The discovery of biomarkers in tears from keratoconous patients will help the diagnosis and future treatment of this disease

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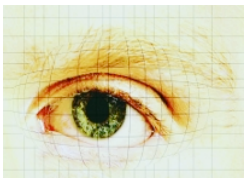

A research collaboration between the Experimental Ophthalmo-Biology GOBE group, directed by Prof. Vecino, the Proteomics group led by Prof. Arizmendi, and clinicians led by Prof. Durán, have described the protein profile of tears from keratoconous patients. The results of this study have been published in the international journal EYE.

Keratoconous is a progressive, non-inflammatory eye disorder that is characterised by the gradual conical-shaping of the cornea, which gradually becomes stretched and increasingly thin towards its centre, thus resulting in distorted and irregular vision.

Although this disorder affects around one person in a thousand, difficulties with its differential diagnosis means that its prevalence remains uncertain.

The exact cause of keratoconous remains unknown but has been associated with damaging enzyme activity within the cornea. Environmental and genetic factors are also considered to be possible causes, but findings in this respect remain inconclusive.

The results of this study have highlighted differences between the tear protein profiles of keratoconous patients and control subjects. Tears from normal subjects and patients with keratoconous were analysed by two-dimensional gel electrophoresis and liquid chromatography-mass spectrometry, which revealed a significant decrease in the levels of members of the cystatin family in the latter. Thus, levels of lipophilin-C, lipophilin-A and phospholipase A2 were lower in tears from keratoconous patients, whereas serum albumin and lipocalin-1 levels were higher.

The changes found are indicative of alterations in tear film stability and interactions with the corneal surface in keratoconous patients. As such, the use of these biomarkers will help in diagnosis of this disorder and the design of future therapeutic treatments.