Primary Sjögren's syndrome (SS) is a chronic inflammatory autoimmune disease affecting mainly the exocrine glands. Its physio-pathology is poorly understood and most of the knowledge has been related to the inflammatory component. The aim of this work was to evaluate gene expression profiling in fractions enriched in epithelial cells from labial salivary glands (LSGs) of patients with primary SS and identify chromosomal regions harboring susceptibility genes expressed in epithelial cells. A combined approach of gene expression and genome-wide association study was used. Enriched epithelial cell fractions were obtained from LSGs of patients and controls. Amplified total RNA was labeled and hybridized to 10K cDNA microarrays. Results were normalized and subjected to statistical and functional analysis. A genome-wide microsatellite screen at 10 cM resolution (393 markers) was performed. In salivary gland-epithelial cells from patients 528 genes were expressed differentially in comparison