2006 SSF Outstanding Abstract Award
ACR

Comparison of Gene Expression Profiles between Patients with Sjogren's Syndrome and Systemic Lupus Erythematosus

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Presentation: 687

Sjogren's syndrome (SS) is a complex autoimmune disease clinically defined by manifestations related to exocrinopathy of the lacrimal and salivary glands. Systemic manifestations in SS patients are common and may include clinical and serological overlap with other autoimmune disease features such as those found in systemic lupus erythematosus (SLE). The pathophysiology of common and distinct features of SS and SLE are poorly understood. Initial studies in our lab using high density microarray technology have revealed over expression of Interferon (IFN) inducible genes in the peripheral blood of primary SS patients when compared with controls. In this study, we have directly compared gene expression profiles in whole blood of SS patients and SLE patients to determine which genes are differentially expressed in both phenotypes, and which genes distinguish the two patient groups. Approximately 22,000 RNA transcripts were interrogated using the Affymetrix U133A GeneChip®. Differentially expressed genes were defined using t-tests with nominal significance of $p<0.001$ and average fold change of >1.5. Our gene expression datasets included 35 Caucasian female SLE patients, 36 Caucasian female SS patients, and 62 Caucasian female controls. We compared each group of SS (n=36) and SLE (n=35) patients separately to the 62 controls. A total of 349 genes were differentially expressed in SS patients and 625 genes were differentially expressed in SLE patients. Of these two gene lists, 95 genes overlapped and were differentially expressed in both SS and SLE patients, the majority of which are IFN-inducible. Among the non-overlapping genes, ribosomal proteins were highly overexpressed in SLE patients but underexpressed in SS patients relative to controls. Genes involved in immune responses and cell proliferation were identified that are overexpressed in SS patients and show no change or reduced expression in SLE patients relative to controls. These results show that SS and SLE patients have identifiable gene expression signatures that are either common or distinct between the two patient populations. Characterization of these profiles has significant potential to facilitate development of improved diagnostic approaches and targeted therapies.