

# **SINGLE-CELL RNA SEQUENCING ANALYSIS OF PERIPHERAL BLOOD MONONUCLEAR CELLS OF A PATIENT WITH EPSTEIN-BARR VIRUS ASSOCIATED HAEMOPHAGOCYtic LYMPHOHISTIOCYTOSIS**

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Epstein-Barr virus (EBV) infects B cells and causes a self-limiting lymphoproliferative disorder known as infectious mononucleosis. However, EBV can also infect T cells which may lead to a potentially life-threatening lymphoproliferative disease known as EBV-associated haemophagocytic lymphohistiocytosis (EBV-HLH). We conduct a pilot study to profile the transcriptome of single EBV-infected cells in EBV-HLH to assess the activation of cellular and viral pathways contributing to the pathogenesis of the disease.

We perform single-cell RNA sequencing on the peripheral blood mononuclear cells (PBMCs) of a paediatric patient with EBV-HLH at diagnosis and at 12 months after the diagnosis, using the BD Rhapsody platform. The analysis is carried out using the Seurat package in R. A total of 17 and 18 cell clusters is found in the acute and the recovery time points, respectively. The CD16<sup>+</sup> monocytes seem to be absent in the acute time point. We confirm that the EBV-infected cells are mainly in the CD8<sup>+</sup> T cell clusters at diagnosis, which are eradicated at the recovery time point. The current work is to compare the cellular and viral transcriptomic profiles at diagnosis and 12 months to assess the activation of cellular and viral pathways possibly related to the pathogenesis.