THE LANDSCAPE OF EBV EXPRESSION IN CANCER AND STROMAL CELLS

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Epstein-Barr virus (EBV) expression in cancer cells is believed to be constrained to different latency programs dependent on the tissue type. In recent years sequencing data generated from multiple primary EBV-associated tumor types have shown that the majority of polyadenylated EBV RNA originates from the BamHI-A region. We have characterized the EBV expression from 52 nasopharyngeal carcinoma (NPC) single-cell sequencing datasets. An ubiquitously expressed EBV RNA originating from the BamHI-A gene RPMS1, was detected in all of the NPC datasets. Also, all NPCs expressed LMP-1/BNLF2, however at highly variable levels. EBV expression was detected in all types of stromal cells and often mirrored the expression of the cancer cells. Intriguingly, EBV reactivation was detected at a high proportion of the stromal cells in a single donor. The separation of the cancer cells from healthy epithelial cells using inferred copy number variation of chromosomes enabled the detection of differentially expressed genes between the cell types from the same individual exposed to the same microenvironment. A downregulation of genes in the extrinsic cell death signaling and interferon signaling pathways were observed in the EBV cancer cells. These findings suggest that the EBV gene expression promotes cell survival and immune escape.