AB0401

ASSESSMENT OF GENES INVOLVED IN SJÖGREN'S SYNDROME RELATED XEROSTOMIA

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Background: Sjögren's syndrome (SS) is characterized by decreased saliva secretion. It is regulated mainly by parasympathetic nervous system. The genes involved in xerostomia can play a neuroprotective role [1]. The expression profiling is helpful to understand the mechanisms of SS related xerostomia.

Objectives: We aimed to investigate and compare gene expression in labial salivary glands from SS patients with xerostomia SS(+) and without xerostomia SS(-) and healthy subjects (HS) by microarray analysis and to find genes potentially involved in xerostomia.

Methods: The study group comprised 11 SS patients (3 SS(+) and 8 SS(-)) and 9 HS. Labial salivary gland samples were processed according to the protocol [2]. Database for Annotation, Visualization and Integrated Discovery (DAVID) and Search Tool for the Retrieval of Interacting Genes (STRING10) were used for the interactions between study groups [3].

Results: Among the genes belonging to "secretion" ontology group, expression of Amyloid Beta Precursor Protein (APP) and Cholinergic Receptor Muscarinic 3 (CHRM3) in both SS(+) and SS(-) groups were lower than in HS. The expression of Visinin Like 1 (VSNL1) in SS(+) and SS(-) was higher than in HS. The expression of Serum Amyloid A1 (SAA1) and Amyloid Beta Precursor like Protein 2 (APLP2) were decreased in SS(+) group and increased in SS(-) compared to HS group. There was no differences between the SS(+) and SS(-) in expression of mentioned genes.

Table 1. Fold changes, adjusted p values of differentially expressed genes in SS(+) and SS(-) groups

Gene symbol	Ratio SS(-)	Ratio SS(+)	adjusted p.value.SS(-)	adjusted p.value.SS(+)
APP	-1,230085	-4,00201	0,9824056	0,00029089
SAA1	1,446255611	-2,222329225	0,831872232	0,046639694
APLP2	1,118778	-2,232646	0,9121355	0,01132797
CHRM3	-1,745830276	-5,359431593	0,867931575	0,000023
VSNL1	1,608504852	3,127527026	0,916228964	0,000513257

Figure 1. STRING-generated interaction network among differentially expressed genes belonging to the "secretion" ontology group.

Conclusion: Decreased expression of APP, SAA1, APLP2 and CHRM3 in SS(+) sufferers compared to HS can reflect the loss of their neuroprotective function and the

cholinergic deficiency in xerostomia. STRING10 software indicates for a central role of APP and genes involved in β -amyloid peptide formation and neurodevelopment and for a close relationships between SS and neurodegenerative diseases [4,5].

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AB0402

DISEASE ACTIVITY AND OBSESSIVE-COMPULSIVE DISORDER IN SYSTEMIC LUPUS ERYTHEMATOSUS

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Background: Obsessive-compulsive disorder (OCD) is more prevalent in systemic autoimmune diseases when compared to healthy controls. This is in part due to inflammatory mechanisms, common across both conditions. Neuroinflammation and specifically problems within the basal ganglia are associated with OCD.

Objectives: The primary objective of this analysis was to investigate the effects of disease activity in systemic lupus erythematosus (SLE) on OCD. Other variables investigated included psychiatric aspects, inflammatory biomarkers and structural brain abnormalities.

Methods: SLE patients who met ACR or SLICC criteria were recruited. Demographic and clinical data were collected and data measuring disease activity (BILAG and SLEDAI-2K), disease damage (SLICC-DI), depression (MADRS, BDI-II, HADS), anxiety (HADS, STAI), fatigue (FSMC), quality of life (LupusQoL and EQ5D), inflammatory and endothelial activation (EA) biomarkers (IL-6, ESR, TNF- α , MCP-1, hsCRP, BLYS, VCAM-1, VEGF, EMVs) and OCD (OCI-R). MRI FLAIR structural scans were also used to examine signal hyperintensities in the brain. Participants with active disease (SLE-F) also had a 2nd visit approx. 4 months later. Non-parametric correlations with the OCI-R were undertaken for all SLE participants and for the change over time scores for the SLE-F participants (n=11).

Results: 39 participants were included in the analysis and were typical for a SLE population. 6 (23%) patients had scores above the threshold for OCD. OCI-R significantly correlated with disease activity, quality of life, fatigue, depression and anxiety measures for all the SLE participants. Change in monocyte chemoattractant protein-1 (MCP-1) correlated with the OCI-R for the within SLE-F group analysis (Table 1). No significant correlations were found with the full SLE group for inflammatory or EA biomarkers or with either group for the structural brain analysis.

Conclusion: OCD in lupus is strongly related to other psychological co-morbidities, fatigue and quality of life. Our results also support a role for inflammatory pathways in mediating some of these changes and so obsessive-compulsive features should be assessed in SLE patients who flare. A larger study is underway to better understand the mechanisms underlying these associations.

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