IN SILICO ANALYSIS AND TRANSCRIPTOMIC PROFILING OF AFFECTED BIOLOGICAL PATHWAYS IN MULTIPLE SCLEROSIS.

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Objective: To assess the underlying reason for development of Grey Matter lesions in Multiple sclerotic patients at the Transcriptomics level.

Methods: The total RNA microarray processed data from GEO for Multiple sclerotic patients was comprehensively analysed to find out underlying differences between Grey Matter lesions, Normal appearing Grey Matter and Control Grey matter at the transcriptomics level. We performed various bioinformatics analyses on transcriptional profiles of a total 184 Total-RNA-Seq samples including 105 Normal appearing Grey Matter (NAMG), 37 Grey Matter lesions (GML), and 42 Healthy controls that were obtained from the NCBI Bio-Project (PRJNA543111).

Results: Conclusively, our study depicted significant differences in the gene expression patterns between GML and CG samples. As a result, 20736 genes (padj. value <0.05, log2 fold change ±0.5) were found to be significantly differentially expressed among these conditions based on differential gene expression analysis. This study discovers new 12 genes like OR10A7, OR11L1, OR2AG1, OR2C3, ORT25, OR4D6,OR52E4, 0R5D16, OR5K1, OR7D4, OR8K1 and ORAI3 as the key features that may substantially contribute to the loss of Olfactory senses in MS patients. Our study also proposes the involvement of Protein Kinase-A in pathogenesis of Multiple sclerosis. Eventually, the results presented here reveal new insights into MS and it's relation with the biological pathways especially Olfactory transduction and Hematopoietic stem cell lineage pathways.

Conclusions: Correlations between novel 12 olfactory genes and olfactory dysfunction in Multiple sclerotic patients suggest loss of smell in MS patients. Transcriptomic profiling of MS patients reveal new insights into MS and it's relation with the biological pathways especially Olfactory transduction and Hematopoietic stem cell lineage pathways.