Differential gene expression analysis and clinical correlations within endemic Burkitt lymphoma

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Endemic Burkitt lymphoma (eBL) is the most common pediatric cancer in equatorial Africa and is associated with malaria and Epstein-Barr virus co-infections. Molecular alterations within the eBL tumor genome and transcriptome have not been adequately investigated or compared to sporadic Burkitt lymphoma (sBL). Given that eBL has distinct clinical presentations in the jaw as opposed to the abdomen which are associated with survival, we hypothesize that transcriptome sequencing (RNA-seq) and potentially underlying genetic alterations will enhance our understanding of pathogenesis. Our results compare genome-wide RNA transcript abundances between eBL tumors from children (ages 6-7 yrs) with Stage I (Jaw tumor, n=14) and Stage II (abdominal, n=24) disease from Western Kenya to previously published work analyzing sBL which present in older children residing in developed countries and that tend not to be associated with EBV. Our initial analysis confirms mutational changes with likely functional alterations in the genes ID3 and TCF3, the key regulators of oncogenic pathways implicated in BL. However, the specific mutations observed in sBL are at lower frequency within eBL cases. This work represents the first comprehensive gene expression profile analysis of different eBL tumors. Hierarchical clustering, gene ontology and pathway analysis will provide insight into pathogenesis and new targets for chemotherapy.