Characterization of Epstein-Barr Virus-Infected Atypical Memory B Cells

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Epstein-Barr Virus (EBV), commonly known as the cause of infectious mononucleosis, infects approximately 95% of the adult human population worldwide (Bjornevik et al., 2022). Recently, EBV infection has been shown to correlate with autoimmune illnesses such as systemic lupus erythematosus, rheumatoid arthritis, and multiple sclerosis (Houen & Trier, 2021). These illnesses could be connected to the B cells in the immune system, specifically the atypical memory B cells (atMBCs) that secrete autoantibodies. Therefore, my purpose was to learn more about the cellular biology of EBV in regard to atypical memory B cells. Using the RNA FlowFISH (fluorescence in situ hybridization) flow cytometry single-cell technique, I observed gene markers of interest, FcRL5 and TBX21, that define a population of atypical memory B cells in EBV-infected lymphoblastoid cell lines (LCLs) transformed from healthy human donors at correlative percentages to single cell RNA-sequencing data of LCLs previously collected by the Luftig Lab. I utilized FlowJo data analysis software to delineate (gate) atMBC populations. Building upon these experiments, other gene markers of interest can now be found in EBV-infected atMBCs through the same, optimized technique. Upregulated genes of interest in EBV-infected atMBCs versus atMBCs may hint toward a correlation between EBV-infected atMBCs and autoimmune disease. From this research, I hope to offer more insight into the consequences of EBV infection in atMBCs, leading to future research in determining the mechanism behind EBV infection in autoimmune disease states.

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