Analyzing Patterns of Gene Expression in Inflamed Microglia Stimulated with a Pro-inflammatory Molecule (TNF Alpha)

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Neurodegenerative diseases are one of the highest causes of death within the world. The WHO reported in 2016 that Alzheimer's Disease and dementia were the 5th highest cause of death internationally. It has been documented by medical studies that in neurodegenerative diseases such as Alzheimer's, Parkinson's, and Multiple Sclerosis, inflammation is an important factor in the progression of the disease. However the effect of these inflammatory diseases on genomic patterns has not been well documented. The purpose of this experiment was to observe the gene expression patterns within introns using microglia, with a control group and a sample manipulated to overexpress the NRA2 gene, which changes a cell's inflammation response. Within each group, there was a set of cells treated with tumor necrosis factor alpha, a pro-inflammatory molecule. The manipulated genes were labeled A2, unmanipulated named VT. The treated samples had 24h tag, indicating they'd been treated for 24 hours, and the untreated had the Unt tag. An interstitial probe was created to find reads within intergenic regions, which were compared with probe trend plots made from the data. The results were that the presence of the TNF alpha agent resulted in higher differentiation of genes within the four samples, and the overexpression of the NRA2 gene resulted in a lower level of differentiation and density of gene reads. Overall, when untreated with TNF Alpha, and unmanipulated with NRA2 gene overexpression, there's a higher level of expression of reads in regards to intronic regions within the inflamed microglia.

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