osin digestion and peptide purification Mass-spectrometry (MS) analyses Bioinformatics analyses



- In total, 261 tear proteins were identified.
- The rank order of cellular localizations of tear proteins was cytoplasm > extracellular space > plasma membrane as shown in Fig. 1A.
- Of the total proteins, 48% function as enzymes, 11% as transporters, 2% as growth factors and 2% as transcription regulators (Fig. 1B).

Protein Localization Protein Function Growth A B Transcription Plasma factors_ regulators Transporters Other 11% Extracellular Cytoplasm Space **Enzymes** 48%

Fig. 1A and 1B: Functional classification of the tear proteome.

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Conclusions

- This is the first study demonstrating the differential expression of a large number of proteins in tears of non-dry eye hard CL and soft CL wearers compared to non-users.
- The findings provide the first evidence of the existence of specific proteome changes attributed to renouncement of CL wear.
- Specific clusters of proteins identified in each CL group may represent potential clinical biomarker candidates indicative of breach of tear and ocular surface homeostasis attributed to CL use.