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Identification of proteolytic profiles diagnostic of Sjögren's

LAY ABSTRACT

The Lay Abstract is for publicity purposes and should use simple language summarizing the proposed research and its significance.

The disease process of Sjögren's Syndrome involves inflammation and destruction of the tear and salivary glands. Enzymes that breakdown the tissue structure are part of this process. Breakdown products, so called peptides, could be early indicators of the disease. We developed new analytical technologies that allow us to detect and characterize these breakdown products in unprecedented molecular detail. We will use this approach to gain unique insights into the disease process. We anticipate that this knowledge will help us to identify patients who are in the early stage of the disease when interventional therapy is most promising.

SCIENTIFIC ABSTRACT

The Scientific Abstract is written for SSF reviewers and a professional audience.

The pathophysiology of Sjögren's Syndrome includes concurrent mechanisms of cell-mediated and humoral autoimmunity that specifically target the lacrimal and salivary glands. The resulting progressive inflammation and tissue destruction is characterized by aberrant proteolytic activity. In the proposed project, we will use activity-based mass spectrometry techniques to comprehensively catalogue proteolytic processes in saliva collected from Sjögren's Syndrome patients. By comparing the degradome to the one of healthy individuals we will be able to draw a map of proteolytic processes occurring in Sjögren's Syndrome and gain unprecedented insights into the molecular pathogenesis of the disease. We expect that the results of our work will be critical for the development of a novel diagnostic molecular signature that will help identifying patients who are in the early stages of Sjögren's Syndrome when interventional therapy is possible and/or for monitoring the progression of the disease.