

## **RNA-sequencing identifies novel differentially expressed coding and non-coding transcripts in multiple sclerosis and Sjögren's syndrome.**

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**Background:** Multiple sclerosis (MS) is an inflammatory disorder of the central nervous system characterized by damage to the myelin sheath. Sjögren's syndrome (SS) is an autoimmune disease characterized by autoantibodies to Ro and/or La proteins and lymphocytic infiltration into exocrine glands. Even though MS and SS have different clinical manifestations, genetic studies have suggested that the underlying etiology is common in both diseases.

**Methods:** We used RNA-seq to compare differentially expressed (DE) protein-coding and non-coding transcripts in 15 MS patients to SS anti-Ro positive (n=27), SS anti-Ro negative (n=30) patients and healthy controls (N=27).

**Results:** Among the DE protein-coding regions, GRIN3B was the most DE transcript in the MS case-control analysis. Of the DE non-protein coding transcripts, we observed DE of a long non-coding RNA (lncRNA) at 5p15.1. Using DE transcripts relevant to distinguish two groups of SS patients, we also found MS patients clustered together with SS Ro-negative patients in the principal components analysis plot.

**Discussion and Conclusion:** Our analysis shows that RNA profiles of MS are more similar to Ro-negative SS than Ro-positive SS. This suggests that MS treatments may be beneficial for Ro-negative SS patients. These data have identified several putative DE in both coding and lncRNA regions in MS. Further comparisons are needed to confirm and expand these findings.

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