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Department of Biology

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(in the field of Genetics)

Title

Evaluation of Microarray-derived Gene Expression Patterns in Animal Models of Multiple Sclerosis Disease Using Bioinformatics Tools

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Abstract

Background: Identification of important mediators of oligodendrocyte degeneration in different experimental models of multiple sclerosis (MS) is important to understand the molecular basis of the demyelination process and to evaluate new therapeutic approaches. In this study, we therefore investigated high-throughput expression profiling to identify similar hub genes in experimental autoimmune encephalomyelitis (EAE) and cuprizone (CPZ), two commonly used animal models of MS, and assessed their compatibility with human MS genes.

Methods: Two microarray-derived mRNA profiles, GSE47900 and GSE100663, were analysed using the software GEO and the computational method GEO2R. For the analysis of signalling pathways and protein-protein interactions (PPI), the co-expression of differentially expressed genes (DEGs) was identified and searched in the Enrichr and STRING databases. The PPI network was created using Cytoscape. Finally, the MS-related genes were collected from the DisGeNET database and the DEGs were compared using duplicate software.

Results: Six similar hub genes including *DEGs*, *LCN2*, *S100A8*, *CD74*, *OPALIN*, *CXCL10* and *CCL2* were identified in both experimental models. These genes were found to be mainly involved in the signalling pathways of interleukin 17 (IL-17), complement cascade, peroxiome proliferator-activated receptor (PPAR), interferon-gamma and inflammatory cytokines. In addition, a comparison of the expression patterns of the experimental models with the MS-related genes in humans revealed that EAE and CPZ were 60 and 40 per cent associated with the expression patterns in humans, respectively.

Conclusion: This study presents a common expression pattern in EAE and CPZ to reveal the molecular mechanisms behind the neurobiology of demyelination and provides a list of candidate factors for evaluating the efficacy of pharmaceutical approaches in experimental models with greater relevance to MS patients.

Keywords: Microarray, Gene Expression, Multiple Sclerosis, Cuprizone, EAE.