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Development of new biomarkers for Dry Eye Disease

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Summary

Biological samples such as tears and conjuctival cells will be collected during the clinical examination of patients suffering from Ocular Surface Diseases and especially from Dry Eye Disease (DED). The proteomic composition of the samples will be evalueted with conventional and novel molecular biology techniques in order to identify differences in the protein expression. The biological data will be then correlated with the clinical phenotype of the patients in order discover potential disease-specific biomarkers that can improve diagnosis and disease management.

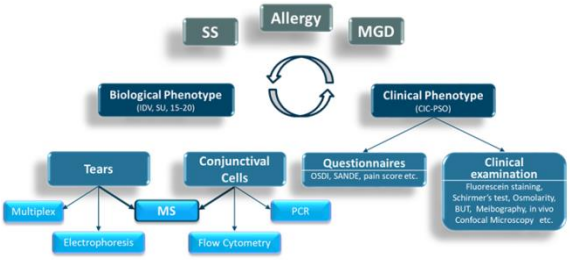
State-of-the-art

Dry Eye Disease (DED) is a multifactorial disease of tears and ocular surface that cannot be characterized by a single process, sign or symptom. Difficulties in diagnosing & managing DED, lack of reliable diagnostic testing and of correlation between signs and symptoms are the main reasons justifying the research for novel potential biomarker for DED.

Tears are a very complex extra-cellular fluid of the ocular surface. Its proteomic composition is known as reflecting altered states in specific eye disorders but also in systemic pathological conditions. Therefore, tears have a great potential to be used as source for the discovery of disease-specific protein biomarkers especially in DED. (Azkargota M. et al., 2016)

The development of high-throughput techniques in proteomics has expanded the search of new biomarkers. Mass spectrometry has become a highly valuable tool to identify and quantify thousands of proteins from complex samples and therefore is the method-of-choice in biomarker development studies.

Today, several techniques for tear collection are available but the most widely used in clinical practice is Schirmer strips. This technique tends to also collect cellular proteins, which may arise from the contact with conjunctiva. (Zhou L. et al, 2012) Therefore, with Schirmer strips we may have the opportunity to investigate simultaneously the proteomic composition of both tears and epithelial cells of the ocular surface.



PhD project plan: correlation of clinical and biological phenotyping to discover disease-specific protein biomarkers.

Techniques

- Clinical examination:
  OSDI questionnaire, Schirmer's test Oxford test, Osmolarity, Break up time, Meibography, in vivo Confocal Microscopy etc.
- Collection of biological samples:
  Schirmer's strips that contain tear fluid and conjunctival cells
- Analysis of biological samples:
  Mass spectrometry, Multiplex Immunoassay, Gel electrophoresis, Flow cytometry, RTqPCR

Task description

Three well-defined and characterized cohorts of patients suffering from ocular surface diseases and one control cohort of healthy subjects will be developed by evaluating their clinical and biological phenotypes.

- Sjögren's Syndrome (SS)
- Chronic allergic conjunctivitis
- Meibomian gland dysfunction (MGD)

The most appropriate biological samples for biomarker research will be identified & investigated using conventional molecular biology and novel mass spectrometry techniques.

The biological data obtained will be statistically correlated with the clinical and morphological parameters in order to identify new biomarkers & potential therapeutic candidates for ocular surface diseases.