The Role of DNA Methylation in the Inflammatory Response Following the Consumption of Glutamate in a Patient With Psoriatic Arthritis: A Case Study in Personalized Medicine

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The usage of DNA methylation at CpG sites within the gene body has the potential to be used as an alternative to promoter methylation for identifying gene expression. In this study, we focused on a single patient with psoriatic arthritis and glutamate sensitivity who still experiences severe inflammation despite taking TNFa inhibitors. Our research questions were which inflammatory genes show differential methylation upon glutamate consumption in a patient with psoriatic arthrtis and concurrently which cytokines show an increased concentration after glutamate consumption. Blood was drawn from the individual before and after glutamate consumption as well as two weeks following consumption. A Human Cytokine Luminex panel was performed. DNA was extracted and sequenced on multiple MinION R10.4 flow cells. Adaptive sampling was used to target a custom panel of 226 inflammatory genes. Methylated bases were then aggregated by target using the wf-human-variation workflow in EPI2ME labs; statistical tests and visualizations were performed using R. We found the targets IL8 and IL6 to be differentially methylated, showing an increase in the relative amount of methylated CpGs within the gene body following the consumption of glutamate which correspond with an increase in both CXCL8 and IL6 cytokines from the Luminex panel. Therefore, what was determined from this case study is that IL6 and IL8 inhibitors should be looked into for this arthritic individual's symptom management. In addition, previous literature has concluded that vitamin c, d, e, magnesium, and omega 3 help to suppress IL6 and IL8 expression. But most importantly, this case study showed that GbM continues to hold promise as a diagnostic tool for individualized medicine of those with psoriatic arthritis.

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